

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 18:35:25 ; Search time 2612 Seconds  
(without alignments)  
11046.851 Million cell updates/sec

Title: US-10-507-132-1  
Perfect score: 516  
Sequence: 1 atgggttcgcaagttcaaaa.....ggagaccttgcgacacaa 516

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues  
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: gb\_esc1:\*  
2: gb\_esc3:\*  
3: gb\_esc4:\*  
4: gb\_esc5:\*  
5: gb\_esc6:\*  
6: gb\_esc7:\*  
7: gb\_esc8:\*  
8: gb\_esc9:\*  
9: gb\_esc10:\*  
10: gb\_esc11:\*  
11: gb\_esc12:\*  
12: gb\_esc13:\*  
13: gb\_esc14:\*  
14: gb\_esc15:\*

Pred.. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512.8	99.4	619	3	BM863356 mgcm006XO
2	511.8	99.4	657	3	BM864194 mgcm008XJ
3	511.2	99.1	664	3	BM863315 mgcm006XK
4	509.6	98.8	649	3	BM863340 mgcm006XK
5	487	94.4	593	3	BM863546 mgcm006XK
6	468.2	90.7	599	3	BM863156 mgcm008XD
7	460.8	89.3	571	3	BM863710 mgcm007XE
8	454.4	88.1	643	3	BM864467 mgcm010XH
9	448	86.8	602	3	BM863558 mgcm006XK
10	434.8	84.3	523	3	BM863209 mgcm005XD
11	422.4	81.9	486	3	BM863639 mgcm007XG
12	406.4	78.8	600	3	BM864472 mgcm010XJ
13	398.8	77.3	781	3	BM864820 mgap007XA
14	394.4	76.4	530	3	BM863357 mgcm006XO
15	392.8	76.1	510	3	BM863374 mgcm006XK
16	384	74.4	504	3	BM863499 mgcm006XL
17	372.4	72.2	515	3	BM861796 mgcm001X1
18	356.6	69.1	430	4	CD028671 mgcm007XH
19	356.4	69.1	473	3	BM864018 mgcm008XG

20	303.8	58.9	366	3	BM864053 mgcm008XJ
21	301.4	58.4	398	3	BM861952 mgcm001XL
22	298.6	57.9	570	4	CD034317 mgcm015XP
23	292.8	56.7	541	4	CD036729 mgcm011XC
24	267	51.7	491	4	CD035038 mgcm018XH
25	260	50.4	552	5	CD275566 mgcm018X1
26	260	50.4	588	5	CD275905 mgcm018X2
27	257.8	50.0	489	3	BM863213 mgcm005XD
28	257	49.8	486	4	CD035120 mgcm018XL
29	239.6	46.4	499	5	CD273332 mgcm018X1
30	237	45.9	530	5	CD275940 mgcm0156
31	232.2	45.0	507	5	CD275678 mgcm018X1
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35	181.6	35.2	377	5	CD276416 mgcm018X2
36	124.2	24.1	670	7	BE188285 PS161P
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42	79.2	15.3	620	4	CD028659 mgcm006XG
43	71.8	13.9	295	3	BM863872 mgcm007XL
44	57.2	11.1	925	14	CNS0091P Drosophila
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## ALIGNMENTS

RESULT 1  
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LOCUS mgcm006XO03f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006XO03 5', mRNA sequence.  
ACCESSION BM863356  
VERSION BM863356.2 GI:30391591  
KEYWORDS EST  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

## REFERENCE

Ebbel, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatterai, K. and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe

## AUTHORS

grisea

## TITLE

Unpublished (2002)

## JOURNAL

On Mar 7, 2002 this sequence version replaced gi:19231038.

## COMMENT

Contact: Ebbel DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbel@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person/Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydrogenase >gi|1127197|pdb|1strd|. . . 367 e-101  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: 0 column: 03  
Seq primer: T3.  
Location/Qualifiers  
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/organism="Magnaporthe grisea"  
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/db\_xref="taxon:148305"  
/clone="mgcm006XO03"  
/sex="Mat1-2 hermaphrodite"

## FEATURES

## source

1. . 619  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm006XO03"  
/sex="Mat1-2 hermaphrodite"

/cell\_type="mycelium"  
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/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
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sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

## ORIGIN

Query Match 99.4%; Score 512.8; DB 3; Length 619;  
Best Local Similarity 99.6%; Pred. No. 4.3e-115;  
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 ATGGGTTCCGAAGTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60
DB 53 ATGGGTTCCGAAGTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 112
OY 61 ACTTGCTATAGTGGGCGAGACGATCAAGCTCCAGAGACTGGGATAGGCTGGCAAG 120
DB 113 ACTTGCTATAGTGGGCGAGACGATCAAGCTCCAGAGACTGGGATAGGCTGGCAAG 172
OY 121 GTCATTGGCCCTAATCTGCGCATTTGATTAACCGCTCTTCTCGACAAAGCTTGGAGGCA 180
DB 173 GTCATTGGCCCTAATCTGCGCATTTGATTAACCGCTCTTCTCGACAAAGCTTGGAGGCA 232
OY 181 ATGCCGCGGAGAGAGTTCCTCGGCATGCTCTCGACAAAGATGCTGGGCGACCCACCC 240
DB 233 ATGCCGCGGAGAGAGTTCCTCGGCATGCTCTCGACAAAGATGCTGGGCGACCCACCC 292
OY 241 CTCGCGACGACGACCTTCACTCGGCGGACGCGCTGGGAGAGGTGTCGAGAGACGAGTTC 300
DB 293 CTCGCGACGACGACCTTCACTCGGCGGACGCGCTGGGAGAGGTGTCGAGAGACGAGTTC 352
OY 301 ATCGGCTACACAGCTGGGCGGCTCCGCGACAGAGTTACAAGACCAACCATGAAGAG 360
DB 353 ATCGGCTACACAGCTGGGCGGCTCCGCGACAGAGTTACAAGACCAACCATGAAGAG 412
OY 361 GTCACCATGAAGGGCGACGCCCACTCGGAAAACCTTCACTGTTGACAAGAGATTCGACG 420
DB 413 GTCACCATGAAGGGCGACGCCCACTCGGAAAACCTTCACTGTTGACAAGAGATTCGACG 472
OY 421 GTCGGAAGTTGCGCGGCTCAAGCCGATATCCGCTGGGGCGAGTTGACATTGACAG 480
DB 473 GTCGGAAGTTGCGCGGCTCAAGCCGATATCCGCTGGGGCGAGTTGACATTGACAG 532
OY 481 ATCTTTGAGAGCGGAGGAGACCTTTGGCGACAA 516
DB 533 ATCTTTGAGAGCGGAGGAGACCTTTGGCGACAA 568

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RESULT 2  
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LOCUS mgcm008xj12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm008xj12 5', mRNA sequence.  
ACCESSION BM864194  
VERSION BM864194.2 GI:30390885  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE  
AUTHORS Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatnagar, K., and Dean, R.A.  
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe

## JOURNAL COMMENT

grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19231876.  
Contact: Ebbole, D.J.  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person: Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi1127197|pdb|1STD|. . . 365 e-100  
PCR primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm008 row: J column: 12  
Seq primer: T3.  
Location/Qualifiers

## FEATURES

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/cell\_type="mycelium"  
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/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

## ORIGIN

Query Match 99.2%; Score 511.8; DB 3; Length 657;  
Best Local Similarity 99.4%; Pred. No. 7.6e-115;  
Matches 513; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY 1 ATGGGTTCCGAAGTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60
DB 91 ATGGGTTCCGAAGTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 150
OY 61 ACTTGCTATAGTGGGCGAGACGATCAAGCTCCAGAGACTGGGATAGGCTGGCAAG 120
DB 151 ACTTGCTATAGTGGGCGAGACGATCAAGCTCCAGAGACTGGGATAGGCTGGCAAG 210
OY 121 GTCATTGGCCCTAATCTGCGCATTTGATTAACCGCTCTTCTCGACAAAGCTTGGAGGCA 180
DB 211 GTCATTGGCCCTAATCTGCGCATTTGATTAACCGCTCTTCTCGACAAAGCTTGGAGGCA 270
OY 181 ATGCCGCGGAGAGAGTTCCTCGGCATGCTCTCGACAAAGATGCTGGGCGACCCACC 240
DB 271 ATGCCGCGGAGAGAGTTCCTCGGCATGCTCTCGACAAAGATGCTGGGCGACCCACC 330
OY 241 CTCGCGACGACGACCTTCACTCGGCGGACGCGCTGGGAGAGGTGTCGAGAGACGAGTTC 300
DB 331 CTCGCGACGACGACCTTCACTCGGCGGACGCGCTGGGAGAGGTGTCGAGAGACGAGTTC 390
OY 301 ATCGGCTACACAGCTCGCGCTCCGCGACAGAGTTACAAGACCAACCATGAAGAG 360
DB 391 ATCGGCTACACAGCTCGCGCTCCGCGACAGAGTTACAAGACCAACCATGAAGAG 450
OY 361 GTCACCATGAAGGGCGACGCCCACTCGGAAAACCTTCACTGTTGACAAGAGATTCGACG 420
DB 451 GTCACCATGAAGGGCGACGCCCACTCGGAAAACCTTCACTGTTGACAAGAGATTCGACG 510

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QY 421 GTCGGAAGTTCGCCGACCTCAAGCCGATATCCGCTGGGGCGAGTTGCACTTTGACAG 480  
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Db 511 GTCGGAAGTTCGCCGACCTCAAGCCGATATCCGCTGGGGCGAGTTGCACTTTGACAG 570  
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QY 481 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAA 516  
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Db 571 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAA 606  
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LOCUS mgcm006xk09f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006xk09 5', mRNA sequence.  
ACCESSION BM63315 GI:30391622  
VERSION BM63315.2 GI:30391622  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
AUTHORS 1 (bases 1 to 664)  
Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatnagar, K., and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
TITLE Unpublished (2002)  
JOURNAL On Mar 7, 2002 this sequence version replaced gi:19230997.  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person/Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 364 e-100  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: E column: 21  
Seg primer: T3.  
Location/Qualifiers  
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XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
rinoculated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and for vector seqs."

QY 99.1%; Score 511.2; DB 3; Length 664;  
Best Local Similarity 99.4%; Pred. No. 1.1e-114;  
Matches 513; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
1 ATGGGTTCCGAAGTTCAGAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60

Db 81 ATGGGTTCCGAAGTTCAGAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 140  
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QY 61 ACTTGCGTTATGAGTGGGCAAGACAGTACGACTCCAGAGACTGGGATAGGCTGGCAAG 120  
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QY 121 GTCATTGCGCTTACTCTGCGATTGACCTACCGCTCTTCTCGA CAAGCTTGGAGGGA 180  
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Db 201 GTCATTGCGCTTACTCTGCGATTGACCTACCGCTCTTCTCGA CAAGCTTGGAGGGA 260  
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QY 181 ATGCCGCGCAGAGAGTTCCTCGGCAATGCTCTCGAGCAAGATGCTGGGCGACCCAC 240  
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QY 361 GTCACCATGAAGGCGCACGCGCACTCGGCAAACTTCACTGATACAAAGATCGACGCG 420  
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QY 421 GTCGGAAGTTCGCCGACCTCAAGCCGATATCCGCTGGGGCGAGTTGCACTTTGACAG 480  
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Db 561 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAA 596  
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LOCUS mgcm006xk09f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006xk09 5', mRNA sequence.  
ACCESSION BM63340 GI:30391603  
VERSION BM63340.2 GI:30391603  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
AUTHORS 1 (bases 1 to 649)  
Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatnagar, K., and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
TITLE Unpublished (2002)  
JOURNAL On Mar 7, 2002 this sequence version replaced gi:19231022.  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person/Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 361 se-99  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: K column: 09  
Seg primer: T3.  
Location/Qualifiers  
1..649  
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 /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
 XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
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 reinoculated into complete medium 24 h, room temperature,  
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 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredPhrap version 991019 and trimmed  
 according to phd files (0.05) and for vector seqs."

## ORIGIN

Query Match 98.8%; Score 509.6; DB 3; Length 649;  
 Best Local Similarity 99.2%; Pred. No. 2.6e-114;

Matches 512; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 1 ATGGGTTGCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCGCTCATG 60
DB 84 ATGGGTTGCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCGCTCATG 143
OY 61 ACTTGCTATGATGAGGCGAGACAGCTTCAAGACTGGATAGGCTGCGAAG 120
DB 144 ACTTGCTATGATGAGGCGAGACAGCTTCAAGACTGGATAGGCTGCGAAG 203
OY 121 GTCATTTGGCCCTACTCTGCGCATGACTACCGCTCTTCTTGACAAAGCTTGGAGGCA 180
DB 204 GTCATTTGGCCCTACTCTGCGCATGACTACCGCTCTTCTTGACAAAGCTTGGAGGCA 263
OY 181 ATGCCGCGGAGAGAGTTCTGCGCATGCTCTGAGCAAGATGCTGGGCGACCCACC 240
DB 264 ATGCCGCGGAGAGAGTTCTGCGCATGCTCTGAGCAAGATGCTGGGCGACCCACC 323
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OY 421 GTCGGAAGTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 504 GTCGGAAGTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 563
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DB 564 ATCTTTGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 599

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RESULT 5  
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 LOCUS mgcm006xf04.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
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 ACCESSION BM863546  
 VERSION BM863546.2 GI:30391437  
 KEYWORDS EST.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE  
 1 (bases 1 to 593)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatteral,K. and Dean,R.A.  
 Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 Unpublished (2002)  
 On Mar 7, 2002 this sequence version replaced gi:19231228.  
 CONTACT: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@amu.edu

Chromatogram file of this sequence is available, see contact  
 person:best nr hit (April. 22, 2003) epI[P56221]SCVD\_MAGGR Scytalone  
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PCR Primers  
 FORWARD: T3 primer

BACKWARD: T7 primer  
 Plate: mgcm006 row: F column: 04  
 Seq primer: T3.

## FEATURES

source Location/Qualifiers

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1..593
/organism="Magnaporthe grisea"
/mol_type="mrna"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xf04"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR library"
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  

XhoI; Unidirectional cloning. EcoRI site has T3 primer and  

predominantly 5' reads. T7 primer on XhoI side of insert.  

Strain inoculated into complete medium grown for two days  

at room temperature, 150 rpm, harvested, blended,  

reinoculated into complete medium 24 h, room temperature,  

150 rpm. Sequences were processed by one of two methods.  

Where a full-length alignment to the M. grisea genome  

sequence was available, the EST sequence was trimmed  

according to the alignment, otherwise sequence quality was  

assessed using phredPhrap version 991019 and trimmed  

according to phd files (0.05) and for vector seqs."
```

## ORIGIN

Query Match 94.4%; Score 487; DB 3; Length 593;  
 Best Local Similarity 97.7%; Pred. No. 9.1e-109;

Matches 504; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

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OY 1 ATGGGTTGCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCGCTCATG 60
DB 79 ATGGGTTGCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCGCTCATG 138
OY 61 ACTTGCTATGATGAGGCGAGACAGCTTCAAGACTGGATAGGCTGCGAAG 120
DB 139 ACTTGCTATGATGAGGCGAGACAGCTTCAAGACTGGATAGGCTGCGAAG 198
OY 121 GTCATTTGGCCCTACTCTGCGCATGACTACCGCTCTTCTTGACAAAGCTTGGAGGCA 180
DB 199 GTCATTTGGCCCTACTCTGCGCATGACTACCGCTCTTCTTGACAAAGCTTGGAGGCA 258
OY 181 ATGCCGCGGAGAGAGTTGCTGCGCATGCTCTGAGCAAGAGATGCTGGGCGACCCACC 240
DB 259 ATGCCGCGGAGAGAGTTGCTGCGCATGCTCTGAGCAAGAGATGCTGGGCGACCCACC 318
OY 241 CTCGCGACGACGACTTCAATCGGCGGACGCGCTGGGAGAGGTGTCGAGACGAGGTC 300
DB 319 CTCGCGACGACGACTTCAATCGGCGGACGCGCTGGGAGAGGTGTCGAGACGAGGTC 378
OY 301 ATCGGCTACACAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360

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Db 379 ATCGGCTACCACGAGCTGCGGTGCGCCAGACAGATACAGACACCATGAAGAG 438  
 Qy 361 GTACACCATGAAGGCCACGCGCACTGGGCAACCTTACTGTATCAAGAGATCGACGC 420  
 Db 439 GTACACCATGAAGGCCACGCGCACTGTGCAACCTTACTGTATCAAGAGATCGACGC 498  
 Qy 421 GTCTGGAGATTGCGCGGCTTCAAGCCCGATATCGCTGGGGCGAGTTGACCTTGAACAG 480  
 Db 499 GTCTGGAGATTGCGCGGCTTCAAGCCCGATATCGCTGGGGCGAGTTGACCTTGAACAG 557  
 Qy 481 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAA 516  
 Db 558 ATCTTTGAGGCGGACGAGACCTTTGGCGACAA 593

## RESULT 6

BM64156 599 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm008XD02f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm008XD02 5', mRNA sequence.

ACCESSION BM64156  
 VERSION BM64156  
 KEYWORDS GI:30390915  
 EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea

REFERENCE Magnaporthe grisea; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.

AUTHORS 1 (bases 1 to 599)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatterai,K. and Dean,R.A.

TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea

JOURNAL Unpublished (2002)  
 COMMENT On Mar 7, 2002 this sequence version replaced gi:19231338.

CONTACT: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483

Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person.Best nr hit (April, 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 302 3e-87

PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer

Plate: mgcm008 row: D column: 02  
 Seq primer: T3.

FEATURES location/Qualifiers  
 source 1..599

/organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:148305"  
 /clone="mgcm008XD02"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
 /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredPhrap version 991019 and trimmed  
 according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 90.7%; Score 468.2; DB 3; Length 599;  
 Best Local Similarity 95.4%; Pred. No. 3,8e-104;  
 Matches 493; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

Qy 1 ATGGGTTCCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACTGGGCTTCATG 60  
 Db 79 ATGGGTTCCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACTGGGCTTCATG 138  
 Qy 61 ACTTGGGTCTATGATGAGGCGACAGACACTGACCTTCAAGAGACTGGGATAGGCTCGAAAG 120  
 Db 139 ACTTGGGTCTATGATGAGGCGACAGACACTGACCTTCAAGAGACTGGGATAGGCTCGAAAG 198  
 Qy 121 GTCAATGGCGCTACTGTGCGCAATTGACTACCGCTCTTCTCGACAAGCTCTGGAGGCA 180  
 Db 199 GTCAATGGCGCTACTGTGCGCAATTGACTACCGCTCTTCTCGACAAGCTCTGGAGGCA 258  
 Qy 181 ATGCGGCGCGGAGAGTTGCTCGCATGTCTCGAGACAGCAATGCTGGGCGACCCACCC 240  
 Db 259 ATGCGGCGCGGAGAGTTGCTCGCATGTCTCGAGACAGCAATGCTGGGCGACCCACCC 318  
 Qy 241 CTCGCGACGACACTTCAATCGCGGCGACGCGCTGGAGAAAGGTGTCGAGACGAGGTC 300  
 Db 319 CTCGCGACGACACTTCAATCGCGGCGACGCGCTGGAGAAAGGTGTCGAGACGAGGTC 378  
 Qy 301 ATCGGCTACACACAGCTGCGCGCTCCGACACAGAGGTACAAGACACCATGAAGAG 360  
 Db 379 ATCGGCTACACACAGCTGCGCGCTCCGACACAGAGGTACAAGACACCATGAAGAG 438  
 Qy 361 GTACACCATGAAGGCCACGCGCACTGGGCAACCTTACTGTGTAAGAAGATCGACGCG 420  
 Db 439 GTACACCATGAAGGCCACGCGCACTGGGCAACCTTACTGTGTAAGAAGATCGACGCG 498  
 Qy 421 GTCTGGAGATTGCGCGGCTTCAAGCCCGATATCGCTGGGGCGAGTTGACCTTGAACAG 479  
 Db 499 GTCTGGAGATTGCGCGGCTTCAAGCCCGATATCGCTGGGGCGAGTTGACCTTGAACAG 558  
 Qy 480 GATCTTTGAGAGCGAGCGGAGAGACTTTGGCGACAA 516  
 Db 559 GATCTTTGAGAGCGAGCGGAGAGACTTTGGCGACAA 595

## RESULT 7

BM63710 571 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm007XE24f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm007XE24 5', mRNA sequence.

ACCESSION BM63710  
 VERSION BM63710  
 KEYWORDS GI:30391295  
 EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea

REFERENCE Magnaporthe grisea; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.

AUTHORS 1 (bases 1 to 571)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatterai,K. and Dean,R.A.

TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea

JOURNAL Unpublished (2002)  
 COMMENT On Mar 7, 2002 this sequence version replaced gi:19231392.

CONTACT: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483

Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person.Best nr hit (April, 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 336 1e-91

PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer

Plate: mgcm007 row: E column: 24  
Seq primer: T3.  
Location/Qualifiers  
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/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm007xE24"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="mycelium"

/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site\_1: EcoRI; Site\_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

## ORIGIN

Query Match 89.3%; Score 460.8; DB 3; Length 571;  
Best Local Similarity 97.5%; Pred. No. 2.5e-102;  
Matches 468; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 1 ATGGGTTCCGAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTAAGCTGGCCCTCATG 60
DB 92 ATGGGTTCCGAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTAAGCTGGCCCTCATG 151
QY 61 ACTTGCGTATAGTGGGCGAGACAGCTCGAATCCAGAGCTGGGATAGGCTGGGCGAAG 120
DB 152 ACTTGCGTATAGTGGGCGAGACAGCTCGAATCCAGAGCTGGGATAGGCTGGGCGAAG 211
QY 121 GTCATTGCGCTACTCTGCGCATTAACCGCTCTCTCGACAAGCTCTTGGAGGCA 180
DB 212 GTCATTGCGCTACTCTGCGCATTAACCGCTCTCTCGACAAGCTCTTGGAGGCA 271
QY 181 ATGCCGCGGAGAGTTCGTGGCATGCTCTGAGCAAGAGATGCTGGGCGAGCCACC 240
DB 272 ATGCCGCGGAGAGTTCGTGGCATGCTCTGAGCAAGAGATGCTGGGCGAGCCACC 331
QY 241 CTCGCGACGAGAGCTTCATCCGCGGCGACGCGCTGGGAGAAAGGTGCCAGAGCGAGTC 300
DB 332 CTCGCGACGAGAGCTTCATCCGCGGCGACGCGCTGGGAGAAAGGTGCCAGAGCGAGTC 391
QY 301 ATCGGCTACCAACAGCTGGCGCTCCCGCAACAGAGGTACAGAGCAACCATGAAGAG 360
DB 392 ATCGGCTACCAACAGCTGGCGCTCCCGCAACAGAGGTACAGAGCAACCATGAAGAG 451
QY 361 GTCACCATGAAAGGCCACGCGCCACTGGCAAACTTCACTGTAACAAGATCGACGGC 420
DB 452 GTCACCATGAAAGGCCACGCGCCACTGGCAAACTTCACTGTAACAAGATCGACGGC 511
QY 421 GTCTGAAGTTCGCGGCGCTCAAGCCGATATCCGCTGGGGGAGGTTTCGACTTTCAGAG 480
DB 512 GTTTGAAGTTTCCGCTCTCAAGCCGATATCCGCTGGGGGAGGTTTCGACTTTCAGAG 571

```

RESULT 8  
BM864467 643 bp mRNA linear EST 06-MAY-2003  
LOCUS BM864467  
DEFINITION mgcm010XH12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
grisea cDNA clone mgcm010XH12 5', mRNA sequence.  
ACCESSION BM864467  
VERSION BM864467.2 GI:30390655  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph): Pyricularia grisea  
ORGANISM Magnaporthe grisea

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19232149.  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact  
person: Beec nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGR\_Scytalone  
dehydratae >911127197|pdb|1STD|. . . 320 8e-87  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm010 row: H column: 12  
Seq primer: T3.  
Location/Qualifiers

## FEATURES

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/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
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/db\_xref="taxon:148305"  
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/sex="Mat1-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site\_1: EcoRI; Site\_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

## ORIGIN

Query Match 88.1%; Score 454.4; DB 3; Length 643;  
Best Local Similarity 97.0%; Pred. No. 9.3e-101;  
Matches 484; Conservative 0; Mismatches 12; Indels 3; Gaps 2;

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QY 1 ATGGGTTCCGAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTAAGCTGGCCCTCATG 60
DB 145 ATGGGTTCCGAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTAAGCTGGCCCTCATG 204
QY 61 ACTTGCGTATAGTGGGCGAGACAGCTCGAATCCAGAGCTGGGATAGGCTGGGCGAAG 120
DB 205 ACTTGCGTATAGTGGGCGAGACAGCTCGAATCCAGAGCTGGGATAGGCTGGGCGAAG 264
QY 121 GTCATTGCGCTACTCTGCGCATTAACCGCTCTCTCGACAAGCTCTTGGAGGCA 180
DB 265 GTCATTGCGCTACTCTGCGCATTAACCGCTCTCTCGACAAGCTCTTGGAGGCA 324
QY 181 ATGCCGCGGAGAGTTCGTGGCATGCTCGACAGAGATGCTGGGCGAGCCACC 240
DB 325 ATGCCGCGGAGAGTTCGTGGCATGCTCGACAGAGATGCTGGGCGAGCCACC 384
QY 241 CTCGCGACGAGAGCTTCATCCGCGGCGACGCGCTGGGAGAAAGTTCGAGAGCAAGGTC 300
DB 385 CTCGCGACGAGAGCTTCATCCGCGGCGACGCGCTGGGAGAAAGTTCGAGAGCAAGGTC 444
QY 301 ATCGGCTACCAACAGCTGGCGCTCCCGCAACAGAGGTACAGAGCAACCATGAAGAG 360

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Db 445 ATGGGCTACACGAGCTGCGCGTCCGACACAGAGTACAGAGACACACCATGAAGAG 504  
QY 361 GTACACATAGAAAGGCCACCGCCACTCGGCAACCTTTCATCGTACAAAGATCGACGGC 420  
Db 505 GTACACATAGAAAGGCCACCGCCACTCGGCAACCTTTCATCGTACAAAGATCGACGGC 564  
QY 421 GTCTGGAAGTTCGCCGAGCTCAAGCCGATATCCGC-TGGAGCGAGTTGCAC--TTTGAC 477  
Db 565 GTTTGGAAGTTCGCCGAGCTCAAGCCGATATCCGC-TGGAGCGAGTTGCAC--TTTGAC 624  
QY 478 AGGATCTTTGAGGACGGAC 496  
Db 625 GGATCTTTGAGGACGGAC 643

RESULT 9  
BM863558 602 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm006xH04.f Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006xH04 5', mRNA sequence.  
ACCESSION BM863558 GI:30391426  
VERSION BM863558.2 GI:30391426  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
REFERENCE 1 (bases 1 to 602)  
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatteirai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
TITLE Unpublished (2002)  
JOURNAL On Mar 7, 2002 this sequence version replaced gi:19231240.  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person:Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 272 3e-72  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: H column: 04  
Seq primer: T3.

FEATURES  
source Location/Qualifiers  
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/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
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/clone="mgcm006xH04"  
/sex="Mati-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphap version 991019 and trimmed  
according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 86.8%; Score 448; DB 3; Length 602;  
Best Local Similarity 93.7%; Pred. No. 3 4e-99;  
Matches 477; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

QY 1 ATGGGTTGCGAAATTCAAAAGAGCCATGATTAACCTTCTCAGACTAGCTGGGCTCATG 60  
Db 95 ATGGGTTGCGAAATTCAAAAGAGCCATGATTAACCTTCTCAGACTAGCTGGGCTCATG 154  
QY 61 ACTTGCTTATGAGTGGGCGACAGCACTGCACTCCAGAGACTGGGATGGCTGCGAAAG 120  
Db 155 ACTTGGCTTATGAGTGGGCGACAGCACTGCACTCCAGAGACTGGGATGGCTGCGAAAG 214  
QY 121 GTCATTTGCGCTACTCTGCGCATTTGACTACGCGCTCTTCTCGAAGCTCTGGAGGCA 180  
Db 215 GTCATTTGCGCTACTCTGCGCATTTGACTACGCGCTCTTCTCGAAGCTCTGGAGGCA 274  
QY 181 ATGCCGCGCGAGAGAGTTCTGTCGCGATGCTTCGAGCAGACAGATGCTGGGCGACCCACC 240  
Db 275 ATGCCGCGCGAGAGAGTTCTGTCGCGATGCTTCGAGCAGACAGATGCTGGGCGACCCACC 334  
QY 241 CTCGCGACGACGACTTTCATCGCGCGACGCGCTGGAGAGAGTGTCCAGAGACGAGTTC 300  
Db 335 CTCGCGACGACGACTTTCATCGCGCGACGCGCTGGAGAGAGTGTCCAGAGACGAGTTC 394  
QY 301 ATGGGCTACACACAGCTGCGGCTCCCGCGACAGAGGTAACAAGACCAATGAAGAG 360  
Db 395 ATGGGCTACACACAGCTGCGGCTCCCGCGACAGAGGTAACAAGACCAATGAAGAG 454  
QY 361 GTACACATAGAAAGGCCACCGCCACTCGGCAACCTTTCATCGTACAAAGATCGACGGC 420  
Db 455 GTACACATAGAAAGGCCACCGCCACTCGGCAACCTTTCATCGTACAAAGATCGACGGC 513  
QY 421 GTCTGGAAGTTCGCCGAGCTCAAGCCGATATCCGC-TGGAGCGAGTTGCACCTTTGACAG 480  
Db 514 GGCTTGGAGTTCGCCGAGCTCAAGCCGATATCCGC-TGGAGCGAGTTGCACCTTTGACAG 573  
QY 481 ATCTTTGAGAGCGAGCGGAGACCTTTGG 509  
Db 574 GTTCTTTGAGAGCGAGCGGAGACCTTTGG 602

RESULT 10  
BM863209 523 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm005xH02.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm005xH02 5', mRNA sequence.  
ACCESSION BM863209  
VERSION BM863209.2 GI:30391705  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
REFERENCE 1 (bases 1 to 523)  
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatteirai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
TITLE Unpublished (2002)  
JOURNAL On Mar 7, 2002 this sequence version replaced gi:19230891.  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person:Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 308 3e-83  
PCR Primers  
FORWARD: T3 primer

BACKWARD: T7 primer  
 Plate: mgcm005 row: D column: 02  
 Seq primer: T3.  
 Location/Qualifiers  
 1..523

/organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm005XD02"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
 /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredPhrap version 991019 and trimmed  
 according to phd files (0.05) and for vector segs."

## ORIGIN

Query Match Score 84.3%; DB 3; Length 523;  
 Best Local Similarity 99.5%; Pred. No. 5.8e-96;

Matches 436; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGGTTTCGCAAGTTCAAAAGAGCGATGATGATTAACCTTCTCAGACTACTGCGGCTCATG 60  
 86 ATGGGTTTCGCAAGTTCAAAAGAGCGATGATGATTAACCTTCTCAGACTACTGCGGCTCATG 145  
 61 ACTTGCGTCTATGAGTGGGCGACAGACTACGACTCCAAAGACTGGGATGCGTGGCAAG 120  
 146 ACTTGCGTCTATGAGTGGGCGACAGACTACGACTCCAAAGACTGGGATGCGTGGCAAG 205  
 121 GTCAATGCGCTACTCTGCGCATTTGACTACCGCTCTTCTCGACAAAGCTCTGGAGGCA 180  
 206 GTCAATGCGCTACTCTGCGCATTTGACTACCGCTCTTCTCGACAAAGCTCTGGAGGCA 265  
 181 ATGCCGCGCGAGAGTTCTCGGCATGTTCTCGAGCAAGCAAGTCTGGGCGACCCACC 240  
 266 ATGCCGCGCGAGAGTTCTCGGCATGTTCTCGAGCAAGCAAGTCTGGGCGACCCACC 325  
 241 CTCGGACGACGACCTTCAATCGCGCGACGCGCTGGGAGAAAGTCTCCAGAGACGAGTTC 300  
 326 CTCGGACGACGACCTTCAATCGCGCGACGCGCTGGGAGAAAGTCTCCAGAGACGAGTTC 385  
 301 ATCGGCTTACCAACAGCTGCGCGCTCCGCGACAGAGGTACAGAGCAACCATGAAGAG 360  
 386 ATCGGCTTACCAACAGCTGCGCGCTCCGCGACAGAGGTACAGAGCAACCATGAAGAG 445  
 361 GTCAACCATGAAGAGGCGCGCGCTCCGCGACAGAGGTACAGAGCAACCATGAAGAG 420  
 446 GTCAACCATGAAGAGGCGCGCGCTCCGCGACAGAGGTACAGAGCAACCATGAAGAG 505  
 421 GTCTGGAAGTTGCGCGCGC 438  
 506 GTCTGGAAGTTGCGCGCGC 523

## RESULT 11

BM863639 486 bp mRNA linear EST 06-MAY-2003  
 LOCUS BM863639  
 DEFINITION mgcm007G13f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 grisea CDNA clone mgcm007G13 5', mRNA sequence.  
 ACCESSION BM863639  
 VERSION BM863639.2 GI:30391353  
 KEYWORDS EST.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

## ORGANISM

Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.  
 1 (bases 1 to 486)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhattacharjee,K. and Dean,R.A.  
 Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea

## JOURNAL

Unpublished (2002)  
 On Mar 7, 2002 this sequence version replaced gi:19231321.

## COMMENT

Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person; Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR\_Scytalome  
 dehydratae >gi|1127197|pdb|1STD|. . . 293 5e-79  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm007 row: G column: 13  
 Seq primer: T3.  
 Location/Qualifiers  
 1..486

## FEATURES

/organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm007G13"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"

/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
 /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredPhrap version 991019 and trimmed  
 according to phd files (0.05) and for vector segs."

## ORIGIN

Query Match Score 81.9%; DB 3; Length 486;  
 Best Local Similarity 98.6%; Pred. No. 6.4e-93;

Matches 426; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGGGTTTCGCAAGTTCAAAAGAGCGATGATGATTAACCTTCTCAGACTACTGCGGCTCATG 60  
 55 ATGGGTTTCGCAAGTTCAAAAGAGCGATGATGATTAACCTTCTCAGACTACTGCGGCTCATG 114  
 61 ACTTGCGTCTATGAGTGGGCGACAGACTACGACTCCAAAGACTGGGATGCGTGGCAAG 120  
 115 ACTTGCGTCTATGAGTGGGCGACAGACTACGACTCCAAAGACTGGGATGCGTGGCAAG 174  
 121 GTCAATGCGCTACTCTGCGCATTTGACTACCGCTCTTCTCGACAAAGCTCTGGAGGCA 180  
 175 GTCAATGCGCTACTCTGCGCATTTGACTACCGCTCTTCTCGACAAAGCTCTGGAGGCA 234  
 181 ATGCCGCGCGAGAGTTCTCGGCATGTTCTCGAGCAAGCAAGTCTGGGCGACCCACC 240  
 235 ATGCCGCGCGAGAGTTCTCGGCATGTTCTCGAGCAAGCAAGTCTGGGCGACCCACC 294  
 241 CTCGGACGACGACCTTCAATCGCGCGACGCGCTGGGAGAAAGTCTCCAGAGACGAGTTC 300  
 295 CTCGGACGACGACCTTCAATCGCGCGACGCGCTGGGAGAAAGTCTCCAGAGACGAGTTC 354

QY 301 ATCGGCTACACCAAGCTGGCGCGTCCGCAACAGAGTAACAAGACCAACCATGAAGAG 360  
 DB 355 ATCGGCTACACCAAGCTGGCGCGTCCGCAACAGAGTAACAAGACCAACCATGAAGAG 414  
 QY 361 GTCCACATGAAGGCGCCGCGCACTCGGCAAACTTCACTGTATCAAGAAGATGACGCGC 420  
 DB 415 GTCCACATGAAGGCGCCGCGCACTCGGCAAACTTCACTGTATCAAGAAGATGACGCGC 474  
 QY 421 GTCTGGAAGTTC 432  
 DB 475 GTCTGGAAGTTC 486

## RESULT 12

BM864472 600 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm010xj04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm010xj04 5', mRNA sequence.

ACCESSION BM864472 GI:30390651

KEYWORDS EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 600)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatterai,K. and Dean,R.A.

AUTHORS Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea

TITLE Unpublished (2002)

JOURNAL On Mar 7, 2002 this sequence version replaced gi:19232154.

COMMENT Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person:best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 268 56-71  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm010 row: J column: 04  
 Seq primer: T3.

## FEATURES

source Location/Qualifiers

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 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:148305"  
 /clone="mgcm010xj04"  
 /sex="Mati-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_1ib="Magnaporthe grisea CM Uni-Zap XR Library"  
 /note="Vector: pBluescriptSK-; Site\_1: EcoRI; Site\_2:  
 XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI site of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredphrap version 991019 and trimmed  
 according to phd files (0.05) and for vector segs."

## ORIGIN

Query Match 78.8%; Score 406.4; DB 3; Length 600;  
 Best Local Similarity 97.0%; Pred. No. 5.6e-89;

Matches 425; Conservative 0; Mismatches 11; Indels 2; Gaps 1;  
 QY 1 ATGGGTTGCAAGTTCAAAAGGCCATGATTAACCTTCTCAGACTACTGGGCTCATG 60  
 DB 145 ATGGGTTGCAAGTTCAAAAGGCCATGATTAACCTTCTCAGACTACTGGGCTCATG 204  
 QY 61 ACTTGCGTTATGAGTGGGCAAGAGCTGCACTCAAGAGCTGGGATAGGCTGCGAAG 120  
 DB 205 ACTTGCGTTATGAGTGGGCAAGAGCTGCACTCAAGAGCTGGGATAGGCTGCGAAG 264  
 QY 121 GTCAATTCGCTACTCTGCGCATTTGACTACCGCTCTTCTCGACAAAGCTTGGAGGCA 180  
 DB 265 GTCAATTCGCTACTCTGCGCATTTGACTACCGCTCTTCTCGACAAAGCTTGGAGGCA 324  
 QY 181 ATGCGCGCCGAGAGTTCGTGGCATGTCTTGAGCAGACAGATGTGGGCGACCCAC 240  
 DB 325 ATGCGCGCCGAGAGTTCGTGGCATGTCTTGAGCAGACAGATGTGGGCGACCCAC 384  
 QY 241 CTCGCGACGACGACCTTCACTCGGCGGACGCGCTGGAGAAAGTGTCCGAGACGAGTTC 300  
 DB 385 CTCGCGACGACGACCTTCACTCGGCGGACGCGCTGGAGAAAGTGTCCGAGACGAGTTC 444  
 QY 301 ATCGGCTACACCAAGCTGGCGCGTCCGCAACAGAGTAACAAGACCAACCATGAAGAG 360  
 DB 445 ATCGGCTACACCAAGCTGGCGCGTCCGCAACAGAGTAACAAGACCAACCATGAAGAG 504  
 QY 361 GTCCACATGAAGGCGCCGCGCACTCGGCAAACTTCACTGTATCAAGAAGATGACGCGC 420  
 DB 505 GTCCACATGAAGGCGCCGCGCACTCGGCAAACTTCACTGTATCAAGAAGATGACGCGC 562  
 QY 421 GTCTGGAAGTTCGCGCGC 438  
 DB 563 GTCTGGAAGTTCGCGCGC 580

## RESULT 13

BM864820 781 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgap007xa05f.b Magnaporthe grisea Ap Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgap007xa05 5', mRNA sequence.

ACCESSION BM864820 GI:30390364

VERSION EST.

KEYWORDS Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 781)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatterai,K. and Dean,R.A.

AUTHORS Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea

TITLE Unpublished (2002)

JOURNAL On Mar 7, 2002 this sequence version replaced gi:19232502.

COMMENT Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person:best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 271 1e-71  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgap007 row: A column: 05  
 Seq primer: T3.

## FEATURES

source Location/Qualifiers  
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 /mol\_type="mRNA"

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/notes="Vector: pBluescriptSK+; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Apresosorium library. Conidia were germ inated on an
inductive surface for 5-8 h. Sequences were processed by
one of two methods. Where a full-length alignment to the
M. grisea genome sequence was available, the EST sequence
was trimmed according to the alignment, otherwise sequence
quality was assessed using phredPhrap version 991019 and
trimmed according to phd files (0.05) and for vector
seqs."

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## ORIGIN

Query Match 77.3%; Score 398.8; DB 3; Length 781;  
 Best Local Similarity 91.1%; Pred. No. 4.2e-87;  
 Matches 468; Conservative 0; Mismatches 42; Indels 4; Gaps 4;

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QY 4 GGTTCGCAAGTTCAAAAGAGCGATGAGATPACTTCTGAGACTACCTGGGCTCATGCT 63
DB 723 GGGTTGTCAATTCAAAAAGCATTAATACCTTGTCTGACTACCTGGG-CTCAATGCT 665
QY 64 TCGCTGTATAGTGGGCGACAGCTACGATCCCAAGAGACTGGATAGGCTG-CGAAGGT 122
DB 664 TCGGTGTATAGT-GGCAGACAGTACGGCTCCCAAGACTGGATAGGCTGAGAAAGGT 606
QY 123 CATTCGCTACTCTCTCGATTCAGTACCGCTCTCTCTGACAAAGCTCTGGAGGCAAT 182
DB 605 CATTCGCTACTCTCTCGATTCAGTACCGCTCTCTCTGACAAAGCTTTTGGAGGCAAT 547
QY 183 GCGCGCGGAGAGTTCGTGGCATGCTCTGACAAAGAGATGCTGGGCGACCCACCT 242
DB 546 GCGCGAGAGAGTTCGTGGCATGCTCTGACAAAGAGTGGGCGACCCACCT 487
QY 243 CCGCAGCAGGACTTTCATGCGCGGCGACGGCTGGGAGAAAGTGTCCGAGAGCAGAGTCAT 302
DB 486 CCGCAGCAGGACTTTCATGCGCGGCGACGGCTGGGAGAAAGTGTCCGAGAGCAGAGTCAT 427
QY 303 CCGCTACCAAGCTCCGCGTCCGCGACGAGAGTACAAAGACCAACCATGAGAGGT 362
DB 426 CCGCTACCAAGCTCCGCGTCCGCGACGAGAGTACAAAGACCAACCATGAGAGGT 367
QY 363 CACCATGAAAGGCGACGCCACTCGGCAAACTTCACCTGATACAGAAATGACGGCGT 422
DB 366 CACCATGAAAGGCGACGCCACTCGGCAAACTTCACCTGATACAGAAATGACGGCGT 307
QY 423 CTGGAAGTTCCGCGGCTCAAGCCGATATCCGCTGGGGGAGTTGAGCTTTGACAGGAT 482
DB 306 CTGGAAGTTCCGCGGCTCAAGCCGATATCCGCTGGGGGAGTTGAGCTTTGACAGGAT 247
QY 483 CTTTGAGAGCAGCAGGAGAGCTTTTGCGCAGAA 516
DB 246 CTTTGAGAGCAGCAGGAGAGCTTTTGCGCAGAA 213

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RESULT 14  
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 LOCUS mgcm006x005f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea CDNA clone mgcm006x005 5', mRNA sequence.  
 ACCESSION BM63357  
 VERSION BM63357.1 GI:19231039  
 KEYWORDS EST.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
 ,REFERENCE 1 (bases 1 to 530)

AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatnagar,K. and Dean,R.A.  
 TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person: Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
 dehydratase >gi|1127197|pdb|1s7d|. . . 276 1e-73  
 PCR primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm006 row: 0 column: 05  
 Seq primer: T3.

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 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredPhrap version 991019 and trimmed  
 according to phd files (0.05) and for vector seqs."

## ORIGIN

Query Match 76.4%; Score 394.4; DB 3; Length 530;  
 Best Local Similarity 99.7%; Pred. No. 4.8e-86;  
 Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGGTTGCAAGTTCAAAAGGCGATGAGATPACTTCTGAGACTACCTGGGCTCATG 60
DB 83 ATGGGTTGCAAGTTCAAAAGGCGATGAGATPACTTCTGAGACTACCTGGGCTCATG 142
QY 61 ACTTGGCTTATAGTGGGCGACAGCTACGATCCCAAGAGACTGGATAGGCTGGGAAG 120
DB 143 ACTTGGCTTATAGTGGGCGACAGCTACGATCCCAAGAGACTGGATAGGCTGGGAAG 202
QY 121 GTCATTCGCGCTACTCTGCGCATTCAGTACCGCTCTCTCTGACAAAGCTCTGGAGGCA 180
DB 203 GTCATTCGCGCTACTCTGCGCATTCAGTACCGCTCTCTCTGACAAAGCTCTGGAGGCA 262
QY 181 ATGCGGCGGAGAGTTCGTGGCATGCTCTGAGCAAGCAGATGCTGGGCGACCCACC 240
DB 263 ATGCGGCGGAGAGTTCGTGGCATGCTCTGAGCAAGCAGATGCTGGGCGACCCACC 322
QY 241 CTCGCGACGACAGCTTCATTCGGCGGCGACGGCTGGGAGAAAGTGTCCGAGAGCAGAGTC 300
DB 323 CTCGCGACGACAGCTTCATTCGGCGGCGACGGCTGGGAGAAAGTGTCCGAGAGCAGAGTC 382
QY 301 ATCGGCTACCAAGCTGCGCTCCGCGACAGAGGTACAAAGAGACCAACCATGAGAGG 360
DB 383 ATCGGCTACCAAGCTGCGCTCCGCGACAGAGGTACAAAGAGACCAACCATGAGAGG 442
QY 361 GTACACATGAAAGGCGACGCCACTCGGCAAACTT 396

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Db 443 GTCACCATGAAAGGCCACGCCCACTGGGCAACCTT 478

RESULT 15  
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mgcm006XC10f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
grisea cDNA clone mgcm006XC10 5', mRNA sequence.

ACCESSION BM863374 GI:30391576  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Magnaporthe grisea (anamorph: Pyricularia grisea)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 510)  
Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatnager, K., and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19231056.  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person; Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGSR Scytalone  
dehydratase >gi|1127137|pdb|1STM|. . . 276 1e-73  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: C column: 10  
Seq primer: T3.

JOURNAL  
COMMENT

TITLE

REFERENCE

AUTHORS

FEATURES

source

location/Qualifiers  
1..510  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm006XC10"  
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/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: BluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

## ORIGIN

Query Match 76.1%; Score 392.8; DB 3; Length 510;  
Best Local Similarity 99.5%; Pred. No. 1.2e-85;  
Matches 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGTTTCGCAATTCGAAAAGAGCGATGAGATTAACCTTCTCAGACTACCTGGGCTCATG 60  
DB 83 ATGGGTTTCGCAATTCGAAAAGAGCGATGAGATTAACCTTCTCAGACTACCTGGGCTCATG 142  
QY 61 ACTTGGCTATAGTAGGGCGAGACAGCTACGACTCCAGGACTGGGATVAGGCTGGCAAG 120  
DB 143 ACTTGGCTATAGTAGGGCGAGACAGCTACGACTCCAGGACTGGGATVAGGCTGGCAAG 202

QY 121 GTCATTGGGCTTACTCTGGGCAATTGACTACCGGCTCTTCTCTGCAACAAGCTCTGGAGGCA 180  
DB 203 GTCATTGGGCTTACTCTGGGCAATTGACTACCGGCTCTTCTCTGCAACAAGCTCTGGAGGCA 262  
QY 181 ATGCCGCGCGAGAGATTCTGCGCATGATCTCTGAGACAGATGCTGGGCGACCCACC 240  
DB 263 ATGCCGCGCGAGAGATTCTGCGCATGATCTCTGAGACAGATGCTGGGCGACCCACC 322  
QY 241 CTCGCGACGACAGACTTTCATTCGCGGACGCGCTGGGAGAAAGTGTCCGAGACGAGGTC 300  
DB 323 CTCGCGACGACAGACTTTCATTCGCGGACGCGCTGGGAGAAAGTGTCCGAGACGAGGTC 382  
QY 301 ATCGCTACACACAGCTGGGCGGTCGCCGACAGAGGTACAGAGACACCAATGAGAG 360  
DB 383 ATCGCTACACACAGCTGGGCGGTCGCCGACAGAGGTACAGAGACACCAATGAGAG 442  
QY 361 GTCACCATGAAAGGCCACGCCCACTGGGCAACCTT 396  
DB 443 GTCACCATGAAAGGCCACGCCCACTGGGCAACCTT 478

Search completed: December 4, 2006, 19:19:10  
Job time : 2616 secs



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Qy 361 GTACACATGAAGGGCCAGCCCACTCGGCAACCTTCACTGGTACAGAGATGACGAGC 420  
Db 361 GTACACATGAAGGGCCAGCCCACTCGGCAACCTTCACTGGTACAGAGATGACGAGC 420  
Qy 421 GTCTGGAAGTTGCGCGGCTCAAGCCCATATCCGCTGGGGCGAGTTGACTTTGACAG 480  
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Qy 481 ATCTTTGAGAGGACGAGCGGAGACCTTTGGCGCAAA 516  
Db 481 ATCTTTGAGAGGACGAGCGGAGACCTTTGGCGCAAA 516

RESULT 2  
US-10-507-132-3

/ Sequence 3, Application US/10507132  
/ Publication No. US20060223136A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Koichiro KAKU et al.  
/ TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO  
/ FILE REFERENCE: 1254-0258PUS1  
/ CURRENT APPLICATION NUMBER: US/10/507,132  
/ PRIOR FILING DATE: 2004-09-10  
/ PRIOR APPLICATION NUMBER: JP 2002-66955  
/ NUMBER OF SEQ ID NOS: 12  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 3  
/ LENGTH: 516  
/ TYPE: DNA  
/ ORGANISM: Pyricularia oryzae  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: (1)..(516)  
US-10-507-132-3

Query Match Best Local Similarity 99.7%; Score 514.4; DB 6; Length 516;

Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGTTGCAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTTACCTGGGCTCATG 60  
Db 1 ATGGGTTGCAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTTACCTGGGCTCATG 60  
Qy 61 ACTTGCGTTATGAGTGGGCGACAGCTTCAAGAGCTGGGATAGGCTGGCAAG 120  
Db 61 ACTTGCGTTATGAGTGGGCGACAGCTTCAAGAGCTGGGATAGGCTGGCAAG 120  
Qy 121 GTCAATGGCGCTACTTGGCGATTGACTACCGCTCTTCTCGACAAGCTTGGAGGCA 180  
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Qy 241 GTCCGAGCGAGACTTATCGCGCGCAGCGCTGGGAGAAAGTGTCCGAGACGAGTTC 300  
Db 241 GTCCGAGCGAGACTTATCGCGCGCAGCGCTGGGAGAAAGTGTCCGAGACGAGTTC 300  
Qy 301 ATGCGGTACACAGCTGGCGGCTCCCGGACCCAGAGTAAAGACCAACCCATGAAAGAG 360  
Db 301 ATGCGGTACACAGCTGGCGGCTCCCGGACCCAGAGTAAAGACCAACCCATGAAAGAG 360  
Qy 361 GTACACATGAAGGGCCAGCCCACTCGGCAACCTTCACTGGTACAGAGATGACGAGC 420

Db 361 GTACACATGAAGGGCCAGCCCACTCGGCAACCTTCACTGGTACAGAGATGACGAGC 420  
Qy 421 GTCTGGAAGTTGCGCGGCTCAAGCCCATATCCGCTGGGGCGAGTTGACTTTGACAG 480  
Db 421 GTCTGGAAGTTGCGCGGCTCAAGCCCATATCCGCTGGGGCGAGTTGACTTTGACAG 480  
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RESULT 3  
US-10-507-132-13

/ Sequence 13, Application US/10507132  
/ Publication No. US20060223136A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Koichiro KAKU et al.  
/ TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO  
/ FILE REFERENCE: 1254-0258PUS1  
/ CURRENT APPLICATION NUMBER: US/10/507,132  
/ PRIOR FILING DATE: 2004-09-10  
/ PRIOR APPLICATION NUMBER: JP 2002-66955  
/ NUMBER OF SEQ ID NOS: 12  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 13  
/ LENGTH: 600  
/ TYPE: DNA  
/ ORGANISM: Pyricularia oryzae  
US-10-507-132-13

Query Match Best Local Similarity 99.7%; Score 514.4; DB 6; Length 600;

Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGTTGCAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTTACCTGGGCTCATG 60  
Db 81 ATGGGTTGCAAGTTCAAAAGAGCGATGAGATTAACCTTCTCAGACTTACCTGGGCTCATG 140  
Qy 61 ACTTGCGTTATGAGTGGGCGACAGCTTCAAGAGCTGGGATAGGCTGGCAAG 120  
Db 141 ACTTGCGTTATGAGTGGGCGACAGCTTCAAGAGCTGGGATAGGCTGGCAAG 200  
Qy 121 GTCAATGGCGCTACTTGGCGATTGACTACCGCTCTTCTCGACAAGCTTGGAGGCA 180  
Db 201 GTCAATGGCGCTACTTGGCGATTGACTACCGCTCTTCTCGACAAGCTTGGAGGCA 260  
Qy 181 ATGCGCGCGAGAGTTGCTGGCATGTCTCGAGAGCAAGTGTGGGCGACCCACCC 240  
Db 261 ATGCGCGCGAGAGTTGCTGGCATGTCTCGAGAGCAAGTGTGGGCGACCCACCC 320  
Qy 241 GTCCGAGCGAGACTTATCGCGCGCAGCGCTGGGAGAAAGTGTCCGAGACGAGTTC 300  
Db 321 GTCCGAGCGAGACTTATCGCGCGCAGCGCTGGGAGAAAGTGTCCGAGACGAGTTC 380  
Qy 301 ATGCGGTACACAGCTGGCGGCTCCCGGACCCAGAGTAAAGACCAACCCATGAAAGAG 360  
Db 381 ATGCGGTACACAGCTGGCGGCTCCCGGACCCAGAGTAAAGACCAACCCATGAAAGAG 440  
Qy 361 GTACACATGAAGGGCCAGCCCACTCGGCAACCTTCACTGGTACAGAGATGACGAGC 420  
Db 441 GTACACATGAAGGGCCAGCCCACTCGGCAACCTTCACTGGTACAGAGATGACGAGC 500  
Qy 421 GTCTGGAAGTTGCGCGGCTCAAGCCCATATCCGCTGGGGCGAGTTGACTTTGACAG 480  
Db 501 GTCTGGAAGTTGCGCGGCTCAAGCCCATATCCGCTGGGGCGAGTTGACTTTGACAG 560  
Qy 481 ATCTTTGAGAGGACGAGCGGAGACCTTTGGCGCAAA 516  
Db 561 ATCTTTGAGAGGACGAGCGGAGACCTTTGGCGCAAA 596

RESULT 4  
US-10-507-132-16  
; Sequence 16, Application US/10507132  
; Publication No. US20060223136A1  
; GENERAL INFORMATION:  
; APPLICANT: Koichiro KAKU et al.  
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITTING RESISTANCE TO  
; FILE REFERENCE: 1254-0258PUS1  
; CURRENT APPLICATION NUMBER: US/10/507,132  
; PRIOR FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: JP 2002-66955  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Pyricularia oryzae  
US-10-507-132-16

Query Match 99.7%; Score 514.4; DB 6; Length 610;  
Best Local Similarity 99.8%; Pred. No. 1.7e-112;  
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGTTCCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60  
DB 81 ATGGGTTCCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 140  
QY 61 ACTTGCGTCTATGATGAGGCGACAGACTACGACTCCAAAGACTGGATAGGCTGCAGAA 120  
DB 141 ACTTGCGTCTATGATGAGGCGACAGACTACGACTCCAAAGACTGGATAGGCTGCAGAA 200  
QY 121 GTCATTGCGCTTACTCTGCGCATTTGACTACCGCTCTCTTCTGCAAGCTCTGGAGGCA 180  
DB 201 GTCATTGCGCTTACTCTGCGCATTTGACTACCGCTCTCTTCTGCAAGCTCTGGAGGCA 260  
QY 181 ATGGCGGCGGAGGATGCTGCGCATGCTGAGCAAGATGCTGGGCGACCCACCC 240  
DB 261 ATGGCGGCGGAGGATGCTGCGCATGCTGAGCAAGATGCTGGGCGACCCACCC 320  
QY 241 CTCGCGACGACGACTTCAATCGGCGGCGACGCGCTGGGAGAAAGTGTCCGAGCAGAGTC 300  
DB 321 CTCGCGACGACGACTTCAATCGGCGGCGACGCGCTGGGAGAAAGTGTCCGAGCAGAGTC 380  
QY 301 ATCGGCTACCAACGCTGCGCTGCCGACACAGAGGTACAGAGCACCAATGAAGAG 360  
DB 381 ATCGGCTACCAACGCTGCGCTGCCGACACAGAGGTACAGAGCACCAATGAAGAG 440  
QY 361 GTCACCATGAAAGGCGACGCGCTGCGCAAACTTCACTGTACAAAGATCCGACGCG 420  
DB 441 GTCACCATGAAAGGCGACGCGCTGCGCAAACTTCACTGTACAAAGATCCGACGCG 500  
QY 421 GTCGTGAAGTTGCGCGGCTCAAGCCCGATATCCGCTGGGGCGAAGTTGCACTTTGACAG 480  
DB 501 GTCGTGAAGTTGCGCGGCTCAAGCCCGATATCCGCTGGGGCGAAGTTGCACTTTGACAG 560  
QY 481 ATCTTTGAGACGAGCGGAGACCTTTGGCGACAA 516  
DB 561 ATCTTTGAGACGAGCGGAGACCTTTGGCGACAA 596

RESULT 5  
US-10-507-132-15  
; Sequence 15, Application US/10507132  
; Publication No. US20060223136A1  
; GENERAL INFORMATION:  
; APPLICANT: Koichiro KAKU et al.  
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITTING RESISTANCE TO  
; FILE REFERENCE: 1254-0258PUS1  
; CURRENT APPLICATION NUMBER: US/10/507,132

; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: JP 2002-66955  
; PRIOR FILING DATE: 2002-03-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 538  
; TYPE: DNA  
; ORGANISM: Pyricularia oryzae  
US-10-507-132-15

Query Match 97.8%; Score 504.8; DB 6; Length 538;  
Best Local Similarity 99.6%; Pred. No. 3e-110;  
Matches 506; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGTTCCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60  
DB 31 ATGGGTTCCGAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 90  
QY 61 ACTTGCGTCTATGATGAGGCGACAGACTACGACTCCAAAGACTGGATAGGCTGCAGAA 120  
DB 91 ACTTGCGTCTATGATGAGGCGACAGACTACGACTCCAAAGACTGGATAGGCTGCAGAA 150  
QY 121 GTCATTGCGCTTACTCTGCGCATTTGACTACCGCTCTCTTCTGCAAGCTCTGGAGGCA 180  
DB 151 GTCATTGCGCTTACTCTGCGCATTTGACTACCGCTCTCTTCTGCAAGCTCTGGAGGCA 210  
QY 181 ATGGCGGCGGAGGATGCTGCGCATGCTGAGCAAGATGCTGGGCGACCCACCC 240  
DB 211 ATGGCGGCGGAGGATGCTGCGCATGCTGAGCAAGATGCTGGGCGACCCACCC 270  
QY 241 CTCGCGACGACGACTTCAATCGGCGGCGACGCGCTGGGAGAAAGTGTCCGAGCAGAGTC 300  
DB 271 CTCGCGACGACGACTTCAATCGGCGGCGACGCGCTGGGAGAAAGTGTCCGAGCAGAGTC 330  
QY 301 ATCGGCTACCAACGCTGCGCTGCCGACACAGAGGTACAGAGCACCAATGAAGAG 360  
DB 331 ATCGGCTACCAACGCTGCGCTGCCGACACAGAGGTACAGAGCACCAATGAAGAG 390  
QY 361 GTCACCATGAAAGGCGACGCGCTGCGCAAACTTCACTGTACAAAGATCCGACGCG 420  
DB 391 GTCACCATGAAAGGCGACGCGCTGCGCAAACTTCACTGTACAAAGATCCGACGCG 450  
QY 421 GTCGTGAAGTTGCGCGGCTCAAGCCCGATATCCGCTGGGGCGAAGTTGCACTTTGACAG 480  
DB 451 GTCGTGAAGTTGCGCGGCTCAAGCCCGATATCCGCTGGGGCGAAGTTGCACTTTGACAG 510  
QY 481 ATCTTTGAGACGAGCGGAGACCTTTG 508  
DB 511 ATCTTTGAGACGAGCGGAGACCTTTG 538

RESULT 6  
US-10-507-132-14  
; Sequence 14, Application US/10507132  
; Publication No. US20060223136A1  
; GENERAL INFORMATION:  
; APPLICANT: Koichiro KAKU et al.  
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITTING RESISTANCE TO  
; FILE REFERENCE: 1254-0258PUS1  
; CURRENT APPLICATION NUMBER: US/10/507,132  
; PRIOR FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: JP 2002-66955  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 545  
; TYPE: DNA  
; ORGANISM: Pyricularia oryzae  
US-10-507-132-14

Query Match 97.8%; Score 504.8; DB 6; Length 545;  
 Best Local Similarity 99.6%; Pred. No. 36-110;  
 Matches 506; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGTTGGCAGTTTCAAAAGAGCGATGATTAACCTTCTCAGACTAAGCTGGGCTCATG 60  
 DB 38 ATGGGTTGGCAGTTTCAAAAGAGCGATGATTAACCTTCTCAGACTAAGCTGGGCTCATG 97  
 QY 61 ACTTGCCTATGATGATGGGCGACAGCTGCACTCAAGGAGTGGGATGAGCTGGGAGG 120  
 DB 98 ACTTGCCTATGATGATGGGCGACAGCTGCACTCAAGGAGTGGGATGAGCTGGGAGG 157  
 QY 121 GTCAATGGCGCTACTCTGCGCATTTGACTACCGCTCTTCTTCTGACAAGCTCTGGAGGCA 180  
 DB 158 GTCAATGGCGCTACTCTGCGCATTTGACTACCGCTCTTCTTCTGACAAGCTCTGGAGGCA 217  
 QY 181 ATGCGGCGCGAGAGTTTCTGCGCATGTTCTGAGCAGACAGATGCTGGGCGAAGCCAC 240  
 DB 218 ATGCGGCGCGAGAGTTTCTGCGCATGTTCTGAGCAGACAGATGCTGGGCGAAGCCAC 277  
 QY 241 CTCCGACGACGACCTTCAATGCGGCGGACGCGCTGGGAGAGAGTGTCCGAGGACGAGGTC 300  
 DB 278 CTCCGACGACGACCTTCAATGCGGCGGACGCGCTGGGAGAGAGTGTCCGAGGACGAGGTC 337  
 QY 301 ATCGGCTACCAACAGCTGCGCTGCCGACAGAGGTACAGAGACCAACCATGAAGAG 360  
 DB 338 ATCGGCTACCAACAGCTGCGCTGCCGACAGAGGTACAGAGACCAACCATGAAGAG 397  
 QY 361 GTACACATTAAGGGCCAGCCCACTGCGCAACCTTCACTTGTGTAACAAGATCGAGGC 420  
 DB 398 GTACACATTAAGGGCCAGCCCACTGCGCAACCTTCACTTGTGTAACAAGATCGAGGC 457  
 QY 421 GTCTGGAAGTTGCGCGGCTCAAGCCCGATATCCGTGGGCGAGTTGCACTTTGACAGG 480  
 DB 458 GTCTGGAAGTTGCGCGGCTCAAGCCCGATATCCGTGGGCGAGTTGCACTTTGACAGG 517  
 QY 481 ATCTTTAGAGACGAGCGGAGACCTTTG 508  
 DB 518 ATCTTTAGAGACGAGCGGAGACCTTTG 545

RESULT 7  
 US-10-507-132-18  
 ; Sequence 18, Application US/10507132  
 ; Publication No. US20060223136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koichiro KAKU et al.  
 ; TITLE OF INVENTION: GENE CODING FOR SCYTLONE DEHYDRATASE EXHIBITING RESISTANCE TO  
 ; FILE REFERENCE: 1254-0258PUS1  
 ; CURRENT APPLICATION NUMBER: US/10/507,132  
 ; PRIOR FILING DATE: 2004-09-10  
 ; PRIOR APPLICATION NUMBER: JP 2002-66955  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 18  
 ; LENGTH: 729  
 ; TYPE: DNA  
 ; ORGANISM: Pyricularia oryzae  
 US-10-507-132-18

Query Match 73.2%; Score 377.8; DB 6; Length 729;  
 Best Local Similarity 84.5%; Pred. No. 3-6e-80;  
 Matches 474; Conservative 0; Mismatches 2; Indels 85; Gaps 1;

QY 41 CAGACTACCTGGGCTCATGACTTGGCTATGATGAGTGGGCAAGCAGCTACGACTCCAGG 100  
 DB 169 CAGACTACCTGGGCTCATGACTTGGCTATGATGAGTGGGCAAGCAGCTACGACTCCAGG 228  
 QY 101 ACTGGATAGGCTGGCAAGAGTATGCGCTACTCTGCGC----- 141  
 DB 229 ACTGGATAGGCTGGCAAGAGTATGCGCTACTCTGCGC----- 288

QY 142 ----- 141  
 DB 289 GTTATTTTACTTTCACACCAAATCCAGACTTTTAACAGCGACGACCAAAAAAAAA 348  
 QY 142 -----ATTGACTACCGCTCTTCTTCTGACAAGCTTGGAGGCAATGCCGGCGAGAG 195  
 DB 349 AAACGATTTGACTACCGCTCTTCTTCTGACAAGCTTGGAGGCAATGCCGGCGAGAG 408  
 QY 196 TTCTGCGGCAATGCTCGAGGAACAGATGCTGGGCGAAGCCCACTTCCGACGACGAC 255  
 DB 409 TTCTGCGGCAATGCTCGAGGAACAGATGCTGGGCGAAGCCCACTTCCGACGACGAC 468  
 QY 256 TTCAATCGGCGGACGCGCTGGGAGAAAGTGTCCGAGGACGAGTCAATCGCTACCAACAG 315  
 DB 469 TTCAATCGGCGGACGCGCTGGGAGAAAGTGTCCGAGGACGAGTCAATCGCTACCAACAG 528  
 QY 316 CTGCGCGTCCCGCACAGAGGTACAGACACCAATGAAGAGTCAACATGAAGGGC 375  
 DB 529 CTGCGCGTCCCGCACAGAGGTACAGACACCAATGAAGAGTCAACATGAAGGGC 588  
 QY 376 CACGCCCACTGGGCAAACTTCACTGTGTAACAAGATCGAGCGCTTGGAAAGTTGCC 435  
 DB 589 CACGCCCACTGGGCAAACTTCACTGTGTAACAAGATCGAGCGCTTGGAAAGTTGCC 648  
 QY 436 GAGCTCAAGCCGCAATATCCGTGGGCGAGTTGCACTTTGACAGGATCTTGAAGACGGA 495  
 DB 649 GAGCTCAAGCCGCAATATCCGTGGGCGAGTTGCACTTTGACAGGATCTTGAAGACGGA 708  
 QY 496 CGGAGACCTTTGGCGACAA 516  
 DB 709 CGGAGACCTTTGGCGACAA 729

RESULT 8  
 US-10-507-132-17  
 ; Sequence 17, Application US/10507132  
 ; Publication No. US20060223136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koichiro KAKU et al.  
 ; TITLE OF INVENTION: GENE CODING FOR SCYTLONE DEHYDRATASE EXHIBITING RESISTANCE TO  
 ; FILE REFERENCE: 1254-0258PUS1  
 ; CURRENT APPLICATION NUMBER: US/10/507,132  
 ; PRIOR FILING DATE: 2004-09-10  
 ; PRIOR APPLICATION NUMBER: JP 2002-66955  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 17  
 ; LENGTH: 732  
 ; TYPE: DNA  
 ; ORGANISM: Pyricularia oryzae  
 US-10-507-132-17

Query Match 72.4%; Score 373.8; DB 6; Length 732;  
 Best Local Similarity 83.9%; Pred. No. 3-2e-79;  
 Matches 474; Conservative 0; Mismatches 2; Indels 89; Gaps 1;

QY 41 CAGACTACCTGGGCTCATGACTTGGCTATGATGAGTGGGCAAGCAGCTACGACTCCAGG 100  
 DB 168 CAGACTACCTGGGCTCATGACTTGGCTATGATGAGTGGGCAAGCAGCTACGACTCCAGG 227  
 QY 101 ACTGGATAGGCTGGCAAGAGTATGCGCTACTCTGCGC----- 141  
 DB 228 ACTGGATAGGCTGGCAAGAGTATGCGCTACTCTGCGC----- 287  
 QY 142 -----ATTGACTACCGCTCTTCTTCTGACAAGCTTGGAGGCAATGCCGGCGGA 191  
 DB 288 GTTATTTTACTTTCACACCAAATCCAGACTTTTAACAGGACGACCAAAAAAAAA 347

Db 348 AAAAAAAAAAGATTGACTACCGCTCTTCTCGACCAAGCTTGGAGGCAATGCCGCCG 407  
QY 192 GGAGTTGTCGCGATGTCCTGAGCAAGAGATGTCGGGCAACCCACCTCCGCAAGCA 251  
Db 408 GGAGTTGTCGCGATGTCCTGAGCAAGAGATGTCGGGCAACCCACCTCCGCAAGCA 467  
QY 252 GCACTTCATCGCGGCGCGCTGGAGAGAGTGTCCGAGAGAGAGTGTCCGCTACCA 311  
Db 468 GCACTTCATCGCGGCGCGCTGGAGAGAGTGTCCGAGAGAGAGTGTCCGCTACCA 527  
QY 312 CCAAGTCGCGGTCCTCGCAACCAAGGTAACAAGACACCAATGAGAGGTCACATGAA 371  
Db 528 CCAAGTCGCGGTCCTCGCAACCAAGGTAACAAGACACCAATGAGAGGTCACATGAA 587  
QY 372 GGGCAAGCGCCCACTCGGCAAACTTCACTGTCAAGAAATGAGAGGTCGAGT 431  
Db 588 GGGCAAGCGCCCACTCGGCAAACTTCACTGTCAAGAAATGAGAGGTCGAGT 647  
QY 432 CGCCGCTCAAGCCCGATTCGCTGGGCGAGTTCGACTTTCAGAGATCTTTAGGA 491  
Db 648 CGCCGCTCAAGCCCGATTCGCTGGGCGAGTTCGACTTTCAGAGATCTTTAGGA 707  
QY 492 CGAGCGGAGACTTTGGCGCAAA 516  
Db 708 CGAGCGGAGACTTTGGCGCAAA 732

## RESULT 9

US-10-449-902-18394  
; Sequence 18394, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agricultural Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18394  
; LENGTH: 3067  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK068793  
; DATABASE ENTRY DATE: 2001-12-06  
; US-10-449-902-18394

Query Match 10.0%; Score 51.6; DB 6; Length 3067;  
Best Local Similarity 46.2%; Pred. No. 0.0069;  
Matches 171; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 79 GCAGACGCTACGACTTCAAGAGCTGAGTAGCTGCAAGAAAGCTTGCCTACTCTG 138  
Db 350 GCGCTCCGACCAATGAACAAGAGGCGGCGCTGTCAAGCTTGCCTCC 409  
QY 139 CGATTTGACTACCGCTCTTCTCTGCAAGCTTGGAGAGCAATGCCGCGCAAGAGTTG 198  
Db 410 ATCTTCTCTCTACTGCGCAAGCGCAACCTTAGAAGGCGCTTTCAGAGTTC 469  
QY 199 GTGCGATGATGTCGAGCAAGAGATGTCGGGCAACCCACCTTCGCAAGCAAGCTTC 258  
Db 470 ATGGGGAAGTACGGCGTGAAGCGGCAAGCGCTGTCAAGCTTCTCTTCGCGCATG 529  
QY 259 ATCGCGGCAAGCGCTTGGAGAAAGTGTTCGAGAGCAAGGTCATCGGCTTACCAACAGCTG 318

Db 530 TCCCGCGGAGAGGCGCGCGAGGCGCGCAGAGACTTGTTCAGCGCACCAAGGCCAC 589  
QY 319 CCGTCTCCCAACAGAGTACCAAGACACCAATGAAGAGTACCAATGAAGGCCAC 378  
Db 590 GTGCGCCCGAGCGGACACCTTTCGAGATTCCTTCGAGAGCGTGGAGAAAGGCGAAGC 649  
QY 379 GCCCACTCGCAAACTTCACTGTGTAACAAGATGACGCGGCTGTGAAGTTTCGCGGC 438  
Db 650 GCCCAAGCGGCGCAAGAGCACTTTCGCGAGATGATTTTCGCGCTGCGGAGCGCGGC 709  
QY 439 CTCAGCCCG 448  
Db 710 AACATGCCG 719

## RESULT 10

US-10-449-902-13052/c  
; Sequence 13052, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agricultural Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13052  
; LENGTH: 3161  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AK110400  
; DATABASE ENTRY DATE: 2001-12-06  
; US-10-449-902-13052

Query Match 9.9%; Score 51; DB 6; Length 3161;  
Best Local Similarity 47.3%; Pred. No. 0.0097;  
Matches 187; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

QY 44 ACTACTGGGCTCTATGACTTGTATGATGAGTGGGCAAGACTTCAAGAGACT 103  
Db 743 ACTCGGGCTTGCACCAAGGCGGCGAGCTGTGCTGTGCAATGACGCGCAGCGGGA 684  
QY 104 GGGATGAGCTCGAAAGTGCATTTGCGCTTACCTTGCATTAACCTCTCTCTG 163  
Db 683 GCGCGGTATGAGCCCGCAAGAGAGAGTGCAGCGGATGACCGGCTCAAGCTCGCA 624  
QY 164 ACAAGCTTGGAGGCAATGCGCGCGAGAGTTCGTGCGCATGTCGAGCAAGCAGA 223  
Db 623 TCGCGTGTGTGATGACGCGGACGTCGTCGATGTGTGCGCATGTCGCGGATCTTA 564  
QY 224 TCGTGGGCAACCCACCTTCGCAAGCAAGCACTTATCGCGGCAAGCGCTGGAGAA 283  
Db 563 CCGCGGGAGTGGCAATGCTGCGGGAAGGCGGGAAGCGCGGCGGAGACAGACTCG 504  
QY 284 TGTCCGAGAGCAAGTGCATCGCTTACCAACAGTGCCTCCCGCAAGAGATCAAG 343  
Db 503 ATTCGCGCGGCA---CTGCGGTGCGCGTGCAGTTTCAAGGCTGAGCT 447  
QY 344 ACACCAACATGAAGAGTGCATTAAGAGGCGCAAGCCACTTCGCAACTTCCTGCT 403  
Db 446 TAGAGTGAAGAGTGTGTGCGCACTGTGTGAGCCCAATCATCGGCAAGGCTGTCT 387  
QY 404 ACAAGAGATGACGAGCGCTTGAAGATTGCGCGC 438

Db 386 CCGGCGTGTGTACCGCGCTCGGCTCGACCGGC 352

## RESULT 11

US-11-056-355B-18159  
; Sequence 18159, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590P052  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 11966  
; SEQ ID NO 18159  
; LENGTH: 760  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc. feature  
; LOCATION: (1)..(760)  
; OTHER INFORMATION: Ceres Seq. ID no. 12416334  
; FEATURE:  
; NAME/KEY: misc. feature  
; LOCATION: (1)..(760)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14306309  
; OTHER INFORMATION: as cited in SEQ ID NO 1394  
; FEATURE:  
; NAME/KEY: misc. feature  
; LOCATION: (1)..(760)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13595377  
; OTHER INFORMATION: as cited in SEQ ID NO 56088  
; FEATURE:  
; NAME/KEY: misc. feature  
; LOCATION: (1)..(760)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598648  
; OTHER INFORMATION: as cited in SEQ ID NO 64497  
US-11-056-355B-18159

Query Match 9.7%; Score 50; DB 9; Length 760;  
Best Local Similarity 47.7%; Pred. No. 0.013;  
Matches 146; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 207 GGTCTGAGCAGCAATGTGCGACCCACCTCTCCGACGACACTTCTATCGCGG 266  
DB 130 GGGCGGCGACGCGAGATGAGAGGTGTTCTGCCCATCGACGCGACGCGCG 189  
QY 267 CACGCGCTGGAGAGAGGTGTCGAGGACGAGTCATCGGCTACACACAGTCGCGTCC 326  
DB 190 GATCTCGGCTCGGAGCTGCGCGGTGACGCGCGCATCTCCCGCCAGAGCTCTC 249  
QY 327 GCAACAAGGTACAGAGACACCATGAGAGGTACCATGAGGCGCCCATCTC 386  
DB 250 GCAAGGCGCGCGAGAGGTGCGCGCATGATGACGAGTGAACAGGACGCGAGCTT 309  
QY 387 GCGAATCTTCACTGTGTAACAAGATCGACGCGCTCTGGAAGTTGCGCGCTCAAGCC 446  
DB 310 CGTGAGCTTCGAGAGTTCAAGGCGTTTCCACGCGCGCGGCGGCGGTGACGACGA 369  
QY 447 CGATATCGGCTGGGCGAGTTGCACTTTGACAGAGATCTTTGAGAGCGGAGACCTT 506  
DB 370 CCGCGAGCTTCGCGCGCTTCAAGCTTACGACGTGACGCGGCGCGCTCCGCGC 429  
QY 507 TGGCGA 512  
DB 430 GGCGCA 435

RESULT 12

US-10-530-643-3

; Sequence 3, Application US/10530643  
; Publication No. US20060259995A1  
; GENERAL INFORMATION:  
; APPLICANT: CAYOUEITE, Michelle  
; APPLICANT: HANSEN, Connie Jo  
; APPLICANT: MCCURE, Amy  
; APPLICANT: SUN, May  
; APPLICANT: GRAMATIKOVA, Svetlana  
; APPLICANT: DYCAICO, Mark  
; APPLICANT: BARTON, Nelson R.  
; APPLICANT: STEGE, Justin T.  
; APPLICANT: ABOUSHADI, Nahla M.  
; TITLE OF INVENTION: PROTEASES, NUCLEIC ACIDS ENCODING THEM  
; FILE REFERENCE: 564462004100  
; CURRENT APPLICATION NUMBER: US/10/530,643  
; CURRENT FILING DATE: 2006-04-07  
; PRIOR APPLICATION NUMBER: PCT/US03/32819  
; PRIOR FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: 60/471,423  
; PRIOR FILING DATE: 2003-05-16  
; PRIOR APPLICATION NUMBER: 60/418,467  
; PRIOR FILING DATE: 2002-10-10  
; NUMBER OF SEQ ID NOS: 255  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1572  
; TYPE: DNA  
; ORGANISM: Bacteria  
US-10-530-643-3

Query Match 9.6%; Score 49.4; DB 6; Length 1572;  
Best Local Similarity 48.7%; Pred. No. 0.02;  
Matches 134; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 85 AGCTACGACTCCAGAGACTGGATGAGTGGCGAAGTCACTGCTACTCTGCGACT 144  
DB 1276 ACCGTCCAGTCCCGGTACCGGTACGCGGCTCAAGCGCCCGCCCTCCAG 1335  
QY 145 GACTACCGCTCTTCTCTGACAGCTCTGGAGGCAATGCCGCGGAGAGTTCGCGC 204  
DB 1336 GTCCGCGTGAACATGTCACACCTACATCGGTGACCTCCAGATCACTGATCCGCC 1395  
QY 205 ATGTCTCGAGCAACAGATGTCGGGACCCACCTCCGACGACACTTCTATCGGC 264  
DB 1396 GACGCTCGGCTTACACCTGAAAGGCTTCGGCACCGGCGGAGCTCGGACATCAAC 1455  
QY 265 GGCACGCGCTGGAGAGGTGTCGAGGACGAGTCACTGCTACCAACAGCTGCGCTC 324  
DB 1456 ACCACGTACAGGCTGAAGCCCTCTCGGAGGTGCGCAACGCGACGTGGAAGCTCCGCTC 1515  
QY 325 CGGACCAAGGTACAGGACCAACCAATGAAGA 359  
DB 1516 ACGAACAACGAGACGCGACCGGCAAGATCGA 1550

## RESULT 13

US-11-218-305-7648  
; Sequence 7648, Application US/11218305  
; Publication No. US2006014195A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McIaird, Paul L.  
; APPLICANT: Tao, Mengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21 (53660) B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01



NUMBER OF SEQ ID NOS: 25043  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 7648  
LENGTH: 1000  
TYPE: DNA  
ORGANISM: Zea mays  
US-11-218-305-7648

Query Match  
Best Local Similarity 48.6%; Score 49.2; DB 9; Length 1000;  
Matches 135; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 82 GACAGCTACGACTCCAGGACTGGGATAGGCTCGAAAGTCACTTGGCTCTGCGC 141  
DB 552 GACCGGAGCTCGGCGGAGTTCTTGGAACGGCGGGTGGCGCCGACCGCGGCGCAGAG 611  
QY 142 ATTGACTACCGCTCTCTTCTCGACAACTCTGGAGGCAATGCGGCGCGAGAGTTCTG 201  
DB 612 GGGGTCCTCTCTTCGACCACTGATCGACAGCTCGACCGGCTGGAGGTCGCACTTAC 671  
QY 202 GGATGATCTCGAGCAAGAGAGCTGGGCGACCCACCTCGGACGAGCACTTCAATC 261  
DB 672 CGGCGCGCGCCCAACAACAGCGGCGGCGGCGGCGCACCTGCGCATCTTCTTC 731  
QY 262 GCGCGCAGCGCTGGGAGAGGTCTCCGAGAGCAAGTCACTCGGCTACCAACGAGTGGC 321  
DB 732 GCGGGAACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 791  
QY 322 GTCCCGCACCAGAGGTACAGACACCAACCATGAGAG 359  
DB 792 AGCTTCGACACTGTCGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 829

RESULT 14  
US-10-449-902-23999  
Sequence 23999, Application US/10449902  
Publication No. US20060123505A1

GENERAL INFORMATION:  
APPLICANT: National Institute of Agrobiological Sciences.  
APPLICANT: Bio-oriented Technology Research Advancement Institution.  
APPLICANT: The Institute of Physical and Chemical Research.  
APPLICANT: Foundation for Advancement of International Science.  
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
FILE REFERENCE: MOA-A0205Y1-US  
CURRENT APPLICATION NUMBER: US/10/449, 902  
CURRENT FILING DATE: 2003-05-29  
PRIOR APPLICATION NUMBER: JP 2002-203269  
PRIOR FILING DATE: 2002-05-30  
PRIOR APPLICATION NUMBER: JP 2002-383870  
PRIOR FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 56791  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 23999  
LENGTH: 749  
TYPE: DNA  
ORGANISM: Oryza sativa  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: AK099441  
DATABASE ENTRY DATE: 2002-08-28  
US-10-449-902-23999

Query Match  
Best Local Similarity 46.9%; Score 48; DB 6; Length 749;  
Matches 150; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 174 GGAGGCAATGCGCGCGAGAGATTCTCGCATGTCTCGAGCAAGAGTGTGGGCGA 233  
DB 212 GGAGTAGCGCCAGAGTGAACGGATGCTCGGCAACGGCGGCTGGAGGCAATCGGCGA 271  
QY 234 CCCACCTCTCGGAGAGAGATTCTCATCGGCGGCGGCGGCTGGAGAGAGTGTCCAGGA 293  
DB 272 CGGACCAAGCGCTCTGCAACATCGCGGCAAGATGCAAGAGAGTGTGATCGCGC 331

QY 294 CGAGTCATCGGCTACCAACGAGTGGCTCCCGACACAGAGTACAAAGACCAACCAT 353  
DB 332 CGGGGACATCATCTCTGTGCGGCTCGGAGCTACCAAGAGCAAGAGCGGAGTATCT 391  
QY 354 GAAGAGGTACCATGAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 413  
DB 392 CAAGTACATGAACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 451  
QY 414 CGACGGCTGTGAAGTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 473  
DB 452 CAGGCTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 511  
QY 474 TGACAGATCTTTGAGGACG 493  
DB 512 CATTCAGTTGAGAGAGAG 531

RESULT 15  
US-10-953-349-26476  
Sequence 26476, Application US/10953349  
Publication No. US20060107345A1

GENERAL INFORMATION:  
APPLICANT: ALEXANDROV, Nikolai et al.  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 26476  
LENGTH: 750  
TYPE: DNA  
ORGANISM: Triticum aestivum  
US-10-953-349-26476

Query Match  
Best Local Similarity 46.9%; Score 48; DB 6; Length 750;  
Matches 150; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 174 GGAGGCAATGCGCGCGAGAGATTCTCGCATGTCTCGAGCAAGAGTGTGGGCGA 233  
DB 236 GGAGTAGCGCGAGAGTGAACGGATGCTCGGCAACGGCGGCTGGAGGCAATCGGCGA 295  
QY 234 CCCACCTCTCGGAGAGAGATTCTCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 293  
DB 296 CGGACCAAGCGCTCTGCAACATCGGCGGCAAGATGCAAGAGAGTGTGATCGCGC 355  
QY 294 CGAGTCATCGGCTACCAACGAGTGGCTCCCGACACAGAGTACAAAGACCAACCAT 353  
DB 356 CGGGGACATCATCTCTGTGCGGCTCGGAGCTACCAAGAGCAAGAGCGGAGCTATCT 415  
QY 354 GAAGAGGTACCATGAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 413  
DB 416 CAAGTACATGAACGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 475  
QY 414 CGACGGCTGTGAAGTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 473  
DB 476 CGGCTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 535  
QY 474 TGACAGATCTTTGAGGACG 493  
DB 536 CATTCAGTTGAGAGAGAG 555

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Job time : 221 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 18:41:36 ; Search time 1111 Seconds  
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5706.949 Million cell updates/sec

Title: US-10-507-132-1

Perfect score: 516  
Sequence: 1 atgggttcgcaagtcacaa.....ggagagacccttgccgacaa 516

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
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13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
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15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq.\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.6	11.4	1479	7	US-10-156-761-6148
2	58.6	11.4	9025608	7	US-10-156-761-1
3	53.4	10.3	113193	12	US-10-478-943D-1
4	53	10.3	7407	7	US-10-246-330-3
5	53	10.3	7407	7	US-10-282-122A-30151
6	52.2	10.1	791	8	US-10-437-963-23119
7	52	10.1	1336	8	US-10-425-114-4414
8	52	10.1	1394	8	US-10-425-114-29012
9	52	10.1	1437	8	US-10-425-114-17854
10	52	10.1	1598	8	US-10-425-114-29011
11	51.4	10.0	2189	7	US-10-353-445-4
12	51.4	10.0	2346	7	US-10-353-445-4
13	51.4	10.0	2346	7	US-10-353-445-5
14	51.4	10.0	2346	7	US-10-353-445-8
15	51.2	9.9	1536	8	US-10-767-701-14768
16	51	9.9	3408	8	US-10-437-963-17000
17	50.8	9.8	1605	10	US-10-858-730-137

18	50.4	9.8	1238	8	US-10-425-114-14248	Sequence 14248, A
19	50.4	9.8	1329	7	US-10-156-761-6352	Sequence 6352, Ap
20	50.4	9.8	1349	8	US-10-425-114-16604	Sequence 16604, A
21	50.4	9.8	1352	8	US-10-425-114-4590	Sequence 4590, Ap
22	50.4	9.8	1488	9	US-10-425-115-10066	Sequence 10066, A
23	50.4	9.8	1492	9	US-10-425-115-10065	Sequence 10065, A
24	50.4	9.8	1511	8	US-10-425-114-4356	Sequence 4356, Ap
25	50.2	9.7	1177	8	US-10-425-114-17800	Sequence 17800, A
26	50	9.7	1821	3	US-09-953-348-82	Sequence 82, Appl
27	50	9.7	2330	8	US-10-267-255-82	Sequence 82, Appl
28	50	9.7	2330	8	US-10-437-963-47924	Sequence 47924, A
29	50	9.7	18034	3	US-09-953-348-75	Sequence 75, Appl
30	50	9.7	18034	7	US-10-267-255-75	Sequence 75, Appl
31	49.8	9.7	1388	8	US-10-425-114-4296	Sequence 4296, Ap
32	49.6	9.6	2559	8	US-10-437-963-39180	Sequence 39180, A
33	49.4	9.6	980	13	US-11-097-143-14525	Sequence 14525, A
34	49.4	9.6	3665	13	US-11-097-143-14524	Sequence 14524, A
35	49	9.5	699	6	US-10-006-922-41	Sequence 41, Appl
36	48.8	9.5	1341	8	US-10-425-114-16569	Sequence 16569, A
37	48.8	9.5	1434	8	US-10-425-114-4374	Sequence 4374, Ap
38	48.8	9.5	1442	8	US-10-425-114-17865	Sequence 17865, A
39	48.8	9.5	1443	8	US-10-425-114-16556	Sequence 16556, A
40	48.8	9.5	1450	8	US-10-425-114-17863	Sequence 17863, A
41	48.8	9.5	1454	8	US-10-425-114-28991	Sequence 28991, A
42	48.8	9.5	1455	8	US-10-425-114-29006	Sequence 29006, A
43	48.8	9.5	1632	7	US-10-369-493-41594	Sequence 41594, A
44	48.8	9.5	1754	9	US-10-425-115-10067	Sequence 10067, A
45	48.6	9.4	13631	13	US-11-097-143-27772	Sequence 27772, A

## ALIGNMENTS

RESULT 1  
US-10-156-761-6148  
Sequence 6148, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHIRA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761  
CURRENT FILING DATE: 2002-05-29  
PRIOR APPLICATION NUMBER: JP 2001-204089  
PRIOR FILING DATE: 2001-05-30  
PRIOR APPLICATION NUMBER: JP 2001-272697  
PRIOR FILING DATE: 2001-08-02  
NUMBER OF SEQ ID NOS: 15109  
SEQ ID NO 6148  
LENGTH: 1479  
TYPE: DNA  
ORGANISM: Streptomyces avermitilis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1479)  
US-10-156-761-6148

Query Match 11.4%; Score 58.6; DB 7; Length 1479;  
Best Local Similarity 50.5%; Pred. No. 7.3e-07;  
Matches 142; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 148 TACCGCTCTCTCGACAGCTTGGAGGAGATCCGCGAGAGATTCTCGGATG 207  
DB 835 TACCTCTTCGCTTCGAGGCTTCACGTCGTCTCCCGAGGCTCTCGCAAG 894  
QY 208 GTCTCGAGAGACAGATGCTGGGCGACCCACCTTCGCGACGACGACTTCATCGGCGC 267

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Db      895 GTGAGAGACGGGACGAGCGATGTCACCCCATCGCGGGACCCGCGCGCGAGC 954
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OKURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      11.4%; Score 58.6; DB 7; Length 9025608;
Best Local Similarity 50.5%; Pred. No. 2.9e-06;
Matches 142; Conservative 0; Mismatches 139; Indels 0; Gaps 0;
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Qy      148 TACCGCTCTTCTCGACAAAGCTCTGGAGGCAATCCGAGCGAGGATTTCGTGGCATG 207
; Sequence 3, Application US/10246330
; Publication No. US20030166030A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Thien-Fah
; APPLICANT: O'Toole, George A.
; TITLE OF INVENTION: METHODS TO STUDY AND MECHANISMS OF
; FILE REFERENCE: 14537-002001
; CURRENT APPLICATION NUMBER: US/10/246,330
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/323,241
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7407
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: CDS
; LOCATION: (1)...(7404)
US-10-246-330-3

Query Match      10.3%; Score 53.4; DB 12; Length 113193;
Best Local Similarity 47.5%; Pred. No. 5e-05;
Matches 159; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
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Qy      136 CTGGCCATTGACTACCGCTCTTCTCGACAAAGCTTGGAGGCAATGCCGCGAGAG 195
; Sequence 1, Application US/10478943D
; Publication No. US20060073574A1
; GENERAL INFORMATION:
; APPLICANT: University College Dublin, National University of Ireland
; TITLE OF INVENTION: Engineered biosynthesis of novel polyenes
; FILE REFERENCE: PC-1636US
; CURRENT APPLICATION NUMBER: US/10/478,943D
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: S2001/0527
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 113193
; TYPE: DNA
; ORGANISM: Streptomyces nodosus
US-10-478-943D-1

Query Match      10.3%; Score 53.4; DB 12; Length 113193;
Best Local Similarity 47.5%; Pred. No. 5e-05;
Matches 159; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
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Qy      136 CTGGCCATTGACTACCGCTCTTCTCGACAAAGCTTGGAGGCAATGCCGCGAGAG 195
; Sequence 3, Application US/10246330
; Publication No. US20030166030A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Thien-Fah
; APPLICANT: O'Toole, George A.
; TITLE OF INVENTION: METHODS TO STUDY AND MECHANISMS OF
; FILE REFERENCE: 14537-002001
; CURRENT APPLICATION NUMBER: US/10/246,330
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/323,241
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7407
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: CDS
; LOCATION: (1)...(7404)
US-10-246-330-3

Query Match      10.3%; Score 53.4; DB 12; Length 113193;
Best Local Similarity 47.5%; Pred. No. 5e-05;
Matches 159; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
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RESULT 3  
US-10-478-943D-1

Query Match 10.3%; Score 53; DB 7; Length 7407;

Best Local Similarity 48.5%; Pred. No. 4.3e-05;  
Matches 146; Conservative 0; Mismatches 155; Indels 0; Gaps 0;  
QY 211 TCGAGCAGCAGATGCTGGGGCCACCCCTCCGACGACAGACTTCATCGCGGACAG 270  
Db 6913 TCCGGGAGACGCTGTGTCTCCGGCCCAACGGCAGTTCCGAGCACTCAACGGCGGAC 6972  
QY 271 CCTGGAGAGAGGTGTCCGAGCAGAGTCACTGGCTACCAACAGCTGGCGCTCCGAC 330  
Db 6973 GGCAGGACCTGATCTTCAACGTGGGACCGGCGATCACTGTGTGGCCGCAACGGCAC 7032  
QY 331 CAGAGGTACAGACACCAACATGAAGAGTCAACATGAAGGCCACCGCCACTCGCA 390  
Db 7033 GACACCATCAAGATCAACCGGACCGATTTCTGATGATGATGCGCGCGCGGTTGAC 7092  
QY 391 AACCTTCACTGTGACAGAGATCGACGGGCTGTGGAAGTTCCCGGCTCAAGCCGAT 450  
Db 7093 ACCCTGTCTCTGGCCAAAGGCTGACCTGACTCAACACCGCTCGGCTCGCACGCTC 7152  
QY 451 ATCCGCTGGGGGAGTTTCACTTTGACAGGATCTTTGAGAGCGAGGAGACCTTGGC 510  
Db 7153 AGCAACCTGAGGCGCATCGAATCTGGCAGAGGCGGATTCGGGTGCGTCTGACCTGACC 7212  
QY 511 G 511  
Db 7213 G 7213

RESULT 5  
US-10-282-122A-30151

; Sequence 30151, Application US/10282122A  
; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

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NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 30151

; LENGTH: 7407  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-10-282-122A-30151

Query Match 10.3%; Score 53; DB 8; Length 7407;

Best Local Similarity 48.5%; Pred. No. 4.3e-05;

Matches 146; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 211 TCGAGCAGCAGATGCTGGGGCCACCCCTCCGACGACAGACTTCATCGCGGACAG 270  
Db 6913 TCCGGGAGACGCTGTGTCTCCGGCCCAACGGCAGTTCCGAGCACTCAACGGCGGAC 6972  
QY 271 CCTGGAGAGAGGTGTCCGAGCAGAGTCACTGGCTACCAACAGCTGGCGCTCCGAC 330  
Db 6973 GGCAGGACCTGATCTTCAACGTGGGACCGGCGATCACTGTGTGGCCGCAACGGCAC 7032  
QY 331 CAGAGGTACAGACACCAACATGAAGAGTCAACATGAAGGCCACCGCCACTCGCA 390  
Db 7033 GACACCATCAAGATCAACCGGACCGATTTCTGATGATGATGCGCGCGGTTGAC 7092  
QY 391 AACCTTCACTGTGACAGAGATCGACGGGCTGTGGAAGTTCCCGGCTCAAGCCGAT 450  
Db 7093 ACCCTGTCTCTGGCCAAAGGCTGACCTGACTCAACACCGCTCGGCTCGCACGCTC 7152  
QY 451 ATCCGCTGGGGGAGTTTCACTTTGACAGGATCTTTGAGAGCGAGGAGACCTTGGC 510  
Db 7153 AGCAACCTGAGGCGCATCGAATCTGGCAGAGGCGGATTCGGGTGCGTCTGACCTGACC 7212  
QY 511 G 511  
Db 7213 G 7213

RESULT 6  
US-10-437-963-23119

; Sequence 23119, Application US/10437963  
; Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbezuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 23119

LENGTH: 791

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

NAME/KEY: unsure

LOCATION: (1)..(791)

OTHER INFORMATION: unsure at all n locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_2822C.1

US-10-437-963-23119

Query Match 10.1%; Score 52.2; DB 8; Length 791;  
Best Local Similarity 46.2%; Pred. No. 5.2e-05;

Matches 171; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 79 GCAGACGCTAGCACTCCAGAGCTGGGATAGCTGCCAGAAAGTCAATTCGGCTACTCTG 138  
Db 404 GCGTCCGACCATGAAAGAGGCGGCGGCTCTGTCACGCTGCGCACCTTCCGCTCC 463



FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 17854  
LENGTH: 1437  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3075-048-C9\_FLI  
US-10-425-114-17854

Query Match 10.1%; Score 52; DB 8; Length 1437;  
Best Local Similarity 47.1%; Pred. No. 6.6e-05;  
Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 133 ACTCTGCGCATTTGACTACCGCTCTCTTCTGACAGAGCTCTGGAGCGCATGCGCGCGAG 192  
DB 379 ATTCTACGCGTGAATTAACCTGTATCAACCGCAAGGGAACCTTGACGCGGCGAGGCCA 438  
QY 193 GAGTTGCGGCGATGCTGCGAGCAAGCATGCTGGCGGACCCCAACCTCCGCGACGCGAG 252  
DB 439 GCGGTGAGAGCAAGAACTCTGACCAAGAGTACGATCGCAAGATCTTCCCACTCG 498  
QY 253 CACTTATCGGCGGACGCGCTGAGAGAGTGTCCGAGGACGAGTCACTGCGCTACAC 312  
DB 499 CTGATGATGAGCTTCTGTAACAAGGAGAGTGTCCGCGGTCAAGCTGCTCACTCCAG 558  
QY 313 CAGCTGCGCTCCCGACCAAGAGTACAGAGCAACCATGAGAGAGTCACTGAG 372  
DB 559 TTCTTCACATGAACATGTACCGGTGACAGACATGCTGATCAAGGACGTGACG 618  
QY 373 GCGCAGCGCCACTCGGCAACCTTCACTGTACAGAGATCGACGCGCTGAGAGTTC 432  
DB 619 GCGCCGCGGACAGCCCAACGAGATGCGATCAAGTGGCACTTCATCCGAGATCAC 678  
QY 433 GCGGCGCTCAAGCCGATATCCGCTGGGCGAGTTGACT 472  
DB 679 ATCACCACACCGTCACTTGGCGTCCGCGAGCATGCACTCT 718

RESULT 10  
US-10-425-114-29011  
; Sequence 29011, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 29011  
; LENGTH: 1598  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4828-011-H12\_FLI  
US-10-425-114-29011

Query Match 10.1%; Score 52; DB 8; Length 1598;  
Best Local Similarity 47.1%; Pred. No. 6.7e-05;  
Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 133 ACTCTGCGCATTTGACTACCGCTCTCTTCTGACAGAGCTCTGGAGCGCATGCGCGCGAG 192  
DB 395 ATTCTACGCGTGAATTAACCTGTATCAACCGCAAGGGAACCTTGACGCGGCGAGGCCA 454

QY 193 GAGTTGCGGCAATGCTTCAGACAGCATGCTGGGCGACCCCAACCTCCGACGCG 252  
DB 455 GCTGTGAGAGCAAGAACTCTGACCAAGAGTACGATCGAAGATCTTCCCACTCG 514  
QY 253 CACTTATCGGCGGACGCGCTGAGAGAGTGTCCGAGGACGAGTCACTGCGCTACAC 312  
DB 515 CTGATGATGAGCTTCTGTAACAAGGAGAGTGTCCGCGGTCAAGCTGCTCACTCCAG 574  
QY 313 CAGCTGCGGTCCCGACCAAGAGTACAGAGACCAACATGAGAGGTCACTGAGAG 372  
DB 575 TTCTTCACATGAACATGTACCGGTGACAGGACATGCTATCAAGGACGTGACCGGACG 634  
QY 373 GCGCAGCGCCACTCGGCAACCTTCACTGATCAAGAGATGACGCGCTGAGAGTTC 432  
DB 635 GCGCCGCGGACAGCCCAACGAGTGGCATTCATGAGGACATCATTCGCGGATCAC 694  
QY 433 GCGGCGCTCAAGCCGATATCCGCTGGGCGGAGTTGACT 472  
DB 695 ATCACCACACCGTCACTTGGCGTCCGCGAGCATGCTCT 734

RESULT 11  
US-10-353-454-45  
; Sequence 45, Application US/10353454  
; Publication No. US20030194809A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. DuPont de Nemours & Company  
; APPLICANT: Yadav, Narendra  
; TITLE OF INVENTION: METHOD OF CONTROLLING SITE-SPECIFIC RECOMBINATION  
; FILE REFERENCE: CL1975 US NA  
; CURRENT APPLICATION NUMBER: US/10/353,454  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 45  
; LENGTH: 2189  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence of 2189 bp Bgl II-Hind III fragment containing  
; OTHER INFORMATION: SCP:Flp:3'pin gene in plasmid pPH12891  
US-10-353-454-45

Query Match 10.0%; Score 51.4; DB 7; Length 2189;  
Best Local Similarity 47.1%; Pred. No. 0.00011;  
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 156 CTTCCTGACAAAGCTCTGGAGGCAATGCGGCGGAGGAGTTGTCGATGAGTTCGAG 215  
DB 859 CTTGAGGCTCTCCCTCAAGAGCTCATCCCGCTGGAGTTCAACCATATCCCTACTA 918  
QY 216 CAAGGATGCTGGGAGCAACCTCTCGACAGCACTTCATCGGCGGACGCGCTG 275  
DB 919 CGGCGAAGACACAGTCCGACATCAACGATCGTGCATCCCTCACTTCACTTCA 978  
QY 276 GGAAGAGTGTCCGAGAGAGAGTCACTGCGCTACCAACGCTGCGGTCCCGACCAAG 335  
DB 979 GTCTTCGAGAGGCTGACAAAGGCAACTCCCACTTCAAGAGATGCTAAAGGCCCTCT 1038  
QY 336 GTACAAGACACCAACATGAAGAGTCACTGAAGAGGCGCAAGCCCACTCGCAACCT 395  
DB 1039 CTCCAGGCGCGAGTCCATCTGGAGATCAACGAGAGATCTTCACTCTTGAAGTAC 1098  
QY 396 TCACTGTACAAAGAGTCAAGCGGTCTGAAAGTTGCGCGGCTTCAAGCCGATATCG 455  
DB 1099 CTCAAGTTCACATAAGACCAAGCCCTTCAACAGTTCTCTTCGCACTTCACTAA 1158  
QY 456 CTGGGCGAGTTCGACTTGAAGAGATCTTGA 488  
DB 1159 CTGGCGAGTTCTGACATCAAGAACGTGA 1191



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RESULT 12
US-10-353-445-4
; Sequence 4, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Rao, Xueni
; APPLICANT: Taglianti, Laura A.
; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign DNA
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence encoding a Cre:FlpM polypeptide, Cre
; OTHER INFORMATION: from Bacteriophage P1 and Flp (Maize preferred
; OTHER INFORMATION: codons) from Saccharomyces
US-10-353-445-4
```

```
Query Match      10.0%; Score 51.4; DB 7; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.00011;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
```

```
QY 156 CTTCCTCGACAGCTCTGGAGGCAATGCCGCGGAGAGTTGTCGGCATGCTCGAG 215
DB 1338 CCTCGAGGCTCTCCCTCAAGAGCTCATCCCGCTGGAGTTCCATCATCCCTACTA 1397
QY 216 CAAGCATGCTGGGGGACCCACCTCGGACGACGACCTTATCGGGGACGCGCTG 275
DB 1398 CGGCCGAGGACACCACTGCAATCCACCATCGTGTATCCCTCCAGCTTCAGTTCA 1457
QY 276 GGAGAGGTGTCCGAGGACGAGGTCAATCGGCTACCAACGCTGCGGCTCCGACCAAG 335
DB 1458 GTCTCCGAGGAGGTGACAGAGGCAACTCCCACTCAAGAAAGATGCTGAAGGCCCTCT 1517
QY 336 GTACAAAGACACCACTGAAGAGGTCAACCATGAAGGCGACGCCACTCGGCAAACT 395
DB 1518 CTCGAGGGGAGGTCTGAGAGATCAACCGAAGATCTCTCACTCTTCAGTACAC 1577
QY 396 TCACGTGTCAAGAAAGATGAGGCGGTCTGGAAGTTGCGCGGCTCAAGCGCGATATCCG 455
DB 1578 CTCGAGGTTCATTAAGCAAGACCTCTACAGTGTCTCTTCGACCACTTCAATCAA 1637
QY 456 CTGGGGCGAGTTGCACTTTGACAGATCTTTGA 488
DB 1638 CTGGCGAGGTTCTCAGACATCAAGAAAGTTGA 1670
```

```
RESULT 13
US-10-353-445-5
; Sequence 5, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
```

```
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Rao, Xueni
; APPLICANT: Taglianti, Laura A.
; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign DNA
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding moCre:FlpM, Cre from Bacteriophage P1 and
; OTHER INFORMATION: Flp from Saccharomyces, both maize preferred
; OTHER INFORMATION: codons
; NAME/KEY: CDS
; LOCATION: (1)..(2346)
US-10-353-445-5
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Query Match      10.0%; Score 51.4; DB 7; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.00011;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
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QY 156 CTTCCTCGACAGCTCTGGAGGCAATGCCGCGGAGAGTTGTCGGCATGCTCGAG 215
DB 1338 CCTCGAGGCTCTCCCTCAAGAGCTCATCCCGCTGGAGTTCCATCATCCCTACTA 1397
QY 216 CAAGCATGCTGGGGGACCCACCTCGGACGACGACCTTATCGGGGACGCGCTG 275
DB 1398 CGGCCGAGGACACCACTGCAATCCACCATCGTGTATCCCTCCAGCTTCAGTTCA 1457
QY 276 GGAGAGGTGTCCGAGGACGAGGTCAATCGGCTACCAACGCTGCGGCTCCGACCAAG 335
DB 1458 GTCTCCGAGGAGGTGACAGAGGCAACTCCCACTCAAGAAAGATGCTGAAGGCCCTCT 1517
QY 336 GTACAAAGACACCACTGAAGAGGTCAACCATGAAGGCGACGCCACTCGGCAAACT 395
DB 1518 CTCGAGGGGAGGTCAATCGGCTACCAACGCTGAGATCAACGAGAAAGATCTCTTCGAGTACAC 1577
QY 396 TCACGTGTCAAGAAAGATGAGGCGGTCTGGAAGTTGCGCGGCTCAAGCGCGATATCCG 455
DB 1578 CTCGAGGTTCATTAAGCAAGACCTCTACAGTGTCTCTTCGACCACTTCAATCAA 1637
QY 456 CTGGGGCGAGTTGCACTTTGACAGATCTTTGA 488
DB 1638 CTGGCGAGGTTCTCAGACATCAAGAAAGTTGA 1670
```

```
RESULT 14
US-10-353-445-8
; Sequence 8, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Rao, Xueni
; APPLICANT: Taglianti, Laura A.
```

```

; TITLE OF INVENTION: A No. US20030119166A1 Method For The Integration Of Foreign DNA
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: encoding a FlpM:Cre polypeptide, Flp from
; OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2346)
; US-10-353-445-8

```

```

Query Match      10.0%; Score 51.4; DB 7; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.00011;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```

```

QY 156 CTTCTCGAACAACCTGAGGAGCATGCGGCGAGAGTTGTCGAGATGTCGAG 215
DB 264 CTTGAGGCTCTCCCTCAAGAGCTCATCCGCTGGAGATTCAACATATCCCTACTA 323
QY 216 CAAGCAGATGCTGGGCGAGCCCACTCCGACGACGACATTATGCGGCGAGCGCTG 275
DB 324 CGGCGAAGACCAACGATCGACATCAACGATCGTGTATCCCTCAGCTTCAAGTTCA 383
QY 276 GAGAGAGTGTCCGAGACGAGGTATCGGCTACACAGCTGCGCTCCGACCAAGAG 335
DB 384 GTCTCCGAGAGCTGACAGAGGCAATCCCACTCAAGAGATGCTGAGAGGCTCTCT 443
QY 336 GTACAGAGACACCAACATGAGAGGTCACCATGAAAGGCGACGCCACTCGGCAACCT 395
DB 444 CTCGAGGCGAGATCTCAATCTGGAGATCACCGAGAGATCTCAACTCTTGGATACAC 503
QY 396 TCACGTGTAACAAGATGACCGCGCTGGAAGTTGCGCGGCTCAAGCCGATATCGG 455
DB 504 CTCAGATTCACTAAGACCAAGACCTCTACCGAGTTCTCTTCTCGCACTTCAACAA 563
QY 456 CTGGGCGAGTTGACTTGAACGATCTTTGA 488
DB 564 CTGGGCGAGTTCTCAGACATCAAGAACGTGA 596

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## RESULT 15

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US-10-767-701-14768/c
; Sequence 14768, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 14768

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; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS2086_1
; US-10-767-701-14768

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Query Match      9.9%; Score 51.2; DB 8; Length 1536;
Best Local Similarity 50.4%; Pred. No. 0.00011;
Matches 125; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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QY 137 TGGCATTGACTACGCTCTCTCTGACACCTCTGGAGGCAATGCCGCGAGAGT 196
DB 1136 TGGTATGACCTGCGCGCACTTCTCAAGCGCGCGGCGGCGCAAGGCGCGGCGATG 1077
QY 197 TCGTGGCATGTGTTGAGACAGCAGATGCTGGGCGACCCACCTCCGACGACGACT 256
DB 1076 CGGACGCGAGCTAACCAATCATGACCTGACCTGGCTCTCTGACAGCGTGGCGAGT 1017
QY 257 TCATCGGCGGACAGCGCTGAGAGAGTGTCCGAGAGAGGTATCGGCTACCAACAGC 316
DB 1016 TGTGAGAGACGTGCGCCAGCTGAGATGCCATGACGTGTGTGTTGCAAGCGCGCG 957
QY 317 TGGCGTCCCGACCAAGAGTAAAGGACCAACCATGAAAGAGTCAACATGAAGGCGC 376
DB 956 TGAACGCGCCACCGCGCAAGACCGCTCTACACCGCGAGGCTTGAAGATGAGGTG 897
QY 377 ACGCCAC 384
DB 896 GCGTCAC 889

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Job time : 1116 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 18:35:54 ; Search time 139 Seconds  
(without alignments)  
6945.987 Million cell updates/sec

Title: US-10-507-132-1

Perfect score: 516

Sequence: 1 atcggttcgcaagtcacaa.....ggagacattggcgacaa 516

Scoring table: IDENTITY\_NUC

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA:\*

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- 2: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/5/COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/6/COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/7/COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/7/COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/H/COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/PCTUS.COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/RE.COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/BACKFLIST.seq:\*
- 10: /EMC\_Celerra\_SIDS3/Pcdata/2/ina/BACKFLIST.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	52.4	10.2	4451	US-08-717-294-42
2	52	10.1	1820	US-08-173-508-7
3	52	10.1	1821	US-08-265-310-7
4	52	10.1	1821	US-08-951-742-7
5	51.4	10.0	1272	US-08-972-258-1
6	51.4	10.0	1272	US-09-263-128-1
7	51.4	10.0	1272	US-09-641-111A-1
8	51.4	10.0	2346	US-09-193-503B-4
9	51.4	10.0	2346	US-09-193-503B-5
10	51.4	10.0	2346	US-09-193-503B-8
11	51.4	10.0	2346	US-09-415-839-4
12	51.4	10.0	2346	US-09-415-839-5
13	51.4	10.0	2346	US-09-415-839-8
14	51.4	10.0	4131	US-09-252-991A-13773
15	51.4	10.0	8211	US-09-252-991A-13656
16	50.8	9.8	561	US-09-252-991A-13572
17	50.6	9.8	1062	US-09-902-540-8032
18	50.6	9.8	6715	US-09-902-540-818
19	50	9.7	1821	US-09-266-965-75
20	48.2	9.3	18034	US-09-266-965-75
21	48.2	9.3	510	US-09-252-991A-15512
22	48.2	9.3	1989	US-09-252-991A-15371
23	48.2	9.3	2058	US-09-252-991A-15462

24	48.2	9.3	2637	US-09-252-991A-15403	Sequence 15403, A
25	47.4	9.2	654	US-10-081-864A-23	Sequence 23, Appl
26	47.4	9.2	707	US-10-081-864A-21	Sequence 21, Appl
27	47.4	9.2	4403765	US-09-103-840A-2	Sequence 2, Appl
28	47.4	9.2	4411529	US-09-103-840A-1	Sequence 1, Appl
29	46.8	9.1	1365	US-09-030-995-1	Sequence 1, Appl
30	46.6	9.0	2358	US-09-902-540-2667	Sequence 2667, Ap
31	46.6	9.0	13706	US-09-902-540-1124	Sequence 1124, Ap
32	46.4	9.0	2208	US-09-902-540-3493	Sequence 3493, Ap
33	46.4	9.0	18471	US-09-902-540-1167	Sequence 1167, Ap
34	46.2	9.0	3282	US-09-902-540-6552	Sequence 6552, Ap
35	46.2	9.0	3666	US-09-902-540-484	Sequence 484, App
36	46.2	9.0	44377	US-08-804-227C-7	Sequence 7, Appl
37	46.2	9.0	44377	US-08-804-198-1	Sequence 1, Appl
38	45.6	8.8	2016	US-10-632-694A-4	Sequence 4, Appl
39	45.6	8.8	2016	US-10-632-694A-5	Sequence 5, Appl
40	45.6	8.8	2595	US-10-132-350-11	Sequence 11, Appl
41	45.6	8.8	3007	US-10-132-350-9	Sequence 9, Appl
42	45	8.7	3401	US-09-907-794A-249	Sequence 249, App
43	45	8.7	3401	US-09-905-125A-249	Sequence 249, App
44	45	8.7	3401	US-09-902-775A-249	Sequence 249, App
45	45	8.7	3401	US-09-906-700-249	Sequence 249, App

#### ALIGNMENTS

RESULT 1  
US-08-717-294-42  
Sequence 42, Application US/08717294

Patent No. 6114148

GENERAL INFORMATION:

APPLICANT: SEED, BRIAN

TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSER: Clark & Edling LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,294

FILING DATE: 20-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Edling, Karen L.

REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786/345001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045

TELEX:

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 4451 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-717-294-42

Query Match 10.2%; Score 52.4; DB 3; Length 4451;  
Best Local Similarity 52.8%; Pred. No. 0.0026;  
Matches 113; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 230 GGCACCCCGACCTCCGACGACCACTTATGCGCGGACGCGCTGGAGAGGTCTCG 289  
DB 2323 GGCACCCCGACGACGCTCGAGAGCACTTACGCGCCACCCCGCTGGAGCGCGAC 2382  
QY 290 AGCAGAGGTCAATCGGCTACACACGCTGCGCGGACGAGGTACAGAGCACCA 349  
DB 2383 AGCGGAGATACCGCGACCACTTCAAGAGGACGAGGATGACTACAGACCA 2442  
QY 350 CCATGAGAGGTACACCATGAGGCGCACGCCACTCGCGCAACCTTCACTGTAACA 409  
DB 2443 CCATGAGCTGAGATGAGAGAGAGAGACTTGAATACGACGAGACGAGAACCA 2502  
QY 410 AGATGACGCGCTCTGGAAGTTGCGCGCGCTCAA 443  
DB 2503 GCCCGCGCTCTTCCAAAAAGAAACCGCGCACTA 2536

RESULT 2  
US-08-173-508-7  
Sequence 7, Application US/08173508  
Patent No. 5616485  
GENERAL INFORMATION:  
APPLICANT: Bartfeld, Daniel  
APPLICANT: Butler, Michael J.  
APPLICANT: Hadary, Dany  
APPLICANT: Jenish, David  
APPLICANT: Krieger, Timothy  
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED  
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,508  
FILING DATE: 23-DEC-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/125/CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 672 5300  
TELEFAX: 202 672 5399  
TELEX: 904136  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1820 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 104..1720  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 104..244  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 245..1720

US-08-173-508-7  
Query Match 10.1%; Score 52; DB 2; Length 1820;  
Best Local Similarity 49.3%; Pred. No. 0.0027;  
Matches 136; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 148 TACCGCTCTTCTTCGACAACTCTGGAGGCAATGCCGCGAGAGATTCTCGCATG 207  
DB 848 TACGCGACCTTCTCTGGGGCGGACCTACGCCGCTGTCTCCGACCGAGCGCGCTG 907  
QY 208 GTCTGAGCAAGACAGATCTGGGCGACCCACCTTCGCGACGACACTTATCGCGGC 267  
DB 908 GTCTGAGCAAGGCGCATGACCCCTCGCTGCGCGCGCGCGCTGAACTTGAGCAAG 967  
QY 268 AGCGCTGGGAGAGGTCTCCGAGGACGAGTCACTGAGCTACACAGCTGCGCTCCG 327  
DB 968 GAGGCTTCGAGACCGCGCTTCCAGTCTTCGGAAGACTGTGAAGAGCGGACTGC 1027  
QY 338 CACGAGAGTACAGACACCACTGAGAGAGTCACTACATGAGGCGCACCGCACTCG 387  
DB 1028 CCCCTCGGACCAAGACACGACCCCGACGAGGTGGCAAGAACTCAAGTCTTCTTC 1087  
QY 388 GCAAACTTCACTGTTACAGAAATCGACCGCTTC 423  
DB 1088 GACGACTGAGACGCGAGCCCTCGCCCGCGCGAC 1123

RESULT 3  
US-08-265-310-7  
Sequence 7, Application US/08265310  
Patent No. 5856166  
GENERAL INFORMATION:  
APPLICANT: Bartfeld, Daniel  
APPLICANT: Butler, Michael J.  
APPLICANT: Hadary, Dany  
APPLICANT: Jenish, David  
APPLICANT: Krieger, Timothy  
APPLICANT: Malek, Lawrence T.  
APPLICANT: Soostmeyer, Gisela  
APPLICANT: Walczyk, Eva  
APPLICANT: Krysman, Phyllis  
APPLICANT: Garven, Sheila  
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED  
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W.  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,310  
FILING DATE: 24-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,508  
FILING DATE: 23-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 18740/133/CACO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 672 5300  
TELEFAX: 202 672 5399  
TELEX: 904136  
INFORMATION FOR SEQ. ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1821 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 104..1720  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 104..244  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 245..1720  
US-08-265-310-7

Query Match 10.1%; Score 52; DB 2; Length 1821;  
Best Local Similarity 49.3%; Pred. No. 0.0027;  
Matches 136; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 148 TACCGCTCTCTCTGACAAAGCTCTGGAGAGCAATGCCGCGAGAGATTGTCGGCATG 207  
DB 848 TACGGACCTTCTTGCGCGGACCTACGCCGTCTGTTCCCGACCGAGCGGCCGCTG 907  
QY 208 GTCTCGAGCAAGAGATGCTGGCGCAACCCACCTCTCGACGAGCACTTCATCGCGGC 267  
DB 908 GTCTCGAGCGCGCGCATGACCCCTCTGCTGCCGCCGCCCTGAACCTGAGAGCAAG 967  
QY 268 AGCGCTGGAGAGGTGTCTCGAGAGAGAGTCAATGGCTACCAACAGCTGGCGCTCCG 327  
DB 968 GAGGGCTTCGAGACGGCGTTCACATCTTGGCAAGAGAGCTGTAAGACGCGGACTGC 1027  
QY 328 CACCAAGGTACAGAGACCAACATGAAGAGGTACCAATGAAGGCCACGCGCACTCG 387  
DB 1028 CCCCTGGGACAGAGACACACCCCGACCAAGGTGGCAAGAACTCAAGTCTTCTTC 1087  
QY 388 GCAAACTTCACTGTGTACAGAAAGATGACGCGCTC 423  
DB 1088 GACGACCTGAGCGGAAAGCCCTGCGCGCGGCGAC 1123

RESULT 4  
US-08-951-742-7  
Sequence 7, Application US/08951742  
Patent No. 6127144  
GENERAL INFORMATION:  
APPLICANT: Bartfeld, Daniel  
APPLICANT: Michael J. Butler  
APPLICANT: Dany Hadary  
APPLICANT: David Jenish  
APPLICANT: Tim Krieger  
APPLICANT: Lawrence T. Malek  
APPLICANT: Gisela Soostmeyer  
APPLICANT: Eva Walczyk  
APPLICANT: Phyllis Kryseman  
APPLICANT: Shella Garven  
TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS IN  
TITLE OF INVENTION: BACTERIAL HOST CELLS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/951,742

FILING DATE: 16-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 0189740/0140  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5339  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1821 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 104..1720  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 104..244  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 245..1720  
US-08-951-742-7

Query Match 10.1%; Score 52; DB 3; Length 1821;  
Best Local Similarity 49.3%; Pred. No. 0.0027;  
Matches 136; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 148 TACCGCTCTCTCTGACAAAGCTCTGGAGAGCAATGCCGCGAGAGATTGTCGGCATG 207  
DB 848 TACGGACCTTCTTGCGCGGACCTACGCCGTCTGTTCCCGACCGAGCGGCCGCTG 907  
QY 208 GTCTCGAGCAAGAGATGCTGGCGCAACCCACCTCTCGACGAGCACTTCATCGCGGC 267  
DB 908 GTCTCGAGCGCGCGCATGACCCCTCTGCTGCCGCCGCCCTGAACCTGAGAGCAAG 967  
QY 268 AGCGCTGGAGAGGTGTCTCGAGAGAGAGTCAATGGCTACCAACAGCTGGCGCTCCG 327  
DB 968 GAGGGCTTCGAGACGGCGTTCACATCTTGGCAAGAGAGCTGTAAGAGCGCGACTGC 1027  
QY 328 CACCAAGGTACAGAGACCAACATGAAGAGGTACCAATGAAGGCCACGCGCACTCG 387  
DB 1028 CCCCTGGGACAGAGACACACCCCGACCAAGGTGGCAAGAACTCAAGTCTTCTTC 1087  
QY 388 GCAAACTTCACTGTGTACAGAAAGATGACGCGCTC 423  
DB 1088 GACGACCTGAGCGGAAAGCCCTGCGCGCGGCGAC 1123

RESULT 5  
US-08-972-258-1  
Sequence 1, Application US/08972258  
Patent No. 5929301  
GENERAL INFORMATION:  
APPLICANT: Baszczyński, Chris  
APPLICANT: Bowen, Benjamin A.  
APPLICANT: Drummond, Bruce J.  
APPLICANT: Gordon-Kamm, William J.  
APPLICANT: Peterson, David J.  
APPLICANT: Sandahl, Gary A.  
APPLICANT: Tagliani, Laura A.  
APPLICANT: Zhao, Zuo-Yu  
TITLE OF INVENTION: No. 5929301el Nucleic Acid Sequence Encoding FLP  
TITLE OF INVENTION: Recombinase and Method of Using Same  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: W. Murray Spruill  
STREET: 3605 Glenwood Ave. Suite 310  
CITY: Raleigh

```
/ STATE: NC
/ COUNTRY: US
/ ZIP: 27622
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/972,258
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Spruill, W. Murray
/ REGISTRATION NUMBER: 32,943
/ REFERENCE/DOCKET NUMBER: 5718-28
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919 420 2202
/ TELEFAX: 919 881 3175
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1272 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: Synthetic sequence (optimized)
/ US-08-972-258-1
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Query Match 10.0%; Score 51.4; DB 2; Length 1272;
Best Local Similarity 47.1%; Pred. No. 0.0035;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
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QY 156 CTTCCCTCGACAAGCTCTGGAGGCAATGCGCGCGAGGATTCGTGGCATGTCCTCGAG 215
DB 264 CTTGAGGCTCTCCCTCAAGAAAGTATCCCGCTGGAGTTACCATATCCCTACTA 323
QY 216 CAAGCAGATGCTGGGCGAACCCTCCGCAAGCAGCATTCATCGGCGGCAAGCGCTG 275
DB 324 CGGCCGAGGACCAATCCGACATCAACCATTCGTATCCCTCAGCTTCAGTTCA 383
QY 276 GGAAGAGTGTCCGAGCAGAGTCAATCGGCTACCAACAGCTGCGGCTCCGACAGAG 335
DB 384 GTCTCCGAGGAGCTGACAGAGGCAATCCCACTCAAGAAAGATCTGAAGCCCTCT 443
QY 336 GTACAAAGACCAACCATGAAGAGTCAACATGAAGGCGCAAGCCCATTCGCAAACT 395
DB 444 CTCGAGGCGAGTCCATCTGGAGATCAACGAAAGATCTCACTCTTCGAGTAC 503
QY 396 TCACTGTACAAGAAATGACAGCGCTCTGAAGTTCCGCGGCTCAAGCCGATATCCG 455
DB 504 CTCGAGGTTCACTAAGAACCAAGACCTCTACCAAGTTCTCTTCGCAACCTTATCA 563
QY 456 CTGGGCGAGTTCGACTTTGACAGATCTTTGA 488
DB 564 CTGGGCGAGTTCCTCAGACATCAAGAACGTGGA 596
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RESULT 6
US-09-263-128-1
/ Sequence 1, Application US/09263128
/ Patent No. 6175058
/ GENERAL INFORMATION:
/ APPLICANT: Barczynski, Chris
/ APPLICANT: Bowen, Benjamin A.
/ APPLICANT: Drummond, Bruce J.
/ APPLICANT: Gordon-Kamm, William J.
/ APPLICANT: Peterson, David J.
/ APPLICANT: Sandahl, Gary A.
/ APPLICANT: Tagliani, Laura A.
/ APPLICANT: Zhao, Zuo-Yu
/ TITLE OF INVENTION: No. 6175058el Nucleic Acid Sequence Encoding RLP
```

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/ Patent No. 6175058
/ TITLE OF INVENTION: Recombinase and Method of Using Same
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: W. Murray Spruill
/ STREET: 3605 Glenwood Ave, Suite 310
/ CITY: Raleigh
/ STATE: NC
/ COUNTRY: US
/ ZIP: 27622
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/263,128
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/972,258
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Spruill, W. Murray
/ REGISTRATION NUMBER: 32,943
/ REFERENCE/DOCKET NUMBER: 5718-28
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919 420 2202
/ TELEFAX: 919 881 3175
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1272 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: Synthetic sequence (optimized)
/ US-09-263-128-1
```

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Query Match 10.0%; Score 51.4; DB 3; Length 1272;
Best Local Similarity 47.1%; Pred. No. 0.0035;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
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QY 156 CTTCTCGACAAGCTCTGGAGGCAATGCGCGCGAGGATTCGTGGCATGTCCTCGAG 215
DB 264 CTTGAGGCTCTCCCTCAAGAAAGTATCCCGCTGGAGTTACCATATCCCTACTA 323
QY 216 CAAGCAGATGCTGGGCGAACCCTCCGCAAGCAGCATTCATCGGCGGCAAGCGCTG 275
DB 324 CGGCCGAGGACCAATCCGACATCAACCATTCGTATCCCTCAGCTTCAGTTCA 383
QY 276 GGAAGAGTGTCCGAGCAGAGTCAATCGGCTACCAACAGCTGCGGCTCCGACAGAG 335
DB 384 GTCTCCGAGGAGCTGACAGAGGCAATCCCACTCAAGAAAGATCTGAAGCCCTCT 443
QY 336 GTACAAAGACCAACCATGAAGAGTCAACATGAAGGCGCAAGCCCATTCGCAAACT 395
DB 444 CTCGAGGCGAGTCCATCTGGAGATCAACGAAAGATCTCACTCTTCGAGTAC 503
QY 396 TCACTGTACAAGAAATGACAGCGCTCTGAAGTTCCGCGGCTCAAGCCGATATCCG 455
DB 504 CTCGAGGTTCACTAAGAACCAAGACCTCTACCAAGTTCTCTTCGCAACCTTATCA 563
QY 456 CTGGGCGAGTTCGACTTTGACAGATCTTTGA 488
DB 564 CTGGGCGAGTTCCTCAGACATCAAGAACGTGGA 596
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RESULT 7
US-09-641-111A-1
/ Sequence 1, Application US/0964111A
/ Patent No. 6720475
```



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; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Drummond, Bruce J.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Peterson, David J.
; APPLICANT: Sandahl, Gary A.
; APPLICANT: Tagilanti, Laura A.
; APPLICANT: Zhao, Zuo-Yu
; APPLICANT: St. Clair, Grace Marie
; TITLE OF INVENTION: No. 6720475el Nucleic Acid Sequence Encoding FLP
; Patent No. 6720475
; TITLE OF INVENTION: Recombinase and Method of Using Same
; FILE REFERENCE: 35718/201942
; CURRENT APPLICATION NUMBER: US/09/641,111A
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 09/263,128
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 08/972,258
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1272)
; OTHER INFORMATION: Optimized sequence
US-09-641-111A-1

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Query Match          10.0%; Score 51.4; DB 3; Length 1272;
Best Local Similarity 47.1%; Pred. No. 0.0035;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```

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QY 156 CTTCCTCGACAACTCTGGAGGCAATGCCGCCGAGAGTGTCTGCTCGAG 215
DB 264 CCTCGAGGCTCTCTCAAGAGCTCATCCCGCTGGAGTTCAACCATCTCCCTACTA 323
QY 216 CAAGCAGATCTGGGCGACCCCACTCCGACGACGACTTATGCGGCGGACGCGCTG 275
DB 324 CGGCCGAGAGCAACAGTCCACATCAACGATCGTCTCATCCCTCAGCTTCAAGTTTCA 383
QY 276 GAGAGAGTGTCTCGAGGAGAGTCAATCGGCTACACAGCTCGGCTCCCGACACAGAG 335
DB 384 GTCCTCCGAGAGAGCTGACAAAGCACTCCCACTCCAAAGATGTGTAAGGCTCTCCT 443
QY 336 GTACAAAGACACCACTGAAGAGGTCAACATGAAGAGGCGACGCCCACTCGGCAAACT 395
DB 444 CTCGAGGGGAGATCTCATCTGGAGATCAACGAGAGATCTCAACTCTTCGAGTACAC 503
QY 396 TCACGTGTAACAAGATGACGAGCGCTCTGAAAGTTCCGCGCTCAAGCCGATATCCG 455
DB 504 CTCAGATTCACTAAGACCAAGACCCCTCTACAGATCTCTCTCGCCACCTTATCAA 563
QY 456 CTGGGGGAGTTGACTTTCATTCACAGATCTTGA 488
DB 564 CTGGGAGGTTCTCAGACATCAAGAACGTGGA 596

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RESULT 8
US-09-193-503B-4
; Sequence 4, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagilanti, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into

```

```

; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/193,503B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
; OTHER INFORMATION: sequence encoding a Cre:FluPm polypeptide, Cre
; OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
; OTHER INFORMATION: codons) from Saccharomyces
US-09-193-503B-4

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Query Match          10.0%; Score 51.4; DB 3; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.004;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

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QY 156 CTTCCTCGACAACTCTGGAGGCAATGCCGCCGAGAGTGTCTGCTCGAG 215
DB 1338 CCTCGAGGCTCTCTCAAGAGCTCATCCCGCTGGAGTTCAACCATCTCCCTACTA 1397
QY 216 CAAGCAGATCTGGGCGACCCCACTCCGACGACGACTTATGCGGCGGACGCGCTG 275
DB 1398 CGGCCGAGAGCAACAGTCCACATCAACGATCGTCTCATCCCTCAGCTTCA 1457
QY 276 GAGAGAGTGTCTCGAGGAGAGTCAATCGGCTACACAGCTCGGCTCCCGACACAGAG 335
DB 1458 GTCCTCCGAGAGAGCTGACAAAGGCACTCCCACTCCAAAGATGTGTAAGGCTCTCCT 1517
QY 336 GTACAAAGACACCACTGAAGAGGTCAACATGAAGAGGCGACGCCCACTCGGCAAACT 395
DB 1518 CTCGAGGGGAGATCTCATCTGGAGATCAACGAGAGATCTCAACTCTTCGAGTACAC 1577
QY 396 TCACGTGTAACAAGATGACGAGCGCTCTGAAAGTTCCGCGCTCAAGCCGATATCCG 455
DB 1578 CTCAGATTCACTAAGACCAAGACCTTACAGATCTCTCTCTCGCCACCTTATCAA 1637
QY 456 CTGGGGGAGTTGACTTTCATTCACAGATCTTGA 488
DB 1638 CTGGGAGGTTCTCAGACATCAAGAACGTGGA 1670

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RESULT 9
US-09-193-503B-5
; Sequence 5, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
; APPLICANT: Baszczyński, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagilanti, Laura A.
; TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/193,503B
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613

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/ PRIOR FILING DATE: 1997-11-18  
/ NUMBER OF SEQ ID NOS: 11  
/ SOFTWARE: Patent In Ver. 2.1  
/ SEQ ID NO 5  
/ LENGTH: 2346  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: sequence  
/ OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacteriophage P1 and  
/ OTHER INFORMATION: FLP from Saccharomyces, both maize preferred  
/ OTHER INFORMATION: codons  
/ NAME/KEY: CDS  
/ LOCATION: (1) .. (2346)  
/ US-09-193-503B-5

Query Match 10.0%; Score 51.4; DB 3; Length 2346;  
Best Local Similarity 47.1%; Pred. No. 0.004;  
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 156 CTTCCTGACAAAGCTCTGGAGGCAATGCGCGCGAGAGTTGTCGGATGATGCTCGAG 215  
DB 1338 CTTGAGGCTCTCCCTCAAGAAAGCTATCCCGCTTGGAGTTCAACATATCCCTTACTA 1397  
QY 216 CAAGCAGATGCTGGGCGAACCCTCCGCAAGCAGCACTTCATCGCGGCGACGCGCTG 275  
DB 1398 CGGCGAAGACACCAATCCGATCAACGATCGTTCATCCCTCAGCTTCAGTTGCA 1457  
QY 276 GGAAGAAGTGTCCGAGAGAGGTCTATCGGCTTACCAACGCTGCGGCTCCCGCAAGAG 335  
DB 1458 GTCTCCGAGAGAGCTGACAAAGGCAATCCCACTCAAGAAAGATCTGAAGGCTCTCT 1517  
QY 336 GTACAAAGACACCAATGAAAGGTCACATGAAGGCGACGCCACTCGGCAAACT 395  
DB 1518 CTCGAGGCGAGTCCATCTGGAGATCAACGAAAGATCTCACTCTTGAAGTAC 1577  
QY 396 TCACGTGTACAAAGATGACGCGCTGTGAAGTTGCGCGGCTCAAGCCGATATCG 455  
DB 1578 CTCGAGTTCACTAAGACCAAGACCTTACAGTTCTTCTCGCACCTTCATCA 1637  
QY 456 CTGGGCGAGTTCGACTTTCAGAGATCTTTGA 488  
DB 1638 CTGCGGAGGTCTTCAGACATCAAGACGTGA 1670

## RESULT 10

US-09-193-503B-8  
/ Sequence 8, Application US/09193503B  
/ Patent No. 6262341  
/ GENERAL INFORMATION:  
/ APPLICANT: Baszczyński, Christopher L.  
/ APPLICANT: Lyznik, Leszek A.  
/ APPLICANT: Gordon-Kamm, William J.  
/ APPLICANT: Guan, Xueni  
/ APPLICANT: Rao, Gurtu  
/ APPLICANT: Taglianti, Laura A.  
/ TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into  
/ FILE REFERENCE: 5718-66 (amended listing)  
/ CURRENT APPLICATION NUMBER: US/09/193,503B  
/ PRIOR FILING DATE: 1998-11-17  
/ PRIOR APPLICATION NUMBER: 60/099,435  
/ PRIOR FILING DATE: 1998-09-08  
/ PRIOR APPLICATION NUMBER: 60/056,627  
/ PRIOR FILING DATE: 1997-11-18  
/ PRIOR APPLICATION NUMBER: 60/065,613  
/ NUMBER OF SEQ ID NOS: 11  
/ SOFTWARE: Patent In Ver. 2.1  
/ SEQ ID NO 8  
/ LENGTH: 2346  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence

/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Sequence  
/ OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from  
/ OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre  
/ OTHER INFORMATION: from Bacteriophage P1  
/ NAME/KEY: CDS  
/ LOCATION: (1) .. (2346)  
/ US-09-193-503B-8

Query Match 10.0%; Score 51.4; DB 3; Length 2346;  
Best Local Similarity 47.1%; Pred. No. 0.004;  
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 156 CTTCCTGACAAAGCTCTGGAGGCAATGCGCGCGAGAGTTGTCGGATGATGCTCGAG 215  
DB 264 CTTGAGGCTCTCCCTCAAGAAAGCTATCCCGCTTGGAGTTCAACATATCCCTTACTA 323  
QY 216 CAAGCAGATGCTGGGCGAACCCTCCGCAAGCAGCACTTCATCGCGGCGACGCGCTG 275  
DB 324 CGGCGAAGACACCAATCCGATCAACGATCGTTCATCCCTCAGCTTCAGTTGCA 383  
QY 276 GGAAGAAGTGTCCGAGAGAGGTCTATCGGCTTACCAACGCTGCGGCTCCCGCAAGAG 335  
DB 384 GTCTCCGAGAGAGCTGACAAAGGCAATCCCACTCAAGAAAGATCTGAAGGCTCTCTCT 443  
QY 336 GTACAAAGACACCAATGAAAGGTCACCAATGAAGGCGACGCCACTCGGCAAACT 395  
DB 444 CTCGAGGCGAGTCCATCTGGAGATCAACGAAAGATCTCACTCTTGAAGTAC 503  
QY 396 TCACGTGTACAAAGATGACGCGCTGTGAAGTTGCGCGGCTCAAGCCGATATCG 455  
DB 504 CTCGAGTTCACTAAGACCAAGACCTTACAGTTCTTCTCGCACCTTCATCA 563  
QY 456 CTGGGCGAGTTCGACTTTCAGAGATCTTTGA 488  
DB 564 CTGCGGAGGTCTTCAGACATCAAGACGTGA 596

## RESULT 11

US-09-415-839-4  
/ Sequence 4, Application US/09415839  
/ Patent No. 6541231  
/ GENERAL INFORMATION:  
/ APPLICANT: Baszczyński, Christopher L.  
/ APPLICANT: Lyznik, Leszek A.  
/ APPLICANT: Gordon-Kamm, William J.  
/ APPLICANT: Guan, Xueni  
/ APPLICANT: Rao, Gurtu  
/ APPLICANT: Taglianti, Laura A.  
/ TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA  
/ FILE REFERENCE: 5718-66 (amended listing)  
/ CURRENT APPLICATION NUMBER: US/09/415,839  
/ PRIOR FILING DATE: 1999-10-12  
/ PRIOR APPLICATION NUMBER: US/09/193,503  
/ PRIOR FILING DATE: 1998-11-17  
/ PRIOR APPLICATION NUMBER: 60/099,435  
/ PRIOR FILING DATE: 1998-09-08  
/ PRIOR APPLICATION NUMBER: 60/056,627  
/ PRIOR FILING DATE: 1997-11-18  
/ PRIOR APPLICATION NUMBER: 60/065,613  
/ PRIOR FILING DATE: 1997-11-18  
/ NUMBER OF SEQ ID NOS: 11  
/ SOFTWARE: Patent In Ver. 2.1  
/ SEQ ID NO 4  
/ LENGTH: 2346  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence:Nucleotide  
/ OTHER INFORMATION: sequence encoding a Cre:FLPm polypeptide, Cre  
/ OTHER INFORMATION: from Bacteriophage P1 and FLP (maize preferred

OTHER INFORMATION: codons) from Saccharomyces  
US-09-415-839-4

Query Match 10.0%; Score 51.4; DB 3; Length 2346;

Best Local Similarity 47.1%; Pred. No. 0.004;  
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```
156 CTCTCCGACAAAGCTCTGGAGGCAATGCCGCGGAGAGTTGATGGCATGATCTCGAG 215
1338 CTTGAGGCTCCCTCAAGAGCTCATCCCGCTGGAGTTACCATATCCCTCTACGA 1397
216 CAAGCAGATCTGGGCGACCCCACTCCGCGACGACGACATTCATGCGGCGGACGCGCTG 275
1398 CGGCGGAGAGCAACAGTCCGACATCCGACATCGTGCATCCCTCAGCTTCAAGTTTCA 1457
276 GGAGAAAGTGTCCGAGGAGAGGTCATCGGCTTACCAACGCGGCTCCCGACCGAGAG 335
1458 GTCTCCGAGAGGCTGACAAAGGCAATCCCACTCAAGAAAGATCTGAAGGCTCTCT 1517
336 GTACAAAGACACCACTGAAAGAGTTCACATGAAGGCGCACGCCCACTCGCAAACT 395
1518 CTCGAGGGCGAGTCATCTGGAGATCAACGAGAAAGATCTCACTCTTGAAGTACAC 1577
396 TCACTGTACAAGAGATGACGCGCTCTGGAAGTTCCGCGGCTCAAGCCGATATCCG 455
1578 CTCAGAGTTCACTAAGACCAAGACCTTACCAAGTTCTTCTCGCCACCTTCA 1637
456 CTGGGCGAGTTTCAGATTTGACAGATCTTTGA 488
1638 CTGCGGAGGTTCTCAGACATCAAGACGTGA 1670
```

RESULT 12

US-09-415-839-5

Sequence 5, Application US/09415839  
Patent No. 6541231

GENERAL INFORMATION:

APPLICANT: Baszczynski, Christopher L.

APPLICANT: Lyznik, Leszek A.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Guan, Xueni

APPLICANT: Rao, Guru

TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA

TITLE OF INVENTION: Into

FILE REFERENCE: 5718-66 (amended listing)

CURRENT APPLICATION NUMBER: US/09/415,839

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: US/09/193,503

PRIOR FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: 60/099,435

PRIOR FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: 60/056,627

PRIOR FILING DATE: 1997-11-18

PRIOR APPLICATION NUMBER: 60/065,613

PRIOR FILING DATE: 1997-11-18

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 2346

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: sequence

OTHER INFORMATION: encoding mcre:FlpM, Cre from Bacteriophage P1 and

OTHER INFORMATION: Flp from Saccharomyces, both maize preferred

FEATURE: NAME/KEY: CDS

LOCATION: (1)..(2346)

US-09-415-839-5

Query Match 10.0%; Score 51.4; DB 3; Length 2346;  
Best Local Similarity 47.1%; Pred. No. 0.004;  
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```
156 CTCTCCGACAAAGCTCTGGAGGCAATGCCGCGGAGAGTTGATGGCATGATCTCGAG 215
1338 CTTGAGGCTCCCTCAAGAGCTCATCCCGCTGGAGTTACCATATCCCTCTACGA 1397
216 CAAGCAGATCTGGGCGACCCCACTCCGCGACGACGACATTCATGCGGCGGACGCGCTG 275
1398 CGGCGGAGAGCAACAGTCCGACATCCGACATCGTGCATCCCTCAGCTTCAAGTTTCA 1457
276 GGAGAAAGTGTCCGAGGAGAGGTCATCGGCTTACCAACGCGGCTCCCGACCGAGAG 335
1458 GTCTCCGAGAGGCTGACAAAGGCAATCCCACTCAAGAAAGATCTGAAGGCTCTCT 1517
336 GTACAAAGACACCACTGAAAGAGTTCACATGAAGGCGCACGCCCACTCGCAAACT 395
1518 CTCGAGGGCGAGTCATCTGGAGATCAACGAGAAAGATCTCACTCTTGAAGTACAC 1577
396 TCACTGTACAAGAGATGACGCGCTCTGGAAGTTCCGCGGCTCAAGCCGATATCCG 455
1578 CTCAGAGTTCACTAAGACCAAGACCTTACCAAGTTCTTCTCGCCACCTTCA 1637
456 CTGGGCGAGTTTCAGATTTGACAGATCTTTGA 488
1638 CTGCGGAGGTTCTCAGACATCAAGACGTGA 1670
```

RESULT 13

US-09-415-839-8

Sequence 8, Application US/09415839  
Patent No. 6541231

GENERAL INFORMATION:

APPLICANT: Baszczynski, Christopher L.

APPLICANT: Lyznik, Leszek A.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Guan, Xueni

APPLICANT: Rao, Guru

TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA

TITLE OF INVENTION: Into

FILE REFERENCE: 5718-66 (amended listing)

CURRENT APPLICATION NUMBER: US/09/415,839

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: US/09/193,503

PRIOR FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: 60/099,435

PRIOR FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: 60/056,627

PRIOR FILING DATE: 1997-11-18

PRIOR APPLICATION NUMBER: 60/065,613

PRIOR FILING DATE: 1997-11-18

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 2346

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Sequence

OTHER INFORMATION: encoding a FlpM, Cre polypeptide, Flp from

OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre

OTHER INFORMATION: from Bacteriophage P1

FEATURE: NAME/KEY: CDS

LOCATION: (1)..(2346)

US-09-415-839-8

Query Match 10.0%; Score 51.4; DB 3; Length 2346;  
Best Local Similarity 47.1%; Pred. No. 0.004;  
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 156 CTTCTCGACAAGCTCTGGGAGGCAATGCCGCCGAGAGTTGTCGCGATGATCTCGAG 215  
DB 264 CTTGAGAGGCTCCCTTAAGAAAGTCAATCCCGCTGGAGTTGACCATATCCCTACTA 323  
QY 216 CAGGATGATCTGGGGGAGCCCACTCCGACGACGACATTCATCGGGGAGACGGCTG 275  
DB 324 CGGCCAAGACACATCCGACATCAACATCGTATCCCTCAGCTTCAGTTGCA 383  
QY 276 GGAGAAGGTGTCGAGGAGAGGTATCGGCTAACCAACGATCGCGGTCCCGCACAGAG 335  
DB 384 GTCCTCCGAGAGGCTGACAAAGGCACTCCCACTCAAGAAAGATGCTAAAGCCCTCT 443  
QY 336 GTACAAGACACCAACCATGAAGGTGACATGAAGGGCCACGCCACTCGCAAACT 395  
DB 444 CTCGAGGGGCGATCATCTGGGAGATCAACGAAAGATCTCACTCTTGAAGTACAC 503  
QY 396 TCACTGTGTAAGAAAGATGACGGCGCTGTGAAGTTGCGCGGCTCAAGCCGATATCG 455  
DB 504 CTCGAGTTCACATAAGACCAAGACCTTACCAAGTTCTTCTCGCACCTTCATCA 563  
QY 456 CTGGGGCGAGTTGACCTTGAACGATCTTGA 488  
DB 564 CTGCGGAGTTTCTGACATCATGAACGTTGA 596

RESULT 14  
US-09-252-991A-13773/c  
; Sequence 13773, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13773  
; LENGTH: 4131  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13773

Query Match 10.0%; Score 51.4; DB 3; Length 4131;  
Best Local Similarity 48.2%; Pred. No. 0.0044;  
Matches 145; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 211 TCGAGCAAGCAGATGCTGGGCGACCCCACTCCGACGACGACATTCATCGGCGGACG 270  
DB 609 TCCGGGAGAGAGTGTCTGTCGGGCGCAAGGAGTTGAGAGCAATCAACGGCGGAC 550  
QY 271 CGCTGGAGAAAGTGTCCGAGACGAGTCACTGACTACACAGCTGCGCTCCGAC 330  
DB 549 GGCAGAGCCTGATCTTCAACGTGGGACGGGATCAAGTGTGGCCGGCAACGGCAAC 490  
QY 331 CAGAGGTACAGACACCAATGAAGAGTCAATGAAGGCCACGCCCACTCGGA 390  
DB 489 GACACCATCCAGATCCCGGACCGATTTCAGCATCATGACGGCGCGGTTGAC 430  
QY 391 AACCTTCACTGTGTAAGAAAGTCAAGGCGGTCTGAAGTTGCGCGGCTCAAGCCGAT 450  
DB 429 ACCCTGTCTTGGCCAAAGGATCGACTGACTACAAAGCGGTGGCAAGCTC 370  
QY 451 ATCCGCTGGGAGAGTTGACTTTGACAGATCTTTGAGAGCAGGAGACCTTTGGC 510  
DB 369 AGCAACCTGAGGCGATCGACTCGGCAAGGGGCACTCGGGTAAAGCTGCTGACCTGACC 310  
QY 511 G 511

DB 309 G 309

RESULT 15  
US-09-252-991A-13656  
; Sequence 13656, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13656  
; LENGTH: 8211  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13656

Query Match 10.0%; Score 51.4; DB 3; Length 8211;  
Best Local Similarity 48.2%; Pred. No. 0.0051;  
Matches 145; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 211 TCGAGCAAGCAGATGCTGGGCGACCCCACTCCGACGACGACATTCATCGGCGGACG 270  
DB 7717 TCCGGGAGAGTGTCTGTCGGGCGCAAGGAGTTGAGAGCAATCAACGGCGGAC 7776  
QY 271 CGCTGGAGAAAGTGTCCGAGACGAGTCACTGACTACACAGCTGCGCTCCGAC 330  
DB 7777 GGCAGAGCCTGATCTTCAACGTGGGACCGCGATCAAGTGTGGCCGGCAACGGCAAC 7836  
QY 331 CAGAGGTACAGACACCAATGAAGAGTCAATGAAGGCCACGCCCACTCGGA 390  
DB 7837 GACACCATCCAGATCAAGGCGGATTCCTGACATCATGAGCGCGGCTTCCAG 7896  
QY 391 AACCTTCACTGTGTAAGAAAGTCAAGGCGGTCTGAAGTTGCGCGGCTCAAGCCGAT 450  
DB 7897 ACCCTGTCTTGGCCAAAGGATCGACTGACTACAAAGCGGTGGCAAGCTC 7956  
QY 451 ATCCGCTGGGAGAGTTGACTTTGACAGATCTTTGAGAGCAGGAGACCTTTGGC 510  
DB 7957 AGCAACCTGAGGCGATCGACTCGGCAAGGGGCACTCGGGTAAAGCTGCTGACCTGACC 8016  
QY 511 G 511  
DB 8017 G 8017

Search completed: December 4, 2006, 18:41:29  
Job time : 142 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 17:46:54 ; Search time 360 Seconds  
(without alignments)  
9993.556 Million cell updates/sec

Title: US-10-507-132-1

Perfect score: 516  
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Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*

- 1: geneeqn1980s:\*
- 2: geneeqn190s:\*
- 3: geneeqn2000s:\*
- 4: geneeqn2001as:\*
- 5: geneeqn2001bs:\*
- 6: geneeqn2002as:\*
- 7: geneeqn2002bs:\*
- 8: geneeqn2003as:\*
- 9: geneeqn2003bs:\*
- 10: geneeqn2003cs:\*
- 11: geneeqn2003ds:\*
- 12: geneeqn2004as:\*
- 13: geneeqn2004bs:\*
- 14: geneeqn2005s:\*
- 15: geneeqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516	100.0	516	10	ADCI6590 Scytalone
2	514.4	99.7	516	10	ADCI6592 Scytalone
3	514.4	99.7	600	10	ADCI6602 Scytalone
4	514.4	99.7	610	10	ADCI6603 Scytalone
5	53.4	10.3	113193	8	AAAD54645
6	53	10.3	7407	8	ACA42281
7	53	10.3	7407	9	ACCS9398
8	52.4	10.2	4451	2	AAV23288
9	52	10.1	1336	13	ADX09839
10	52	10.1	1394	13	ADX54272
11	52	10.1	1437	13	ADX55034
12	52	10.1	1598	13	ADX54271
13	52	10.1	1821	2	AAO99366
14	52	10.1	1821	3	AAV84068
15	52	10.1	1821	3	AAAC61406
16	51.6	10.0	1395	11	ACI29101
17	51.4	10.0	1272	2	AAK61296
18	51.4	10.0	2189	10	AAO63718

19	51.4	10.0	2346	4	AAAD10219	AAAD10219	Chimeric
20	51.4	10.0	2346	4	AAAD10217	AAAD10217	Chimeric
21	51.4	10.0	2346	4	AAAD10216	AAAD10216	Chimeric
22	51.4	10.0	2346	9	ACD26378	ACD26378	DNA encod
23	51.4	10.0	2346	9	ACD26379	ACD26379	DNA encod
24	51.4	10.0	2346	9	ACD26381	ACD26381	DNA encod
25	51.4	10.0	2346	10	AAAD65095	AAAD65095	Cre:FLPm
26	51.4	10.0	2346	10	AAAD65097	AAAD65097	Cre:FLPm
27	51.4	10.0	2346	10	AAAD65094	AAAD65094	Cre:FLPm
28	51.4	10.0	4131	11	ABD15169	ABD15169	Pseudomon
29	51.4	10.0	8211	11	ABD15052	ABD15052	Pseudomon
30	50.8	9.8	561	11	ABD14968	ABD14968	Pseudomon
31	50.6	9.8	1062	14	ACL71569	ACL71569	M. xanthu
32	50.6	9.8	6715	14	ACL64355	ACL64355	M. xanthu
33	50.4	9.8	1238	13	ADX31428	ADX31428	Plant ful
34	50.4	9.8	1349	13	ADX33784	ADX33784	Plant ful
35	50.4	9.8	1352	13	ADX10015	ADX10015	Plant ful
36	50.4	9.8	1511	13	ADX09781	ADX09781	Plant ful
37	50.2	9.7	1177	13	ADX34980	ADX34980	Plant ful
38	50	9.7	585	11	ACL34434	ACL34434	Rice abio
39	50	9.7	1821	3	AACS5846	AACS5846	Mitomycin
40	50	9.7	1821	10	ADE10327	ADE10327	S. lavend
41	50	9.7	18034	3	AACS5841	AACS5841	Complete
42	50	9.7	18034	10	ADE10260	ADE10260	S. lavend
43	49.8	9.7	1388	13	ADX09721	ADX09721	Plant ful
44	49.4	9.6	980	4	AB115123	AB115123	Drosophila
45	49.4	9.6	1572	12	ADM99120	ADM99120	Bacterial

## ALIGNMENTS

RESULT 1	ADCI6590	standard; DNA; 516 BP.
ID	ADCI6590	
XX	ADCI6590;	
AC	18-DEC-2003	(first entry)
XX		
DE	Scytalone dehydrogenase gene #SEQ ID 1.	
XX		
KM	Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;	
KM	gene; db.	
XX		
OS	Magnaporthe grisea.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..516
FT		/*tag= a
FT		/product= "scytalone dehydrogenase"
FT		/partial
FT		/note= "no stop codon"
XX		
PN	WO200307628-A1.	
XX		
PD	18-SEP-2003.	
XX		
PF	24-FEB-2003; 2003WO-JP001980.	
XX		
PR	12-MAR-2002; 2002JP-0006955.	
XX		
PA	(TSUB) KUMIAI CHEM IND CO LTD.	
XX		
PI	Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;	
XX		
DR	WPI; 2003-748394/70.	
XX	P-PSDB; ADCI6591.	
PT	Gene encoding for scytalone dehydrogenase (SCDH), useful for screening	
XX	for SCDH inhibitors and evaluating sensitivity to them.	
PS	Example 2; SEQ ID NO 1; 50pp; Japanese.	

XX The invention relates to a gene encoding scytalone dehydrogenase (SCDH),  
CC that functions in the presence of an inhibitor, comprising an optionally  
CC mutated, defined amino acid sequence given in the specification. Also  
CC disclosed is a method for evaluating rice blast fungus (Pyricularia  
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase  
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and  
CC evaluating sensitivity to them. The current sequence represents the  
CC scytalone dehydrogenase gene sequence.

XX  
SQ Sequence 516 BP; 119 A; 151 C; 155 G; 91 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 10; Length 516;  
Best Local Similarity 100.0%; Pred. No. 9,5e-108;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTTGCCAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60  
DB 1 ATGGGTTGCCAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60  
QY 61 ACTTGCGCTATGATGAGGCGAGACAGCTTCACTCCAGAGACTGGGATGAGGCTGCGAAG 120  
DB 61 ACTTGCGCTATGATGAGGCGAGACAGCTTCACTCCAGAGACTGGGATGAGGCTGCGAAG 120  
QY 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
DB 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
QY 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
DB 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
QY 181 ATGCCGCGCGAGAGTTCTGCGCATGCTCGAGCAAGTCTGGGCGACCCACCC 240  
DB 181 ATGCCGCGCGAGAGTTCTGCGCATGCTCGAGCAAGTCTGGGCGACCCACCC 240  
QY 241 CTCGCGACGACAGCTTCACTGCGGCGAGCGGCTGGGAGAGGTGTCGAGACGAGTTC 300  
DB 241 CTCGCGACGACAGCTTCACTGCGGCGAGCGGCTGGGAGAGGTGTCGAGACGAGTTC 300  
QY 301 ATCGGCTACCAACAGCTGCGGCTCCGCAACAGAGGTAACAAGACACCATGAAGAG 360  
DB 301 ATCGGCTACCAACAGCTGCGGCTCCGCAACAGAGGTAACAAGACACCATGAAGAG 360  
QY 361 GTCACCATGAAGGGCGACGCCCACTGGGCAAACTTCTGATCAAGAAAGATCGACG 420  
DB 361 GTCACCATGAAGGGCGACGCCCACTGGGCAAACTTCTGATCAAGAAAGATCGACG 420  
QY 421 GTCGGAAGTTGCCCGGCTCAAGCCCATATCCGCTGGGGCGAAGTTGCACTTTGACAG 480  
DB 421 GTCGGAAGTTGCCCGGCTCAAGCCCATATCCGCTGGGGCGAAGTTGCACTTTGACAG 480  
QY 481 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAAA 516  
DB 481 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAAA 516

## RESULT 2

ADCI6592  
ID ADCI6592 standard; DNA; 516 BP.

XX  
AC ADCI6592;

XX  
DT 18-DEC-2003 (first entry)

XX  
DE Scytalone dehydrogenase gene #SEQ ID 3.

XX  
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;

XX  
KM gene; de.

XX  
OS Magnaporthe grisea.

XX  
FH Key Location/Qualifiers

XX  
CDS 1..516

XX  
FT /tag= a  
FT /product= "scytalone dehydrogenase"  
FT /partial

PT /note= "no stop codon"

XX  
PN MO2003076628-A1.

XX  
PD 18-SEP-2003.

XX  
PF 24-FEB-2003; 2003WO-JP001980.

XX  
PR 12-MAR-2002; 2002JP-0006955.

XX  
PA (TSUB ) KOMIAT CHEM IND CO LTD.

XX  
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

XX  
DR MPI; 2003-748394/70.

XX  
P-PSDB; ADCI6593.

PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening  
for SCDH inhibitors and evaluating sensitivity to them.

PS Example 2; SEQ ID NO 3; 50pp; Japanese.

CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),  
CC that functions in the presence of an inhibitor, comprising an optionally  
CC mutated, defined amino acid sequence given in the specification. Also  
CC disclosed is a method for evaluating rice blast fungus (Pyricularia  
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase  
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and  
CC evaluating sensitivity to them. The current sequence represents the  
CC scytalone dehydrogenase gene sequence.

SQ Sequence 516 BP; 118 A; 151 C; 156 G; 91 T; 0 U; 0 Other;

Query Match 99.7%; Score 514.4; DB 10; Length 516;  
Best Local Similarity 99.8%; Pred. No. 2.2e-107;  
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGTTGCCAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60  
DB 1 ATGGGTTGCCAAGTTCAAAAGAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 60  
QY 61 ACTTGCGCTATGATGAGGCGAGACAGCTTCACTCCAGAGACTGGGATGAGGCTGCGAAG 120  
DB 61 ACTTGCGCTATGATGAGGCGAGACAGCTTCACTCCAGAGACTGGGATGAGGCTGCGAAG 120  
QY 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
DB 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
QY 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
DB 121 GTCATTGCGCCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
QY 181 ATGCCGCGCGAGAGTTCTGCGCATGCTCGAGCAAGTCTGGGCGACCCACCC 240  
DB 181 ATGCCGCGCGAGAGTTCTGCGCATGCTCGAGCAAGTCTGGGCGACCCACCC 240  
QY 241 CTCGCGACGACAGCTTCACTGCGGCGAGCGGCTGGGAGAGGTGTCGAGACGAGTTC 300  
DB 241 CTCGCGACGACAGCTTCACTGCGGCGAGCGGCTGGGAGAGGTGTCGAGACGAGTTC 300  
QY 301 ATCGGCTACCAACAGCTGCGGCTCCGCAACAGAGGTAACAAGACACCATGAAGAG 360  
DB 301 ATCGGCTACCAACAGCTGCGGCTCCGCAACAGAGGTAACAAGACACCATGAAGAG 360  
QY 361 GTCACCATGAAGGGCGACGCCCACTGGGCAAACTTCTGATCAAGAAAGATCGACG 420  
DB 361 GTCACCATGAAGGGCGACGCCCACTGGGCAAACTTCTGATCAAGAAAGATCGACG 420  
QY 421 GTCGGAAGTTGCCCGGCTCAAGCCCATATCCGCTGGGGCGAAGTTGCACTTTGACAG 480  
DB 421 GTCGGAAGTTGCCCGGCTCAAGCCCATATCCGCTGGGGCGAAGTTGCACTTTGACAG 480  
QY 481 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAAA 516  
DB 481 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAAA 516

## RESULT 3

ADCl6602 standard; DNA; 600 BP.

ADCl6602;

18-DEC-2003 (first entry)

Scytalone dehydrogenase DNA #1.

Scytalone dehydrogenase, SCDH; rice blast fungus; enzyme; inhibitor; gene; ds.

Magnaporthe grisea.

MO2003076628-A1.

18-SEP-2003.

24-FEB-2003; 2003MO-JP001980.

12-MAR-2002; 2002JP-00066955.

(TSUB ) KUMIAI CHEM IND CO LTD.

Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

WPI; 2003-748394/70.

Gene encoding for scytalone dehydrogenase (SCDH), useful for screening for SCDH inhibitors and evaluating sensitivity to them.

Example 2; Fig 3; 50bp; Japanese.

The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is given in ADCl6590.

Sequence 600 BP; 146 A; 176 C; 168 G; 110 T; 0 U; 0 Other;

Query Match 99.7%; Score 514.4; DB 10; Length 600;

Best Local Similarity 99.8%; Pred. No. 2.2e-107;

Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGGTTCCGAATTCAAAAGACGATGATTAACCTTCTCAAGACTACCTGGGCTCATG 60

81 ATGGGTTCCGAATTCAAAAGACGATGATTAACCTTCTCAAGACTACCTGGGCTCATG 140

61 ACTTGCTCATAGTGGGCGACAGCTACGACTCCAAAGACTGGGTAAGGCTGGCAAG 120

141 ACTTGCTCATAGTGGGCGACAGCTACGACTCCAAAGACTGGGTAAGGCTGGCAAG 200

121 GTCATTGCGCTACTCTGGCGATTGACTACCGCTCTTCTCGACAAGCTTGGAGGCA 180

201 GTCATTGCGCTACTCTGGCGATTGACTACCGCTCTTCTCGACAAGCTTGGAGGCA 260

181 ATGGCGCGCGAGAGTTCTCGCGCATGCTTCGAGCAAGATGCTGGGCGACCCGACC 240

261 ATGCGCGCGCGAGAGTTCTCGCGCATGCTTCGAGCAAGATGCTGGGCGACCCGACC 320

241 CTCGCGACGAGCACTTCATCGCGCGACGCGCTGGGAGAAAGTGTCCGAGACGAGTC 300

321 CTCGCGACGAGCACTTCATCGCGCGACGCGCTGGGAGAAAGTGTCCGAGACGAGTC 380

301 ATGGGCTACCAAGCTGCGCGTCCGCGACCAAGGTAACAAGACCAACATGAAGAG 360

DB 381 ATCGGCTACCAAGCTGCGCGTCCGCGACGAGGTAACAAGACCAACATGAAGAG 440

QY 361 GTCACCATGAGAGGCGACGCGCATCGGCAACCTTCACTGTTACAGAAAGATCGAGCG 420

DB 441 GTCACCATGAGAGGCGACGCGCATCGGCAACCTTCACTGTTACAGAAAGATCGAGCG 500

QY 421 GTCTGGAAGTTGCGCGGCTCAAGCCCGATATCCGCTGGGCGAGTTGCACTTTGACAG 480

DB 501 GTCTGGAAGTTGCGCGGCTCAAGCCCGATATCCGCTGGGCGAGTTGCACTTTGACAG 560

QY 481 ATCTTTGAGACGACGAGCGGAGACCTTTGGCGCAAA 516

DB 561 ATCTTTGAGACGACGAGCGGAGACCTTTGGCGCAAA 596

## RESULT 4

ADCl6603 standard; DNA; 610 BP.

ADCl6603;

18-DEC-2003 (first entry)

Scytalone dehydrogenase DNA #2.

Scytalone dehydrogenase, SCDH; rice blast fungus; enzyme; inhibitor; gene; ds.

Magnaporthe grisea.

MO2003076628-A1.

18-SEP-2003.

24-FEB-2003; 2003MO-JP001980.

12-MAR-2002; 2002JP-00066955.

(TSUB ) KUMIAI CHEM IND CO LTD.

Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

WPI; 2003-748394/70.

Gene encoding for scytalone dehydrogenase (SCDH), useful for screening for SCDH inhibitors and evaluating sensitivity to them.

Example 2; Fig 4; 50bp; Japanese.

The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is given in ADCl6592.

Sequence 610 BP; 148 A; 179 C; 170 G; 113 T; 0 U; 0 Other;

Query Match 99.7%; Score 514.4; DB 10; Length 610;

Best Local Similarity 99.8%; Pred. No. 2.3e-107;

Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGGTTCCGAATTCAAAAGACGATGATTAACCTTCTCAAGACTACCTGGGCTCATG 60

81 ATGGGTTCCGAATTCAAAAGACGATGATTAACCTTCTCAAGACTACCTGGGCTCATG 140

61 ACTTGCTCATAGTGGGCGACAGCTACGACTCCAAAGACTGGGTAAGGCTGGCAAG 120

141 ACTTGCTCATAGTGGGCGACAGCTACGACTCCAAAGACTGGGTAAGGCTGGCAAG 200



OY 121 GTGATTCGCGCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 180  
 FT |||||  
 Db 201 GTGATTCGCGCTACTCTGCGCATTTGACTACCGCTCTCTCGACAAAGCTCTGGAGGCA 260  
 FT |||||  
 OY 181 ATGCCGCGCGAGAGTTGCTGCGCATGCTCTGACGACAAAGATGCTGGCGCAACCCACC 240  
 FT |||||  
 Db 261 ATGCCGCGCGAGAGTTGCTGCGCATGCTCTGACGACAAAGATGCTGGCGCAACCCACC 320  
 FT |||||  
 OY 241 CTCGCGACGACAGCTTCAATCGGCGGACGCGCTGGGAGAGGTTCCGAGGACGAGTTC 300  
 FT |||||  
 Db 321 CTCGCGACGACAGCTTCAATCGGCGGACGCGCTGGGAGAGGTTCCGAGGACGAGTTC 380  
 FT |||||  
 OY 301 ATCGGCTACCAACAGCTGCGCGCTCCGCAACAAGGTAACAAGACCAACAATGAAGAG 360  
 FT |||||  
 Db 381 ATCGGCTACCAACAGCTGCGCGCTCCGCAACAAGGTAACAAGACCAACAATGAAGAG 440  
 FT |||||  
 OY 361 GTGACCATGAAGGGCCAGCGCCCACTGCGAAACCTTCACTGGTAACAAGATCGAGGCG 420  
 FT |||||  
 Db 441 GTGACCATGAAGGGCCAGCGCCCACTGCGAAACCTTCACTGGTAACAAGATCGAGGCG 500  
 FT |||||  
 OY 421 GTCTGGAAGTTGCGCGCGCTCAAGCCCGATATCCGCTGGGCGAGTTGACTTGAACAG 480  
 FT |||||  
 Db 501 GTCTGGAAGTTGCGCGCGCTCAAGCCCGATATCCGCTGGGCGAGTTGACTTGAACAG 560  
 FT |||||  
 OY 481 ATCTTTGAGACGCGACGCGGAGACCTTTGGCGACAAA 516  
 FT |||||  
 Db 561 ATCTTTGAGACGCGACGCGGAGACCTTTGGCGACAAA 596  
 FT |||||

RESULT 5  
 AAD54645  
 ID AAD54645 standard; DNA; 113193 BP.

AC AAD54645;  
 XX  
 XX 26-JUN-2003 (first entry)  
 DT  
 XX Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.  
 DE  
 XX Polyene; antibiotic; amphotericin; amph; polyketide; enzyme; gene; ds.  
 KM  
 XX Streptomyces nodosus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH complement(4..1824)  
 FT /tag= a  
 FT /product= "ABC transporter encoded by S. nodosus amphg  
 FT gene"  
 FT CDS  
 FT /tag= b  
 FT /product= "ABC transporter encoded by S. nodosus amphH  
 FT gene"  
 FT CDS  
 FT /tag= c  
 FT /product= "GDP-mannose dehydratase encoded by S. nodosus  
 FT amphDIII gene"  
 FT CDS  
 FT /tag= d  
 FT /product= "Polyketide synthase multienzyme housing  
 FT extension modules 9, 10, 11, 12, 13 and 14 encoded by S.  
 FT CDS  
 FT /tag= e  
 FT /product= "Polyketide synthase multienzyme housing  
 FT extension modules 15, 16 and 17 encoded by S. nodosus  
 FT amphU gene"  
 FT CDS  
 FT /tag= f  
 FT /product= "Polyketide synthase multienzyme housing  
 FT extension modules 18 and thioesterase encoded by S.  
 FT CDS  
 FT /tag= g  
 FT /product= "Polyketide synthase multienzyme housing  
 FT extension modules 18 and thioesterase encoded by S.  
 FT CDS  
 FT /tag= g

FT /product= "Cytochrome P450 encoded by S. nodosus amphL  
 FT gene"  
 FT CDS  
 FT /tag= h  
 FT /product= "ORF1, hypothetical protein"  
 FT complement(58756..59610)  
 FT CDS  
 FT /tag= i  
 FT /product= "ORF2, hypothetical protein"  
 FT 59869..61470  
 FT CDS  
 FT /tag= j  
 FT /product= "ORF3, hypothetical protein"  
 FT /transl\_except= (pos:59869..59871, aa:Met)  
 FT CDS  
 FT /tag= k  
 FT /product= "Ferredoxin encoded by S. nodosus amphM gene"  
 FT complement(62051..63250)  
 FT CDS  
 FT /tag= l  
 FT /product= "Cytochrome P450 encoded by S. nodosus amphN  
 FT gene"  
 FT CDS  
 FT /tag= m  
 FT /product= "NDP-sugar aminotransferase encoded by S.  
 FT nodosus amphDII gene"  
 FT CDS  
 FT /tag= n  
 FT /product= "Glycosyl transferase encoded by S. nodosus  
 FT amphDI gene"  
 FT /transl\_except= (pos:65773..65775, aa:Met)  
 FT CDS  
 FT /tag= o  
 FT /product= "Polyketide synthase multienzyme housing  
 FT loading module encoded by S. nodosus amphA gene"  
 FT 70366..79938  
 FT CDS  
 FT /tag= p  
 FT /product= "Polyketide synthase multienzyme housing  
 FT extension modules 1 and 2 encoded by S. nodosus by amphB  
 FT gene"  
 FT CDS  
 FT /tag= q  
 FT /product= "Polyketide synthase multienzyme housing  
 FT extension modules 3, 4, 5, 6, 7 and 8 encoded by S.  
 FT nodosus by amphC gene"  
 FT  
 XX WO200297082-A2.  
 PN  
 XX  
 XX 05-DEC-2002.  
 PD  
 XX  
 XX 27-MAY-2002; 2002WO-1E000071.  
 PF  
 XX  
 XX 31-MAY-2001; 2001IE-00000527.  
 PR  
 XX  
 XX (UYDU-) UNIV COLLEGE DUBLIN.  
 PA  
 XX  
 XX Caffrey JP;  
 PI  
 XX  
 XX WPI; 2003-201271/19.  
 DR P-PSDB; AAE36116, AAE36117, AAE36118, AAE36119, AAE36120, AAE36121,  
 DR AAE36122, AAE36123, AAE36124, AAE36125, AAE36126, AAE36127, AAE36128,  
 DR AAE36129, AAE36130, AAE36131, AAE36132.  
 XX  
 XX Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, useful  
 PT for preparing amphotericin derivative or analog antibiotic agent with  
 PT altered properties, in biosynthesis of polyketide other than  
 PT amphotericin.  
 XX  
 XX Claim 1, Page 52-114; 276pp; English.  
 PS  
 XX  
 XX The invention relates to the gene cluster encoding the polyketides  
 CC responsible for the biosynthesis of the polyene antibiotic amphotericin  
 CC (amph) of Streptomyces nodosus. Polynucleotides of the invention are  
 CC useful for preparing amphotericin derivatives or analogue antibiotic  
 CC agents with altered properties and in the biosynthesis of polyketides  
 CC other than amphotericin. amphDII, amphDI or amphDI mutants are useful





ACC59398  
 ID ACC59398 standard; DNA; 7407 BP.  
 AC ACC59398;  
 XX  
 XX  
 DT 28-AUG-2003 (first entry)  
 DE Microbial resistance gene PA1874 coding sequence.  
 XX  
 XX Biofilm; microbial resistance; gene; ds.  
 KW  
 XX  
 OS Unidentified.  
 XX  
 XX WO2003041483-A2.  
 PN  
 XX  
 PD 22-MAY-2003.  
 XX  
 XX 18-SEP-2002; 2002WO-US029565.  
 PR 18-SEP-2001; 2001US-0323241P.  
 XX  
 XX (DART-) DARTMOUTH COLLEGE.  
 PA  
 XX O'toole GA, Mah T;  
 PI  
 XX WPI; 2003-468567/44.  
 DR P-PSDB; ABP59933.  
 XX  
 XX  
 PT Identifying modulators of microbial resistance of organisms in biofilm,  
 PT e.g. inhibitor of biofilm formation, by employing expression controls, or  
 PT efflux pumps containing polypeptides, of genes associated with biofilm  
 resistance.  
 PS  
 XX Disclosure; Fig 7; 102pp; English.  
 XX  
 CC The present invention relates to a method of identifying a compound  
 CC capable of altering the sensitivity of a microorganism to an  
 CC antimicrobial agent by employing efflux pumps comprising polypeptides  
 CC encoded by the following genes: PA1874, PA4142, PA2389, PA1876, PA4143,  
 CC PA2390 or PA1163. The method is useful for identifying modulators of  
 CC microbial resistance of an organism in a biofilm. The methods are also  
 CC useful for identifying genes that encode proteins that play a role in  
 CC biofilm resistance. The method is particularly useful for screening  
 CC compounds or discovering compositions that will inhibit biofilm formation  
 CC and overcome their resistance mechanisms. These methods are particularly  
 CC useful in medical, industrial or natural settings, where formation of  
 CC biofilms can have serious negative consequences and result in high costs  
 CC both in human health and economic terms. The present invention is a  
 CC coding/control sequence shown in the exemplification of the invention  
 CC  
 SQ Sequence 7407 BP; 1387 A; 2763 C; 2378 G; 879 T; 0 U; 0 Other;  
 XX  
 Query Match 10.3%; Score 53; DB 9; Length 7407;  
 Best Local Similarity 48.5%; Pred. No. 0.026;  
 Matches 146; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

211 TCAGAGCAAGCATGCTGGGCGAAGCCACCTCCGACGACGACCTTCATTCGGCGGACG 270  
 |||||  
 DB 6913 TCCGGGAGAGAGCTGCTGTCCTGGCGCAACGGCAGTTCCGAGACATCAACGGCGGCGAC 6972  
 |||||  
 QY 271 CGCTGGAGAGAGTGTCCGAGACGAGTTCATGCTACCAACGCTGCGCGTCCGCGAC 330  
 |||||  
 DB 6973 GGGAGGACCTGATCTTCAACGTGGGACCGGCGATCACTGTGTGCGCGGCAACGGCAAC 7032  
 |||||  
 QY 331 CAGAGGTACAGAGACCAACCATGAAGAGGTGCATGAAGGGGCAACGCCACTCGGGA 390  
 |||||  
 DB 7033 GACACCATCCAGATCCGAGACGATTCGTGATCATGATGCGGCGCGGCTTCGAC 7092  
 |||||  
 QY 391 AACCTTCACTGTATCAAGAGATGACGGCGTCTGGAAGTTCCGCGCTCAAGCCCGAT 450  
 |||||  
 DB 7093 ACCCTGTCTGTGCGCAACGGCATCGACTGATCAAGCCGCTCGGCTGGCAAGCTC 7152  
 |||||  
 QY 451 ATCCGCTGGGCGAGTTGCACTTTGAACAGATCTTTGAGAGCGAGCGGAGACCTTTGGC 510  
 |||||

DB 7153 AGCAACTCGAGCGCATGACTCGGCAAGGCGCATTCGGGTAGCGTCTGACCTGACC 7212  
 |||||  
 QY 511 G 511  
 |||||  
 DB 7213 G 7213  
 |||||

RESULT 8  
 AAV23288  
 ID AAV23288 standard; DNA; 4451 BP.  
 AC AAV23288;  
 XX  
 XX  
 DT 17-AUG-1998 (first entry)  
 DE Synthetic human Factor-VIII gene lacking central B domain.  
 XX  
 XX Factor-VIII; blood clotting; human; synthetic gene; codon usage; ss.  
 KW  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO9812207-A1.  
 PN  
 XX  
 XX 26-MAR-1998.  
 PD  
 XX  
 XX 18-SEP-1997; 97MO-US016639.  
 PF  
 XX 20-SEP-1996; 96US-00717294.  
 PR  
 XX (GENO ) GEN HOSPITAL CORP.  
 PA  
 XX  
 XX Seed B, Haas J;  
 PI  
 XX  
 XX WPI; 1998-217200/19.  
 DR  
 XX  
 XX New synthetic eukaryotic gene(s) - in which non-preferred or less  
 PT preferred codon(s) are replaced to provide high level expression in  
 PT mammalian cell(s).  
 PS  
 XX Claim 20; Fig 13; 92pp; English.  
 XX  
 CC This synthetic gene codes for a human Factor-VIII protein that lacks the  
 CC central B domain (amino acids 760-1639) of the native protein. In the  
 CC synthetic gene, non-preferred or less preferred codons of the native gene  
 CC (see AAV23339) are replaced by codons favored by highly expressed human  
 CC genes to provide high-level expression in mammalian cells. The synthetic  
 CC gene was assembled from 29 pairs of oligonucleotides (see AAV23340-97)  
 CC which served as PCR templates. Synthetic genes of the invention (see also  
 CC AAV23289-91) are used for production of recombinant proteins in mammalian  
 CC cells at levels of at least 500% of those obtained using the natural  
 CC genes. They can also be used in gene therapy. An expression vector  
 CC comprising a synthetic gene and a mammalian cell harboring a synthetic  
 CC gene are also claimed  
 CC  
 SQ Sequence 4451 BP; 972 A; 1568 C; 1234 G; 677 T; 0 U; 0 Other;  
 XX  
 Query Match 10.2%; Score 52.4; DB 2; Length 4451;  
 Best Local Similarity 52.8%; Pred. No. 0.033;  
 Matches 113; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

230 GCGACCCCACTCCGACGACGACCTTCATTCGCGGACGCGCTGGGAGAAGTGTCCG 289  
 |||||  
 DB 2323 GCGACCCCAAGCGGTGACGAGAGCTTCAACGCCACCCCGCTGTGAAGGCCCAAC 2382  
 |||||  
 QY 290 AGAGAGAGGTATCGGCTTACCAACAGTTCGCGCTCCGACCAAGAGTACAGACACCA 349  
 |||||  
 DB 2383 AGCGGAGATCACCCGACCAACCTTGCAAGCGACAGAGAGATGATCTACGACGACA 2442  
 |||||  
 QY 350 CCATGAAGAGGTGACCATGAAGGGGCCAGCCCACTCGCAAACTTCACTGTGTAACA 409  
 |||||  
 DB 2443 CCATGAGCGTGAATGAAGAGAGACTTTCGATCTTACGACGAGGACGAAACAGAA 2502  
 |||||

QY 410 AGATCGACGGCGCTGTGAAGTTCCCGGCTCA 443  
DB 2503 GCCCGCGCTCTTCCAAAAGAAAACCCGCCACTA 2536

RESULT 9  
ADX09839  
ID ADX09839 standard; cDNA; 1336 BP.

AC ADX09839;

DT 21-APR-2005 (first entry)

DE Plant full length insert polynucleotide seqid 4414.

KM plant protectant; plant growth regulant; gene therapy; plant;  
KM recombinant DNA construct; physical array; plant breeding marker;  
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KM extreme osmotic condition; pathogen tolerance; pest tolerance;  
KM growth rate; cell cycle pathway; disease resistance;  
KM galactomannan production; lignin production; plant growth regulator;  
KM yield; plant growth; plant development; seed oil; protein yield;  
KM protein content; gene; ss.

OS Unidentified.

PN US2004034888-A1.

PD 19-FEB-2004.

PF 28-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

XX (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TABA/) TABASKA J E.

PA (CAOV/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

DR WPI; 2004-180133/17.

PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.

PS Claim 1; SEQ ID NO 4414; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.

SQ Sequence 1336 BP; 331 A; 405 C; 358 G; 242 T; 0 U; 0 Other;

Query Match 10.1%; Score 52; DB 13; Length 1336;  
Best Local Similarity 47.1%; Pred. No. 0.034;  
Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 133 ACTCTGCGCATTTAGTACCGCTCTCTCTGACAACTCTGGAGAGCAATGCCGCGAG 192

DB 372 ATTCTACGCGTGGAATPACTGTGTCATCACCGGCAAGGAAACCTTAGACGGGAGGCCCA 431

QY 193 GAGTTCTGCGCATGTGCTCGAGCAAGCATGCTGGCGGACCCACCTTCGCGACGCA 252

DB 432 GCCGTGTGAGCAAGAACTCTGCAACCAAGAAATGATGATGCAAGATCCTTCCCACTCG 491

QY 253 CACTTCATGCGGGGAGCAGCGGCTGGGAGAGGTGTCGAGAGAGATGATTCGGCTAAC 312

DB 492 CTGTGATGATGACTTGTGTGAACAACGGGGAGGTGTCGGGGTACGCTGCTCAATCCAA 551

QY 313 CAGCTGCGCGCTCCGACAGAGTACAGAGACACCATGAAAGAGGTACACATGAAG 372

DB 552 TTCTTCCATATGAACATGTACCGGTGCAAGCATGTGATCAAGACGTGACCGTGAAG 611

QY 373 GGCCACGCGCCACTCGGCAAACTTCACTGTGTAACAAGATGACGCGCTTGGAAATTG 432

DB 612 GCGCCCGGGGAGACGCCCAACACGAGTGGCATTCACATGCGGAGACTATCCGGATCAC 671

QY 433 GCGGCTCAAGCCGATATCCGCTGGGGCGAGTTCGACT 472

DB 672 ATCACCACACCGTCATTTGGCGTGGCGACGACTGATCT 711

RESULT 10

ADX54272

ID ADX54272 standard; cDNA; 1394 BP.

XX ADX54272;

DT 21-APR-2005 (first entry)

DE Plant full length insert polynucleotide seqid 29012.

XX plant protectant; plant growth regulant; gene therapy; plant;  
XX recombinant DNA construct; physical array; plant breeding marker;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
XX extreme osmotic condition; pathogen tolerance; pest tolerance;  
XX growth rate; cell cycle pathway; disease resistance;  
XX galactomannan production; lignin production; plant growth regulator;  
XX yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.

OS Unidentified.

PN US2004034888-A1.

PD 19-FEB-2004.

PF 28-APR-2003; 2003US-00425114.

PR 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

XX (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.

PA (SCRE/) SCREEN S E.

PA (TABA/) TABASKA J E.

PA (CAOV/) CAO Y.

PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

DR WPI; 2004-180133/17.

PT New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.

PS Claim 1; SEQ ID NO 29012; 15bp; English.

XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.

XX  
XX Sequence 1394 BP; 349 A; 418 C; 365 G; 262 T; 0 U; 0 Other;

XX  
XX Query Match 10.1%; Score 52; DB 13; Length 1394;

XX  
XX Best Local Similarity 47.1%; Pred. No. 0.034; Mismatches 180; Indels 0; Gaps 0;

XX  
XX Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 133 ACTCTGCGGATTGACTACCGCTCTCTCTCGACAGAGCTCGGAGGCAATGCCGCGGAG 192  
DB 361 ATTCTACCGGTGGATATACCTGGTCAACCGGAGAGAAACCTTGACGGGCGGCGCA 420  
QY 193 GAGTTGCTGGGAGTGTCTCGAGCAAGCATGCTGGGAGCCCACTTCGCGACGCG 252  
DB 421 GCTGTGTGAGAGAAAGTCTCTGCAAGAAAGTCAAGATCTCTTCCCAACTCG 480  
QY 253 CACTTCATCGGGGGGCGCGGCTGGGAGAAAGTGTCCGAGAGAGAGTCAATCGGCTACAC 312  
DB 481 CTGTGTATGATCTCTCTGAAACAAGGAGGTGTCCGAGGTCACTGCTCAACTCCAG 540  
QY 313 CAGCTGCGGTCCCGACCAAGAGTACAGAGCAACCATGAGAGGCTCACTGAAG 372  
DB 541 TTCTTCCATGATAGATGATACCGGTGCAAGGATCTGATCAAGAGACCTGACCGTGAAG 600  
QY 373 GGGCAGCGCCACTCGGCAAACTTCACTGCTACAGAGATGACGCGCTTGGAAAGTTG 432  
DB 601 GCGCCCGGGGAGACGCGCCCAACAGGATGCGATCCATGAGGCGGCACTCATCCGCGATCAC 660  
QY 433 GCGGCGCTCAAGCGCGATATCGCTGGGGGCGAGTTGCACT 472  
DB 661 ATTCACCAACCGCTCATTTGGCGGTGGGAGACTGATCT 700

RESULT 11

ADX35034  
ID ADX35034 standard; cDNA; 1437 BP.

XX  
XX ADX35034;

XX  
XX 21-APR-2005 (first entry)

XX  
XX Plant full length insert polynucleotide seqid 17854.

XX  
XX plant protectant; plant growth regulator; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;

KW protein content; gene; ss.  
XX  
XX Unidentified.

XX  
XX US2004034888-A1.

XX  
XX 19-FEB-2004.

XX  
XX 28-APR-2003; 2003US-00425114.

XX  
XX 06-MAY-1999; 99US-00304517.

XX  
XX 05-NOV-2001; 2001US-00985678.

XX  
XX (LIU/) LIU J.

XX  
XX (ZHOU/) ZHOU Y.

XX  
XX (KOVA/) KOVALIC D K.

XX  
XX (SCRE/) SCREEN S E.

XX  
XX (TAB/) TABASKA J E.

XX  
XX (CAO/) CAO Y.

XX  
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX  
XX WPI; 2004-180133/17.

XX  
XX Claim 1; SEQ ID NO 17854; 15bp; English.

XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.

XX  
XX Sequence 1437 BP; 364 A; 426 C; 375 G; 272 T; 0 U; 0 Other;

XX  
XX Query Match 10.1%; Score 52; DB 13; Length 1437;

XX  
XX Best Local Similarity 47.1%; Pred. No. 0.035; Mismatches 180; Indels 0; Gaps 0;

XX  
XX Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 133 ACTCTGCGGATTGACTACCGCTCTCTCTCGACAGAGCTCGGAGGCAATGCCGCGGAG 192  
DB 379 ATTCTACCGGTGGATATACCTGGTCAACCGGAGAGAAACCTTGACGGGCGGCGCA 438  
QY 193 GAGTTGCTGGGAGTGTCTCGAGCAAGCATGCTGGGAGCCCACTTCGCGACGCG 252  
DB 439 GCTGTGTGAGAGAAAGTCTCTGCAAGAAAGTCAAGATCTCTTCCCAACTCG 498  
QY 253 CACTTCATCGGGGGGCGCGGCTGGGAGAAAGTGTCCGAGAGAGTCAATCGGCTACAC 312  
DB 499 CTGTGTATGATCTCTCTGAAACAAGGAGGTGTCCGAGGTCACTGCTCAACTCCAG 558  
QY 313 CAGCTGCGGTCCCGACCAAGAGTACAGAGCAACCATGAGAGGCTCACTGAAG 372  
DB 559 TTCTTCCATGATAGATGATACCGGTGCAAGGATCTGATCAAGAGACCTGACCGTGAAG 618  
QY 373 GGGCAGCGCCACTCGGCAAACTTCACTGCTACAGAGATGACGCGCTTGGAAAGTTG 432

Db 619 GCCCGCGGAGACGCCCAACGAGATGCGATCCACATGGCGAGCTCATCCGGGATCACC 678  
 QY 433 GCGGCGCTCAAGCCGATATCCGCTGGGGGAGTTGACT 472  
 Db 679 ATCACCACACCGTCATTTGGCGTGGGAGAGCTGCATCT 718

## RESULT 12

ADXS4271  
 ID ADXS4271 standard; cDNA; 1598 BP.

AC ADXS4271;  
 XX

DT 21-APR-2005 (first entry)  
 XX

DE Plant full length insert polynucleotide seqid 29011.  
 XX

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KM recombinant DNA construct; physical array; plant breeding marker;

KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;

KM growth rate; cell cycle pathway; disease resistance;  
 KM galactomannan production; lignin production; plant growth regulator;

KM yield; plant growth; plant development; seed oil; protein yield;  
 KM protein content; gene; ss.

XX Unidentified.  
 OS

XX US2004034888-A1.  
 PN

XX 19-FEB-2004.  
 PD

XX 28-APR-2003; 2003US-00425114.  
 PF

XX 06-MAY-1999; 99US-00304517.  
 PR

XX 05-NOV-2001; 2001US-00985678.  
 PR

XX (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.

PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.

PA (TABAS/) TABASKA J E.  
 PA (CAOY/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 PI

XX MPI; 2004-180133/17.  
 DR

XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.

XX Claim 1; SEQ ID NO 29011; 15pp; English.  
 PS

XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence

CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for

CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in

CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,

CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of

CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert

CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC

CC invention.  
 XX Sequence 1598 BP; 408 A; 453 C; 400 G; 337 T; 0 U; 0 Other;  
 SQ Query Match 10.1%; Score 52; DB 13; Length 1598;  
 Best Local Similarity 47.1%; Pred. No. 0.035;  
 Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 133 ACTCTGCGATGACTGATCAGCGCTCTCTCCGACAGAGCTGAGGAGCATGCGGCGAG 192  
 Db 395 ATCTACGCGTGAATACCTGCTCATCACCAGGAGAACTTGAACGAGGAGGAGGAG 454

QY 193 GAGTTGCTGCGATGCTGCGACAGAGATGCTGGGAGACCCACCTCCGACAGCAG 252  
 Db 455 GCTGTGTGAGAGCAAGAACTCTCCGACAGAGATGAGATGCAAGATCTTCCCACTG 514

QY 253 CACTTCATGCGGCGACGCGCTGGAGAGAGTGTCCGAGAGAGAGTATCGGCTTCCAC 312  
 Db 515 CTGCTGATGACTTGTGTAACACGCGGAGGTGTCCGAGGATCAGCTGCTCAACTCAAG 574

QY 313 CAGTTCGCGTCCCGACAGAGTACAGAGACACCATGAGAGAGTCAACATGAG 372  
 Db 575 TTCTTCCATGAATACATGTACCGGTGCAAGAGATGATCAAGAGCGTGAACGAGC 634

QY 373 GGCACAGCCCACTCGGCAACCTTCACTGTCAAGAGATGACGCGCTTGAAGTTG 432  
 Db 635 GCGCCCGGGAGACGCCCAACAGAGATGATGATGATGATGATGATGATGATGATGAT 694

QY 433 GCGGCGCTCAAGCCGATATTCGCTGGGCGAGTTGACT 472  
 Db 695 ATCACCACACCGTCATTTGGCGTGGCGAGAGCTGATCT 734

XX RESULT 13  
 AAQ9366  
 ID AAQ9366 standard; DNA; 1821 BP.  
 XX

XX AAQ9366;  
 AC

DT 25-MAR-2003 (revised)  
 DT 04-DEC-1995 (first entry)  
 XX

DE S. lividans protease P5-6 gene.  
 XX

KM Protease; metalloendoprotease; tripeptidyl aminopeptidase;  
 KM protease-deficiency; protein secretion; ds.  
 KM

XX Streptomyces lividans.  
 XX

XX Key Location/Qualifiers  
 FH CDS 104..1723  
 FT /\*tag= a  
 FT sig\_peptide 104..244  
 FT /\*tag= b  
 FT mat\_peptide 245..1720  
 FT /\*tag= c  
 FT /product= "P5-6."  
 FT

XX WO9517512-A2.  
 PN

XX 29-JUN-1995.  
 PD

XX 22-DEC-1994; 94WO-US014772.  
 PP

XX 23-DEC-1993; 93US-00173508.  
 PR

XX (CANG-) CANGENE CORP.  
 PA

PI Bartfeld D, Butler MJ, Hadary D, Jenish DL, Krueger TV, Malek LT;  
 PI Walczyk E, Soostmeyer G,  
 XX

XX MPI; 1995-240673/31.  
 DR

XX P-PSDB; AAR80506.  
 DR





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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 17:53:24 / Search time 2492 Seconds  
(without alignments)  
13241.119 Million cell updates/sec

Title: US-10-507-132-1  
Sequence: 1 atgggtcgcgaagttccaaaa.....ggagagaccttgcgcgacaa 516

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues  
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_dl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vl:\*  
11: gb\_ov:\*  
12: gb\_hlg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	514.4	99.7	807 4	AB004741 Magnaporthe
2	251.2	48.7	770 4	AB100172 Bipolaris
3	234.8	45.5	1151 4	COGSCD1 DB6079 Colletotrich
4	219	42.4	1477 4	AF316575 Ophiostom
5	192	37.2	415 4	AY098662 Ophiostom
6	191.8	37.2	1215 4	AY214004 Ceratocys
7	190	36.8	414 4	AY098664 Ophiostom
8	189.4	36.7	414 4	AY098663 Ophiostom
9	187.8	36.4	433 4	AY098658 Ophiostom
10	185.6	36.0	427 4	AY098656 Ophiostom
11	182.6	35.4	424 4	AY098657 Ophiostom
12	182.4	35.3	428 4	AY098659 Ophiostom
13	179.2	34.7	421 4	AY098661 Ophiostom
14	179.2	34.7	423 4	AY098660 Ophiostom
15	179.2	34.7	423 4	AY098666 Ophiostom
16	171.8	33.3	422 4	AY098665 Ophiostom
17	167.8	32.5	573 4	AF575152 Sordaria
18	162.4	31.5	1447 4	AF095042 Aspergillus

19	160	31.0	433 4	AY098655	AY098655 Ceratocys
20	155.8	30.2	432 4	AY098654	AY098654 Ceratocys
21	58.6	11.4	110000 15	BA000030	Continuation (75 o
22	55.2	10.7	110000 15	AP006840	Continuation (17 o
23	54.4	10.5	110000 15	CR55306	Continuation (38 o
24	53.6	10.4	110000 15	CP000251	Continuation (11 o
25	53.4	10.3	110000 4	AP008209	Continuation (140
26	53.4	10.3	113193 2	AF703543	Continuation (140
27	53.4	10.3	113193 15	AF357202	Continuation (140
28	53.4	10.3	161676 4	AC135907	Continuation (140
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33	52.2	10.1	110000 15	AE016825	Continuation (140
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35	52	10.1	1233 4	ZMPGAL17	Continuation (140
36	52	10.1	1562 4	ZMPGAL2	Continuation (140
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38	52	10.1	1820 2	STMSLPD	Continuation (140
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40	52	10.1	1821 2	AR111405	Continuation (140
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43	51.6	10.0	3067 4	AK068793	Continuation (140
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45	51.6	10.0	110000 4	AP008210	Continuation (140

## ALIGNMENTS

RESULT 1	AB004741	807 bp	mRNA	linear	PLN 13-NOV-1998
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DEFINITION	AB004741.1 GI:3798733				
ACCESSION	AB004741				
VERSION	AB004741.1				
KEYWORDS	scytalone dehydratase; sdh1.				
SOURCE	Magnaporthe grisea				
ORGANISM	Magnaporthe grisea				
REFERENCE	Magnaporthe grisea				
AUTHORS	Fukuyama, T., Imanishi, K. and Yamaguchi, I.				
TITLE	1 (sites)				
REFERENCE	Motowaka, T., Imanishi, K. and Yamaguchi, I.				
JOURNAL	CDNA cloning, expression, and mutagenesis of scytalone dehydratase				
PUBMED	needed for pathogenicity of the rice blast fungus, Pyricularia				
AUTHORS	Oryzae				
TITLE	Biosci. Biotechnol. Biochem. 62 (3), 564-566 (1998)				
REFERENCE	9571787				
AUTHORS	2 (bases 1 to 807)				
TITLE	Motowaka, T.				
JOURNAL	Direct Submission				
COMMENT	Submitted (09-JUN-1997) Takayuki Motowaka, The Institute of				
FEATURES	Physical and Chemical Research (RIKEN), Microbial Toxicology Lab.;				
source	2-1 Hitosawa, Wako-shi, Saitama 351-0198, Japan				
1..807	(E-mail:tmotowaka@postman.riken.go.jp, Tel:++81-48-467-9518)				
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whose telomorphic form is unknown"					
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ORIGIN

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YHOLRVPHORVYKDTMTKEVTVMGHAHSAHLHMVKKIDGVWKFPAGLKPDIRMEGFDFDR  
IFEDRETFEGDK"

Query Match 99.7%; Score 514.4; DB 4; Length 807;  
Best Local Similarity 99.8%; Pred. No. 2.2e-118;  
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGTTCCCAAGTTTAAAGAGCGATGATTAACCTTCTCAGACTAAGCTGGGCTCATG 60  
DB 81 ATGGGTTCCCAAGTTTAAAGAGCGATGATTAACCTTCTCAGACTAAGCTGGGCTCATG 140  
QY 61 ACTTGCGTATAGTGGGCGAGACAGCTAGCTCAAGAGACTGGGATAGGCTGGCAAG 120  
DB 141 ACTTGCGTATAGTGGGCGAGACAGCTAGCTCAAGAGACTGGGATAGGCTGGCAAG 200  
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QY 241 CTCGCGACGACAGACTTTCATCGGCGGACGCGCTGGGAGAGAGTGTCCGAGGACGAGTTC 300  
DB 321 CTCGCGACGACAGACTTTCATCGGCGGACGCGCTGGGAGAGAGTGTCCGAGGAGTTC 380  
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DB 381 ATCGGCTACACAGCTGCGCGCTGCCGACACAGAGGTACAGAGACACACATGAAGAG 440  
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DB 441 GTCAACATGAAGGCGGACCGCCACATCGGAGAACTTTCATCGTGAAGAGATTCAGCGGC 500  
QY 421 GTCTGGAAGTTGCGCGGCTCAAGCCGATATCCGCTGGGCGAGATTTCATTTGACAGG 480  
DB 501 GTCTGGAAGTTGCGCGGCTCAAGCCGATATCCGCTGGGCGAGATTTCATTTGACAGG 560  
QY 481 ATCTTTGAGAGCGGACGCGAGACCTTTGGCGACAA 516  
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RESULT 2  
ABI00172 770 bp DNA linear PLN 01-APR-2004  
LOCUS AB100172 Bipolaris oryzae BSCD1gene for scytalone dehydratase, complete cds.  
DEFINITION AB100172  
ACCESSION AB100172  
VERSION AB100172.1 GI:32879676  
KEYWORDS  
SOURCE  
ORGANISM

Bipolaris oryzae  
Bipolaris oryzae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.  
1 Kihara,J., Moriawaki,A., Ueno,M., Tokunaga,T., Arase,S. and Honda,Y.  
Cloning, functional analysis and expression of a scytalone  
dehydratase gene (SCD1) involved in melanin biosynthesis of the  
phytopathogenic fungus Bipolaris oryzae  
Curr. Genet. 45 (4), 197-204 (2004)  
14716498  
2 (bases 1 to 770)  
Kihara,J. and Moriawaki,A.  
Direct Subregion  
Submitted (16-JAN-2003) Junichi Kihara, Shimeane University, Faculty  
of Life and Environmental Science; Nishikawatsuru 1060, Matsue,  
Shimane 690-8504, Japan (E-mail:j-kihara@life.shimane-u.ac.jp,  
Tel:81-852-32-6520, Fax:81-852-32-6597)  
Location/Qualifiers

FEATURES

source

1..770  
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ORIGIN

Query Match 48.7%; Score 251.2; DB 4; Length 770;  
Best Local Similarity 70.8%; Pred. No. 3.1e-52;  
Matches 334; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 41 CAGACTACCTGGGCTCATGACTTGGCTATGAGTGGGCGAGACAGCTACGATCCAAAG 100  
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QY 101 ACTGGGATGAGGTGGGAAAGGTCATTTGGGCTACTCTGCGCATTTGACTTACCGCTCTTC 160  
DB 182 ACTGGGAGGCTGTGGCAAGTGGCGATGCTCGACTCTGAAGTATGACTTACCGGCTCTTCT 241  
QY 161 TCGACAAAGCTTGGAGGCAATGCGGCGGAGAGTGTGGCGCATGTCTTGAAGCAAGC 220  
DB 242 TCGACAAAGTATGGAGGCGATGCGAGGATGATTTGTGGCCATGGGCTCTGAACCTG 301  
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DB 302 CGGTCTGGGCAACCCCTCTCAAGACACAGCACTTATCGGCGGAAACGCGTGGAGA 361  
QY 281 AGGTGCGGAGGACGAGGTCATCGGCTACACACAGCTGGGCTCCGACGAGAGTACA 340  
DB 362 AGACGCGCGAGATGATTAAGGATTAACGAGTACACAGCTGAGTGTCTTACACAGCATACA 421  
QY 341 AGACACACACATGAAGAGGTACCATGAAGGCGCACGCCCATTCGCGAACTTCACT 400  
DB 422 CGGATGAGTCAAGGGCGACGCGTGCAGTCAAGGGCGCACGCCCATTCGCGAACT 481  
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QY 461 GCGAGTTCGACTTTCAGAGATCTTTGAGAGGACGAGGAGACCTTTGGCGGA 512  
DB 542 ACGAGTATGACTTTGACAAAGTGTTTGACAGAGGCGCGAGACGCTGGCGGA 593

RESULT 3

COGSCD1 1151 bp DNA linear PLN 25-DEC-2002  
LOCUS COL1021richum lagenarium DNA for scytalone dehydratase, complete  
DEFINITION cds.  
ACCESSION D86079  
VERSION D86079.1 GI:1395159  
KEYWORDS melanin biosynthesis; scytalone dehydratase.  
SOURCE Colletotrichum lagenarium  
ORGANISM Colletotrichum lagenarium

REFERENCE  
AUTHORS Kubo,Y., Takano,Y., Endo,N., Yasuda,N., Tajima,S. and Furusawa,I.  
TITLES Cloning and structural analysis of the melanin biosynthesis gene  
SCD1 encoding scytalone dehydratase in Colletotrichum lagenarium

JOURNAL Appl. Environ. Microbiol. 62 (12), 4340-4344 (1996)  
PUBMED 8953707  
REFERENCE 2 (bases 1 to 1151)  
AUTHORS Kubo, Y., Takano, Y., Noriko, E., Yasuda, N., Tajima, S. and Furusawa, I.  
TITLE Cloning and structural analysis of the melanin biosynthesis gene encoding scytalone dehydratase of *Colletotrichum lagenarium*  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1151)  
AUTHORS Kubo, Y.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUN-1996) Yasuyuki Kubo, Laboratory of Plant Pathology, Faculty of Agriculture, Kyoto Prefectural University, Shimogamo, Kyoto 606, Japan (E-mail: y\_kubo@kpu.ac.jp, Tel: 075-702-0957, Fax: 075-702-0957)  
FEATURES  
source Location/Qualifiers  
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/organism="Colletotrichum lagenarium"  
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intron 422..488  
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Query Match 45.5%; Score 234.8; DB 4; Length 1151;  
Best Local Similarity 76.7%; Pred. No. 4.2e-48;  
Matches 287; Conservative 0; Mismatches 87; Indels 0; Gaps 0;  
142 ATTGACTACCGCTCTCTCGACGAGCTCTGGAGGACATGCGGCCGAGAGTTCGTC 201  
Db 489 ATGACTACCGCTCTCTCGACGAGCTCTGGAGGACATGCGGCCGAGAGTTCATC 548  
QY 202 GGCATGATCTCGAGCAGATGCTGGGCAACCCACCTCCGACGACGACTTCATC 261  
Db 549 GGCATATCTCGACAAAGTCCGTCCTCGGCAACCCGCTCTCAAGACGACGACTTCATC 608  
QY 262 GGGGCGACGCGCTGGGAGAAAGTGTCCGAGAGCAGAGTCACTGGCTACCACTGCGC 321  
Db 609 GGGGCGTCCCGCTGGGAGAAAGTGTCTCGACACGAGGTCACTGCGACCACTGCGC 668  
QY 322 GTCCCGACGAGGTACAGACACACCATGAGAGGTCACTGAAGGGGCGACGCC 381  
Db 669 GTCCCGACCAAAAGTACCGACGAGCTCGCGACCGAGGTCCGCTCAAGGGGCGACGCC 728  
QY 382 CACTCGCAAACTTCACTGGTACCAAGAGATGACGCGCGCTTGGAAGTTCCGCGCCTC 441

Db 729 CACAGTACAAATCATGCTGATCCGCAAGGTCAACGCGGTGTGGAAGTTCGCCGCTCG 788  
QY 442 AAGCCGATATTCGCTGGGCGAGTTCGACTTGAACAGATCTTTGAGAGCAGCGAG 501  
Db 789 AACCCGAGATCCGGGTGCGGATGACCTTTGACGCCGCTTCGCGACGCGCGAC 848  
QY 502 ACCTTGGCGCA 515  
Db 849 TCGTACGCGACCGA 862  
RESULT 4  
AF316575  
LOCUS Ophiostoma floccosum strain 387N scytalone dehydratase (OSD1) gene,  
DEFINITION complete cds.  
ACCESSION AF316575  
VERSION AF316575  
KEYWORDS AF316575.1 GI:12964737  
SOURCE Ophiostoma floccosum  
ORGANISM Ophiostoma floccosum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
REFERENCE Wang, H. L., Kim, S. H. and Breuill, C.  
TITLE A scytalone dehydratase gene from *Ophiostoma floccosum* restores the melanization and pathogenicity phenotypes of a melanin-deficient *Colletotrichum lagenarium* mutant  
JOURNAL Mol. Genet. Genomics 266 (1), 126-132 (2001)  
PUBMED 11589570  
REFERENCE 2 (bases 1 to 1477)  
AUTHORS Wang, H. and Breuill, C.  
TITLE Direct Submission  
JOURNAL Submitted (25-OCT-2000) Wood Science, University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada  
FEATURES  
source Location/Qualifiers  
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CDS join(316..394,471..571,635..>1105)  
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ORIGIN  
Query Match 42.4%; Score 219; DB 4; Length 1477;  
Best Local Similarity 74.4%; Pred. No. 4e-44;  
Matches 276; Conservative 0; Mismatches 95; Indels 0; Gaps 0;  
145 GACTACCGCTCTCTCGACGAGCTCTGGAGGCAATGCGGCCGAGAGTTCGTCGCGC 204  
Db 635 GACTACCGCTCTCTCTGAACAAGCTGTGGAGGCGCATGCCGCGAAGAGTTTATCGGC 694  
QY 205 ATGATCTCGAGCAAGCAATGCTGGGCGACCCACCTCCGACGACGAGCACTTCATCGC 264  
Db 695 ATGATCTCGAGCCCAAGGCTTCGCGCAACCCCGTGTGCGACCAACACTTCTTCGCG 754  
QY 265 GGCACGCGCTGGAGAGGTGTCCGAGCAGAGGTCACTGGCTACCAACAGCTGCGCGTC 324

Db 755 GCCTGCGCTGGAGCGCATCTCCGACACCGAGGTGCGGCTTACCATCAGCTGCGCGTC 814

QY 325 CGGCACAGAGGTATCAAGGACACCATGAAAGAGTCAACATGAAAGGCCACCGCCAC 384

Db 815 CCCACACAGGTCTACACATACACTCTCACAGAGTTCGCCGTCAAGGGCCACGCCAC 874

QY 385 TCGGCAACCTTCACTGTGTACAAAGATGACGCGGTCTGAAAGTTGCGCGGCTCAAG 444

Db 875 TCGGCAACACCCACTGTGTACCGCAAGGTGACGCGGTCTGAAAGTTTTCGCCGCTCGAT 934

QY 445 CCGCATATCCGCTGGGCGAGTTTCGCTTTGACAGATCTTTGAGAGACCGGAGGAGACC 504

Db 935 CCGAAGATCGCTGTGTCAATACGATTTTGATTAAGGTGTTTCCAGCGCGGACGACG 994

QY 505 TTGCGGCAAA 515

Db 995 TTGCGACCGA 1005

RESULT 5  
AY098662 415 bp DNA linear PLN 16-JAN-2003

LOCUS Ophiostoma piliferum isolate Cartapip scytalone dehydratase (SD)

DEFINITION Gene, partial cds.

ACCESSION AY098662

VERSION AY098662.1 GI:21238833

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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/db\_xref="GI:21238834"

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AASANTHWKXVDGVMKFPAG"

ORIGIN

Query Match 37.2%; Score 192; DB 4; Length 415;

Best Local Similarity 78.0%; Pred. No. 2.2e-37;

Matches 231; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 142 ATTGACTACGCTCTCTCTCGACAAGCTCTGGAGGCAATGCGGCCGAGAGTTCGT 201

Db 120 ATGCACTACGCGCTGTTCTCTCAACAGCTCTGGAGGCAATGCGGCCGAGAGTTCATC 179

QY 202 GGCATGCTCTCGACGAAGATGTGGGCGACCCACCTCCGACGACGACCTTCATC 261

Db 180 GGCATGATCTCCGATCCAGCGGTGCTCCGCAATCCGCTGTCGCGACCCAGACATTCCTTC 239

QY 262 GCGGCGACGCGCTGGGAGAAAGGTGTCGAGGACGAGGTCATCGGTACACAGCTGGGC 321

Db 240 GCGGCTGCGCTGGGAGCGCATCTCCGACACCGAGGTGTGGGACACACAGGCTGGGC 299

QY 322 GTCCGACACAGAGGTATCAAGGACACCATGAAAGAGTTCACCATGAAAGGCCACGCC 381

Db 300 GTCCCGACACAGGTATTACACGATGCTCCACCTCTCACACAGGTGCGCGTCAAGGGCCACGCC 359

QY 382 CACTCGCAACCTTCACTGTGTACAAAGATGACGCGGTCTGGAAGTTGCGCGG 437

Db 360 CACTCGCAACACCCACTGTGTACCGCAAGGTGACGCGGTCTGGAAGTTGCGCGG 415

RESULT 6  
AY214004 1215 bp DNA linear PLN 10-MAR-2004

LOCUS Ceratocystis resinifera scytalone dehydratase I (SD1) gene,

DEFINITION complete cds.

ACCESSION AY214004

VERSION AY214004.1 GI:37787189

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .1215

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/specific\_host="Pinus contorta"

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ORIGIN





/product="scytalone dehydratase"  
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AHSANTHWKRVKDVGWKFA"

## ORIGIN

Query Match 36.0%; Score 185.6; DB 4; Length 427;  
Best Local Similarity 76.7%; Pred. No. 9e-36;  
Matches 227; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 142 ATTTACTACCGCTCTCTCTCGACAAGCTCTGGAGGCAATGCCGCCGAGAGTTGTC 201  
DB 132 ATCGACTACCGCTCTCTCTCGACAAGCTCTGGAGGCAATGCCGCCGAGAGTTTATC 191  
QY 202 GGCATGATCTCGACCAAGCATGCTGGGCGACCCCACTCTCGACGACGACCTTCATC 261  
DB 192 GGCATGATCTCGACCAAGCATGCTGGGCGACCCCACTCTCGACGACGACCTTCATC 251  
QY 262 GGCAGCAGCGCTGGGAGAAAGTGTCCGAGACAGATCATGGGCTACCAACGAGCTGGC 321  
DB 252 GGCAGCAGCGCTGGGAGAGCATCTCCGACACCGAGGTGTTGGCTACCAACGAGCTGGC 311  
QY 322 GTCCCGCACAGAGTACAAAGACACACCATGAGAGGCTCACATGAAGGCCACGCGC 381  
DB 312 GTCCCGCACAGAGTACAAAGATACCATCTCACAAAGTTGCCGTCAAGGCCACGCGC 371  
QY 382 CACTCGGCAAACTTCACTGTGTACAAAGATGACGCGGTCTGGAAGTTCCGCG 437  
DB 372 CACTCGGCAAACTTCACTGTGTACCGCAGAGTGCAGCGGTCTGGAAGTTCCGCG 427

## RESULT 11

AY098657 424 bp DNA linear PLN 16-JAN-2003  
LOCUS Ophiostoma floccosum isolate GR10 scytalone dehydratase (SD) gene,  
DEFINITION partial cds.  
VERSION AY098657  
KEYWORDS  
SOURCE  
ORGANISM

Ophiostoma floccosum  
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
INFORMERS  
GENETIC ANALYSIS OF SCYTALONE DEHYDRATASE CONFIRM  
THE PRESENCE OF DHN-MELANIN PATHWAY IN SAPSTAIN FUNGI  
Mycol. Res. 106 (11), 1331-1339 (2002)

2 (bases 1 to 424)  
Fleet, C. and Breuil, C.  
Direct Submission  
Submitted (22-APR-2002) Wood Science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

Location/Qualifiers

## FEATURES

source

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## CDS

gene

mrna

## CDS

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## ORIGIN

Query Match 35.4%; Score 182.6; DB 4; Length 424;  
Best Local Similarity 76.5%; Pred. No. 5.1e-35;  
Matches 224; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 142 ATTTACTACCGCTCTCTCTCGACAAGCTCTGGAGGCAATGCCGCCGAGAGTTGTC 201  
DB 132 ATCGACTACCGCTCTCTCTCGACAAGCTCTGGAGGCAATGCCGCCGAGAGTTTATC 191  
QY 202 GGCATGATCTCGACCAAGCATGCTGGGCGACCCCACTCTCGACGACGACCTTCATC 261  
DB 192 GGCATGATCTCGACCAAGCATGCTGGGCGACCCCACTCTCGACGACGACCTTCATC 251  
QY 262 GGCAGCAGCGCTGGGAGAAAGTGTCCGAGACAGATCATGGGCTACCAACGAGCTGGC 321  
DB 252 GGCAGCAGCGCTGGGAGAGCATCTCCGACACCGAGGTGTTGGCTACCAACGAGCTGGC 311  
QY 322 GTCCCGCACAGAGTACAAAGACACACCATGAGAGGCTCACATGAAGGCCACGCGC 381  
DB 312 GTCCCGCACAGAGTACAAAGATACCATCTCACAAAGTTGCCGTCAAGGCCACGCGC 371  
QY 382 CACTCGGCAAACTTCACTGTGTACAAAGATGACGCGGTCTGGAAGTTCCG 434  
DB 372 CACTCGGCAAACTTCACTGTGTACCGCAGAGTGCAGCGGTCTGGAAGTTCCG 424

## RESULT 12

AY098659 428 bp DNA linear PLN 16-JAN-2003  
LOCUS Ophiostoma minus isolate OM3 scytalone dehydratase (SD) gene,  
DEFINITION partial cds.  
VERSION AY098659  
KEYWORDS  
SOURCE  
ORGANISM

Ophiostoma minus  
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
INFORMERS  
GENETIC ANALYSIS OF SCYTALONE DEHYDRATASE CONFIRM  
THE PRESENCE OF DHN-MELANIN PATHWAY IN SAPSTAIN FUNGI  
Mycol. Res. 106 (11), 1331-1339 (2002)

2 (bases 1 to 428)  
Fleet, C. and Breuil, C.  
Direct Submission  
Submitted (22-APR-2002) Wood Science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

Location/Qualifiers

## FEATURES

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gene

mrna

CDS



## ORIGIN

Query Match 35.3%; Score 182.4; DB 4; Length 428;  
Best Local Similarity 76.0%; Pred. No. 5.7e-35;  
Matches 225; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 142 ATTGACTACCGCTCTCTCTCTCGACAGCTCTGGAGGCAATGCGGCGGAGAGTTCTGTC 201  
DB 133 ATGACTACCGCTCGTTCTTAACAAGCTCTGGAGGCGCATGCGGCAACAGGTTATC 192  
QY 202 GGCATGATCTCGAGCAAGAGATGCTGGGCGAACCCCTCCGACCGAGCACTTCATC 261  
DB 193 ACATGATCTCGAGCAAGAGATGCTGGGCGAACCCCTCCGACCGAGCACTTCATC 252  
QY 262 GGCAGCAGCGCTGGAGAGAGTGTCCGAGGAGAGTCACTGAGTCACTGAGGCGCC 321  
DB 253 GGCAGCAGCGCTGGAGAGAGTGTCCGAGGAGAGTCACTGAGTCACTGAGGCGCC 312  
QY 322 GTCCCGCACCAAGGTACAGGACACCATGAAAGAGTCACTGAAAGGCGCACGCC 381  
DB 313 GTCCCGCACCAAGGTACAGGACACCATGAAAGAGTCACTGAAAGGCGCACGCC 372  
QY 382 CACTCGGCAACCTTCACTGTGTAACAAGATCGAGGCGTCTGGAAGTTCCCGG 437  
DB 373 CACTCGGCAACCTTCACTGTGTAACAAGATCGAGGCGTCTGGAAGTTCCCGG 428

## RESULT 13

AY098661

LOCUS AY098661 421 bp DNA linear PLN 16-JAN-2003  
DEFINITION Ophiostoma piceae isolate W5 scytalone dehydratase (SD) gene,  
partial cds.

ACCESSION AY098661  
VERSION AY098661.1 GI:21238831

KEYWORDS  
SOURCE

ORGANISM

Ophiostoma piceae  
Ophiostoma piceae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.

REFERENCE 1 (bases 1 to 421)  
Fleet, C. and Breuil, C.  
Inhibitors and genetic analysis of scytalone dehydratase confirm

JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)  
AUTHORS the presence of DHN-melanin pathway in sapstain fungi  
TITLE 2 (bases 1 to 421)  
Fleet, C. and Breuil, C.

JOURNAL Direct Submision  
TITLE Submitted (22-APR-2002) Wood Science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

FEATURES  
source Location/Qualifiers  
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gene  
mrna  
CDS

ORIGIN

Query Match

34.7%; Score 179.2; DB 4; Length 421;

Best Local Similarity 75.3%; Pred. No. 3.7e-34;  
Matches 223; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 142 ATTGACTACCGCTCTCTCTCTCGACAGCTCTGGAGGCAATGCGGCGGAGAGTTCTGTC 201  
DB 136 ATGACTACCGCTCGTTCTTAACAAGCTCTGGAGGCGCATGCGGCAACAGGTTATC 185  
QY 202 GGCATGATCTCGAGCAAGAGATGCTGGGCGAACCCCTCCGACCGAGCACTTCATC 261  
DB 166 GGCATGATCTCGAGCAAGAGATGCTGGGCGAACCCCTCCGACCGAGCACTTCATC 245  
QY 262 GGCAGCAGCGCTGGAGAGAGTGTCCGAGGAGAGTCACTGAGTCACTGAGGCGCC 321  
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QY 322 GTCCCGCACCAAGGTACAGGACACCATGAAAGAGTCACTGAAAGGCGCACGCC 381  
DB 306 GTCCCGCACCAAGGTACAGGACACCATGAAAGAGTCACTGAAAGGCGCACGCC 365  
QY 382 CACTCGGCAACCTTCACTGTGTAACAAGATCGAGGCGTCTGGAAGTTCCCGG 437  
DB 366 CACTCGGCAACCTTCACTGTGTAACAAGATCGAGGCGTCTGGAAGTTCCCGG 421

RESULT 14

AY098660

LOCUS AY098660 423 bp DNA linear PLN 16-JAN-2003  
DEFINITION Ophiostoma piceae isolate 187-1 scytalone dehydratase (SD) gene,  
partial cds.

ACCESSION AY098660  
VERSION AY098660.1 GI:21238829

KEYWORDS  
SOURCE

ORGANISM

Ophiostoma piceae  
Ophiostoma piceae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.

REFERENCE 1 (bases 1 to 423)  
Fleet, C. and Breuil, C.  
Inhibitors and genetic analysis of scytalone dehydratase confirm

JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)  
AUTHORS the presence of DHN-melanin pathway in sapstain fungi  
TITLE 2 (bases 1 to 423)  
Fleet, C. and Breuil, C.  
Direct Submision  
TITLE Submitted (22-APR-2002) Wood Science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

FEATURES  
source Location/Qualifiers  
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gene  
mrna  
CDS

ORIGIN

Query Match

34.7%; Score 179.2; DB 4; Length 423;

Best Local Similarity 75.3%; Pred. No. 3.7e-34;  
Matches 223; Conservative 0; Mismatches 73; Indels 0; Gaps 0;



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QY 142 ATGACTACCGCTCTCTCTCGACAAGCTCTGGAGGCAATGCCGCCGAGAGTTGTC 201
DB 128 ATGATTTACCGGCTGTTTCTGAAACAAGCTCTGGAGGCAATGCCGCCGAGAGTTTATC 187
QY 202 GGCATGCTCTCGAGCAAGCATGCTGGGAGACCCCACTCCGACGACGACTTCATC 261
DB 188 GGCATATATCTCGAAGCCCAACGCTCTCGGCAACCCCTGCTACGACACAACACTTCTT 247
QY 262 GCGGCAAGCGCTGGAGGAAGTGTCCGAGGACAGGTCATCGGCTACCAACGAGTCCGC 321
DB 248 GGGGCTCTCGGCTGGAGAACCGCTCTCCGATACGAGAGTTATGGCTACCAACGAGTCCGC 307
QY 322 GTCCGACACGAGTACAGAGACACCAACCATGAGAGGTCAACATGAGGCGCACGCC 381
DB 308 GTCCCCCACCAGGTTACACCAACGAGCTCCCTGTGACCGTTGCGCAAGGCGCACGCCA 367
QY 382 CACTCGGCAAACTTCACTGTGTACAGAGATGACGCGCTCTGGAAGTTCCCGG 437
DB 368 CACTCGGCAACCAAGACTGTGTACCGGAGTTGACGCGCTCTGGAAGTTCCCGG 423

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## RESULT 15

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LOCUS AY098666 423 bp DNA linear PLN 16-JAN-2003
DEFINITION Ophiostoma setosum isolate NZFS3734 scytalone dehydratase (SD)
ACCESSION AY098666
VERSION AY098666.1 GI:21238841
KEYWORDS
SOURCE
ORGANISM

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REFERENCE
AUTHORS Fleet,C. and Breuil,C.
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm

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JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE 2 (bases 1 to 423)
AUTHORS Fleet,C. and Breuil,C.
TITLE Direct Submission

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JOURNAL Submitted (22-APR-2002) Wood Science, University of British
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

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FEATURES
source 1..423
Location/Qualifiers

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/organism="Ophiostoma setosum"
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/isolate="NZFS3734"
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/gene="SD"
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/product="scytalone dehydratase"
join(<1..69,128..>423)

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/gene="SD"
/codon_start=1

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/product="scytalone dehydratase"
/protein_id="AAM34812.1"

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/db_xref="GI:21238842"
/translation="EWADRYDSDKMDRLKCIAPTLRIDYRSPINKMEAMPDEPIV
MISDPSVLGNPLIRTOHPFGASRWERVSDTEVIGYHQLRVPHOYTDAASLSTAVAKGH
AHSANQHWYRKXDVWVKFAG"

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## ORIGIN

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Query Match 34.7%; Score 179.2; DB 4; Length 423;
Best Local Similarity 75.3%; Pred. No. 3,7e-34;
Matches 223; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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QY 142 ATGACTACCGCTCTCTCTCGACAAGCTCTGGAGGCAATGCCGCCGAGAGTTGTC 201
DB 128 ATGATTTACCGGCTGTTTCTGAAACAAGCTCTGGAGGCAATGCCGCCGAGAGTTTATC 187

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Search completed: December 4, 2006, 18:35:10
Job time : 2495 secs

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QY 202 GGCATGCTCTCGAGCAAGCATGCTGGGAGACCCCACTCCGACGACGACTTCATC 261
DB 188 GGCATATATCTCGAAGCCCAACGCTCTCGGCAACCCCTGCTACGACACAACACTTCTT 247
QY 262 GCGGCAAGCGCTGGAGGAAGTGTCCGAGGACAGGTCATCGGCTACCAACGAGTCCGC 321
DB 248 GGGGCTCTCGGCTGGAGAACCGCTCTCCGATACGAGAGTTATGGCTACCAACGAGTCCGC 307
QY 322 GTCCGACACGAGTACAGAGACACCAACCATGAGAGGTCAACATGAGGCGCACGCC 381
DB 308 GTCCCCCACCAGGTTACACCAACGAGCTCCCTGTGACCGTTGCGCAAGGCGCACGCCA 367
QY 382 CACTCGGCAAACTTCACTGTGTACAGAGATGACGCGCTCTGGAAGTTCCCGG 437
DB 368 CACTCGGCAACCAAGACTGTGTACCGGAGTTGACGCGCTCTGGAAGTTCCCGG 423

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:27:41 ; Search time 52 Seconds  
(without alignments)  
269.524 Million cell updates/sec

Title: US-10-507-132-2

Perfect score: 942  
Sequence: 1 MSGQVQKSDPITFSDYLGLM.....WGFEDFDRIFFDGRFTGDK 172

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

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4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7 COMB.pep: \*  
5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/8 COMB.pep: \*  
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7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfill1.pep: \*

Pred. No. is the number of results predicted by chance to a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94.5	10.0	153	US-09-328-352-4170	Sequence 4170, Ap
2	84	8.9	338	US-09-543-681A-4649	Sequence 4649, Ap
3	84	8.9	349	US-09-625-634A-3	Sequence 3, Appl1
4	81	8.6	349	US-09-625-634A-2	Sequence 2, Appl1
5	77	8.2	700	US-09-252-991A-29072	Sequence 29072, A
6	76	8.1	602	US-09-248-796A-15811	Sequence 15811, A
7	74.5	7.9	437	US-09-477-135A-136	Sequence 136, App
8	74	7.9	768	US-09-489-039A-11131	Sequence 11131, A
9	72.5	7.7	388	US-08-282-197C-56	Sequence 56, Appl
10	72.5	7.7	518	US-09-489-039A-8407	Sequence 8407, Ap
11	72	7.6	396	US-09-328-352-7847	Sequence 7847, Ap
12	71.5	7.6	500	US-09-949-016-11697	Sequence 11697, A
13	71.5	7.6	613	US-09-149-727-5	Sequence 5, Appl1
14	71.5	7.6	651	US-09-270-957-16	Sequence 16, Appl
15	71.5	7.6	1207	US-10-098-6008-16	Sequence 16, Appl
16	71.5	7.6	1207	US-10-098-6008-16	Sequence 16, Appl
17	71.5	7.6	1207	US-09-949-002-376	Sequence 376, App
18	71.5	7.6	1271	US-09-540-236-3740	Sequence 3740, Ap
19	71.5	7.6	1384	US-08-976-255-11	Sequence 11, Appl
20	71	7.5	251	US-09-248-796A-16943	Sequence 16943, A
21	71	7.5	728	US-09-543-681A-8132	Sequence 8132, Ap
22	70.5	7.5	110	US-08-194-290-9	Sequence 9, Appl1
23	70.5	7.5	184	US-08-614-377A-9	Sequence 9, Appl1
24	70.5	7.5	184	US-09-142-648B-9	Sequence 9, Appl1
25	70.5	7.5	471	US-08-914-375C-70	Sequence 70, Appl
26	70.5	7.5	590	US-10-104-047-3415	Sequence 3415, Ap

27	70	7.4	176	2	US-09-543-681A-6922	Sequence 6922, Ap
28	70	7.4	243	2	US-09-252-991A-26765	Sequence 26765, A
29	69.5	7.4	146	2	US-09-270-767-33395	Sequence 33395, A
30	69.5	7.4	146	2	US-09-270-767-48612	Sequence 48612, A
31	69.5	7.4	166	2	US-09-328-352-7279	Sequence 7279, Ap
32	69.5	7.4	524	2	US-09-242-913B-15	Sequence 15, Appl
33	69.5	7.4	524	3	US-10-347-252-15	Sequence 15, Appl
34	69.5	7.4	653	2	US-09-171-937C-27	Sequence 27, Appl
35	69.5	7.4	779	2	US-09-171-937C-25	Sequence 25, Appl
36	69	7.3	224	2	US-09-134-000C-4000	Sequence 4000, Ap
37	69	7.3	614	2	US-09-328-352-4504	Sequence 4504, Ap
38	69	7.3	2154	1	US-08-841-349-4	Sequence 4, Appl1
39	69	7.3	2154	2	US-09-431-184A-4	Sequence 4, Appl1
40	69	7.3	2364	2	US-09-538-092-1243	Sequence 1243, Ap
41	68.5	7.3	331	2	US-09-107-433-4641	Sequence 4641, Ap
42	68.5	7.3	442	2	US-09-252-991A-31597	Sequence 31597, A
43	68.5	7.3	484	7	5171673-8	Sequence 31597, A
44	68.5	7.3	487	7	5171673-6	Patent No. 5171673
45	68.5	7.3	493	2	US-08-999-774A-12	Sequence 12, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-328-352-4170
; Sequence 4170, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4170
; LENGTH: 153
; TYPE: PRN
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4170

Query Match      10.0%; Score 94.5; DB 2; Length 153;
Best Local Similarity 23.0%; Pred. No. 0.008;
Matches 31; Conservative 28; Mismatches 59; Indels 17; Gaps 6;

QY 15 DYGLMTCYEMADSDSKMDRLKRVIAPTLRIDRSFLDKLMEAMPAEFVGMYSKO 74
   ||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 13 DYRRILEVITRFQVLVDQKNWDAFDELADOLEVDLQFRGEPLCVVSCHEYRG--SRQ 70
QY 75 MLDGPTLFTQHFHIGTRWEKVSDEVYIGVHQLRPHQRXKDTTWKEVTMKGHASNLHW 134
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Db 71 ALSH--LRLOHNLNRP-LRIBDDA---WLECNVQIYR-----FSENDYHSGRY 117
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 135 Y--KKIDGVWKPAGL 147
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 118 FTLAKQGGIWKITGI 132

RESULT 2
US-09-543-681A-4649
; Sequence 4649, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709,1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
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; SEQ ID NO 4649  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Proteus mirabilis  
 US-09-543-681A-4649

Query Match 8.9%; Score 84; DB 2; Length 338;  
 Best Local Similarity 25.5%; Pred. No. 0.38;  
 Matches 39; Conservative 18; Mismatches 42; Indels 54; Gaps 10;

QY 35 WDRLRVIAPIALRIDRSLFDKMEMPAEFYGMVSSKOMLDPILR-TQHFIGSTRWE 93  
 DB 94 WDKAQK-----EDVLDKMFETAP-QSFV-----MLADLCIRGAKHTLQRTSWE 135  
 QY 94 KYSEDEVIGYHQR-----VPHQRKDTMKKEVTMKGHAHSAHLHWYK--IDGYW 142  
 DB 136 GI---EIT--ERLKAQGRNVIFWVPHGMADVPAMLIAAKGQMAAMFHQKDPVTDYIA 190  
 QY 143 -----KFAGLKPDIR-----WGEF 156  
 DB 191 NKARYHFGRLHSREAGIKPFISTVRQGFWGY 223

RESULT 3  
 US-09-625-634A-3  
 ; Sequence 3, Application US/09625634A  
 ; Patent No. 6653448  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Verneet, Corine  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Herrmann, John  
 ; TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING  
 ; FILE REFERENCE: Cura-244 (15966-744) US  
 ; CURRENT APPLICATION NUMBER: US/09/625,634A  
 ; CURRENT FILING DATE: 2000-07-26  
 ; PRIOR APPLICATION NUMBER: USSN 60/194,256  
 ; PRIOR FILING DATE: 2000-04-03  
 ; PRIOR APPLICATION NUMBER: USSN 60/192,838  
 ; PRIOR FILING DATE: 2000-03-29  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: Mus sp.  
 US-09-625-634A-3

Query Match 8.9%; Score 84; DB 2; Length 349;  
 Best Local Similarity 31.1%; Pred. No. 0.4;  
 Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

QY 84 OHFIGSTRW--EKVSEDEVIGHQLRVPHQRKDTMKKEVTMKGHAH-----ANLH- 133  
 DB 74 QHOFRRGRMCSALGKTVFQG-OLRVGSRBAFT--VAITAGVAHVAITAACSGGNLSN 130  
 QY 134 -----WYKKIDGVWKFAGLKPDIRWGEFDPDIRPFEDGRE 167  
 DB 131 CGCDREKQGYNNQAG-KWKGGCSADVRYG-IDFSRRFVDARE 171

RESULT 4  
 US-09-625-634A-2  
 ; Sequence 2, Application US/09625634A  
 ; Patent No. 6653448  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Verneet, Corine  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Herrmann, John  
 ; TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING  
 ; FILE REFERENCE: Cura-244 (15966-744) US  
 ; CURRENT APPLICATION NUMBER: US/09/625,634A

; CURRENT FILING DATE: 2000-07-26  
 ; PRIOR APPLICATION NUMBER: USSN 60/194,256  
 ; PRIOR FILING DATE: 2000-04-03  
 ; PRIOR APPLICATION NUMBER: USSN 60/192,838  
 ; PRIOR FILING DATE: 2000-03-29  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-625-634A-2

Query Match 8.6%; Score 81; DB 2; Length 349;  
 Best Local Similarity 31.2%; Pred. No. 0.88;  
 Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

QY 91 RW--EKVSEDEVIGHQLRVPHQRKDTMKKEVTMKGHAH-----ANLH----- 133  
 DB 81 RWNCSALGKTVFQG-OLRVGSRBAFT--VAITAGVAHVAITAACSGGNLSNCGDREK 137  
 QY 134 --WYKKIDGVWKFAGLKPDIRWGEFDPDIRPFEDGRE 167  
 DB 138 QGYNNQAG-KWKGGCSADVRYG-IDFSRRFVDARE 171

RESULT 5  
 US-09-252-991A-29072  
 ; Sequence 29072, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 29072  
 ; LENGTH: 700  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-29072

Query Match 8.2%; Score 77; DB 2; Length 700;  
 Best Local Similarity 28.1%; Pred. No. 6.6;  
 Matches 25; Conservative 15; Mismatches 35; Indels 14; Gaps 4;

QY 59 EMMPAEFVGM-VSSKOMLGPDLATQHFIGSTR-----EKVSEDEVIGHQLRVPHQ 111  
 DB 141 EDQPAEQRGQRVAAGHILGYPEDVVAHVQRSPQCRQAVAEVVGQEDVGHIIIEGHQ 200  
 QY 112 RYK-----DTMKKEVTMKGH--AHSANLH 133  
 DB 201 RHRRQOEGDSALLEAVPDABHSIHRSVTLH 229

RESULT 6  
 US-09-248-796A-15811  
 ; Sequence 15811, Application US/09248796A  
 ; Patent No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstein et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
 ; FILE REFERENCE: 107196.132  
 ; CURRENT APPLICATION NUMBER: US/09/248,796A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,725

;; PRIOR FILING DATE: 1998-02-13  
;; PRIOR APPLICATION NUMBER: US 60/096,409  
;; PRIOR FILING DATE: 1998-08-13  
;; NUMBER OF SEQ ID NOS: 28208  
;; SEQ ID NO 15811  
;; LENGTH: 602  
;; TYPE: PRT  
;; ORGANISM: Candida albicans  
US-09-248-796A-15811

Query Match 8.1%; Score 76; DB 2; Length 602;  
Best Local Similarity 21.3%; Pred. No. 7;  
Matches 36; Conservative 24; Mismatches 61; Indels 48; Gaps 6;

QY 4 QVCKSPDITSDVIGMTCYEWADSYDSKDW-----DLKRVIAPTLRIDYRSPFLDKLME 59  
DB 103 QEASSVEITTEENTEGHSPIYIKREFTAKESMTVNNKGRATESKIKDRTYFNQLDNLCH 162  
QY 60 AMPAE---EFVG-----WVSSKQMLGDPPTLRTOH-----FIGGT-----RWE 93  
DB 163 FLPOERVAEFAGLSPEKLMETERLTGSHLLIMHEDLIKDNESQGLGNKIKIDIGRLA 222  
QY 94 KXSED-----EVIGYHQLRVPHORYKDTTMEVYTMK 124  
DB 223 KLHEDRSKLEEARKLEEDYDKSEEDVNHRLIIPYAKYQDLKNQRTILK 271

RESULT 7  
US-09-477-135A-136  
; Sequence 136, Application US/09477135A  
; Patent No. 6572865  
; GENERAL INFORMATION:  
; APPLICANT: Nano, Francis  
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding  
; FILE REFERENCE: 52888  
; CURRENT APPLICATION NUMBER: US/09/477.135A  
; CURRENT FILING DATE: 2000-01-03  
; PRIOR APPLICATION NUMBER: 08990823  
; PRIOR FILING DATE: 1997-12-15  
; PRIOR APPLICATION NUMBER: US 96/10375  
; PRIOR FILING DATE: 1996-06-14  
; PRIOR APPLICATION NUMBER: 60/000,254  
; PRIOR FILING DATE: 1995-06-15  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 136  
; LENGTH: 437  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
US-09-477-135A-136

Query Match 7.9%; Score 74.5; DB 2; Length 437;  
Best Local Similarity 20.5%; Pred. No. 6.7;  
Matches 34; Conservative 23; Mismatches 48; Indels 61; Gaps 9;

QY 58 WEAMPAEFPGWSSKQMLGD-----PTLRTOHFIGTTRKXSE----- 97  
DB 43 WSHPEQ---SSAERELIRFQDRFPTLSVKLIDAKXDVEVAQKFNALLIGTDVDDVV 99  
QY 98 -----DEVIGYHQLRVPHORYKDTTMEVYTMK-----HANSANTL 132  
DB 100 LDDRRWTFHAFALSGVLTALDDLFG--QVGVDTTDDYDUSLADYEFNRRHAAVYARSTPL 157  
QY 133 HMYKKIDGVKKFAGLKPD---IMGEFD-----PDRIFEDGETFG 170  
DB 158 FYVTK--AAWQOAGL--PDRGPQSWSEPDWGPBLQRYVAGRSANHG 200

RESULT 8  
US-09-489-039A-11131  
; Sequence 11131, Application US/09489039A  
; Patent No. 6610836

;; GENERAL INFORMATION:  
;; APPLICANT: Gary Breton et. al  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
;; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 2709.2004001  
;; CURRENT APPLICATION NUMBER: US/09/489,039A  
;; CURRENT FILING DATE: 2000-01-27  
;; PRIOR APPLICATION NUMBER: US 60/117,747  
;; PRIOR FILING DATE: 1999-01-29  
;; NUMBER OF SEQ ID NOS: 14342  
;; SEQ ID NO 11131  
;; LENGTH: 768  
;; TYPE: PRT  
;; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11131

Query Match 7.9%; Score 74; DB 2; Length 768;  
Best Local Similarity 20.6%; Pred. No. 17;  
Matches 45; Conservative 31; Mismatches 66; Indels 76; Gaps 11;

QY 8 SDEITSDVIGMTCYEWADSYDS--KQWDRL-----RKVIA-----P 44  
DB 383 ADFFALASPDG--TSLYERSDPREGYHDMNTLLINYGREVSNNYVGNALYIERPGID 440  
QY 45 TLRID-----YRSFLDKLWEAMPAE-----EFVGVWSSKQMLGDP-----L 81  
DB 441 ALRVDAVASMIYRDYRKAGWEIPIREYGGRENLEAIEF--LRNTNRILSGQTGAATMAE 498  
QY 82 RTQHFITGTR-----WEKVSDEVIGYHQLRVPHORYKDTTMEVYTMKGH--- 126  
DB 499 ESTDFAGVTRPPAGGIGFWMFKNNLGMHMDTLDYMLDPVHRHRYHDKMTFCMLVYVTEN 558  
QY 127 -----AHSANIKHYKKI-----DGVWKFAGKPDRIW 153  
DB 559 FVLPUSHDEVHGKSIDLRMPGDANQKFNALPAYGW 596

RESULT 9  
US-08-282-197C-56  
; Sequence 56, Application US/08282197C  
; Patent No. 5871730  
; GENERAL INFORMATION:  
; APPLICANT: Brzezinski, Ryszard  
; APPLICANT: Dery, Claude V  
; APPLICANT: Beaulieu, Carole  
; TITLE OF INVENTION: Thermostable Xylanaase DNA, Protein and  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Releasee #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/282,197C  
; FILING DATE: 23-JUL-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cimballa, Michele A  
; REGISTRATION NUMBER: 33,851  
; REFERENCE/DOCKET NUMBER: 1050.0410000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 388 amino acids  
TYPE: amino acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-282-197C-56

Query Match 7.7%; Score 72.5; DB 1; Length 388;  
Best Local Similarity 21.9%; Pred. No. 9.6;  
Matches 33; Conservative 23; Mismatches 68; Indels 27; Gaps 5;

QY 31 DSKMDRLKVIAPTLRIYRSFLDKLMEAMPAEEFVGVSSKOMLGDPFLRTQHFIGGT 90  
DB 176 DKSMDVNEVEIEPN---DEGGRNSPMYQITGETEYI-----EVAFRATREAGS 222  
QY 91 RMEKVESEDEVIGYH-----QLRVPHORYKDTTMEKVTMKGHASHANLHWY-----KKIDG 140  
DB 223 DKLKLYND-----YNTDDPKYKRDILYELVKNLEKGVPIQGVGHQTHIDYINPEVERILIS 278  
QY 141 VVKFAGLKPDIRWGEFDPRIEFDEGRETGCD 171  
DB 279 IKKFAGLGDNITTELDMSIYSWNRSDYGD 309

RESULT 10  
US-09-489-039A-8407  
; Sequence 8407, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 8407  
; LENGTH: 518  
; TYPE: PR1  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-8407

Query Match 7.7%; Score 72.5; DB 2; Length 518;  
Best Local Similarity 26.1%; Pred. No. 14;  
Matches 36; Conservative 16; Mismatches 53; Indels 33; Gaps 6;

QY 33 KDMDLRKVIAPTLRI--DYRSFLDKLMEAMPAEEFVGVSSKOMLGDPFLRTQHFIGGT 90  
DB 164 KETDALPEGERANLRVITQNRRTALNQLTAVLPDSDKIVMSILRFSGTQPLTYT----- 216  
QY 91 RMEKVESEDEVIGYHOLRVPHORYKDTTMEKVTMKGHASHANLHWYKKIOWMKFAGLKP- 149  
DB 217 ---LSDGVLNNQTHVKYRPNNV-----GFYQSLN-----ADSGWNEKLSFG 258  
QY 150 ---DIRWGEFDPRIEF 164  
DB 259 YTVTIGMD--NFTRVFHD 274

RESULT 11  
US-09-328-352-7847  
; Sequence 7847, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7847

LENGTH: 396  
TYPE: PR1  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-7847

Query Match 7.6%; Score 72; DB 2; Length 396;  
Best Local Similarity 18.9%; Pred. No. 11;  
Matches 35; Conservative 27; Mismatches 41; Indels 82; Gaps 8;

QY 9 DEITSFDVIGMTQCYENADSYD-----SKDM---DLRKVIAPTLRIDYRSFL 54  
DB 52 DELFFDKCDPRAKOVFDGIEFTPIDELIKOVHKLKPMFDELLEKHLTPGQRAE----- 106  
QY 55 DKLMEAMPAEEFVGVSSKOMLGDPFLRTQH--FIGTR----- 91  
DB 107 --LQAKGSLBELMKRLER-----LREQHKHGGGRNRMVGTGTSFPGAGDHPGEGV 157  
QY 92 -----WEK-----VSEDEVIGYHOLRVPHORYK-----DTMKE 120  
DB 158 IGGPKRKSAYKVEQRKYQNLDDQVLGTRQMQIALRRLRKFAQGAABELVDVGTIRE 217  
QY 121 VTMKG 125  
DB 218 TAKOG 222

RESULT 12  
US-09-949-016-11697  
; Sequence 11697, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11697  
; LENGTH: 500  
; TYPE: PR1  
; ORGANISM: Human  
US-09-949-016-11697

Query Match 7.6%; Score 71.5; DB 2; Length 500;  
Best Local Similarity 26.0%; Pred. No. 18;  
Matches 34; Conservative 19; Mismatches 51; Indels 27; Gaps 6;

QY 29 SYDSKMDRLKVIAPTLRIDY-----RSFLDK-----LMEAMPAEEFVGVSSKOMLG 78  
DB 43 SRECKELDGLW-----SFRADPSDNRRRGFEQWYRRPLMESGPTVDMVPSSFNDISQD 97  
QY 79 PTLRTQHFIGGTRMEKVESEDEVIGYHOLRVPHORYKDTTMEKVTMKGHASHANLHWYKKI 138  
DB 98 WRLR--HFGWGWYER---EVI-----LPERMTQDLATRLVLRIGSAHSAIYWVANGV 145  
QY 139 DGWKKFAGLKP 149  
DB 146 DTLEHEGGYLP 156

RESULT 13  
US-09-149-727-5  
; Sequence 5, Application US/09149727  
; Patent No. 6391547  
; GENERAL INFORMATION:

```

1  APPLICANT: Jefferson, Richard A.
2  APPLICANT: Kilian, Andrzej
3  APPLICANT: Reese, Paul Konrad
4  TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
5  TITLE OF INVENTION: USES THEREOF
6  FILE REFERENCE: 190106.405
7  CURRENT APPLICATION NUMBER: US/09/149,727
8  CURRENT FILING DATE: 1998-09-08
9  EARLIER APPLICATION NUMBER: US 60/058,263
10 EARLIER FILING DATE: 1997-09-09
11 NUMBER OF SEQ ID NOS: 71
12 SOFTWARE: PatentIn Ver. 2.0
13 SEQ ID NO 5
14 LENGTH: 613
15 TYPE: PR1
16 ORGANISM: Homo sapiens
17 US-09-149-727-5

```

Query Match	7.6%	Score 71.5;	DB 2;	length 613;
Best Local Similarity	26.0%;	Pred. No. 23;		
Matches	34;	Conservative	19;	Mismatches 51;
				Indels 27;
				Gaps 6;

[illegible]

```

RESULT 14
US-09-270-957-16
: Sequence 16, Application US/09270957
: Patent No. 6641996
: GENERAL INFORMATION:
: APPLICANT: Richard A. Jefferson and Jorge E. Mayer
: TITLE OF INVENTION: MICROBIAL-GLUCONIDASE GENES, GENE
: FILE OF INVENTION: PRODUCTS, AND USES THEREOF
: FILE REFERENCE: 190106.405C1
: CURRENT APPLICATION NUMBER: US/09/270.957
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ ID NOS: 112
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 16
: LENGTH: 613
: TYPE: PRT
: ORGANISM: Homo sapien
US-09-270-957-16

```

	Query Match	7.6%;	Score 71.5;	DB 2;	Length 613;
	Best Local Similarity	26.0%;	Pred. No. 23;		
	Matches	34;	Conservative	19;	Mismatches 51; Indels 27; Gaps 6
Oy	29	SYDSKDMRLRKVIAPLTRIDY----	-RSFLDK-----	LMEAMPAAEFVGVWSKOMTGD	78
Dd	15	SRECELDGLW-----	SFRADPSDNRRRGFEQWRRLPLMESGPIVDMPVPSSFNDISQD		69
Oy	79	PTLRTQHFIIGGTWRWEKSDEVEYGHLRVPHQRKYKDTMTKEVTMKGAHANSNLHWYKKI			138
Dd	70	WRLR--HEVGWWMYER----	EVI-----	LPERTQTDLRTLVLRIGSASHSAIYTWNGV	117
Oy	139	DGVWKFAGLKP	149		
Dd	118	DTLEHGGLP	128		

RESULT 15  
US-09-715-858-2

```

? Sequence 2, Application US/09715858
? Patent No. 6582692
? GENERAL INFORMATION:
? APPLICANT: Podsakoff, Gregory
? APPLICANT: Watson, Gordon
? APPLICANT: Conito, Linda B.
? APPLICANT: Yang, Bin
? TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR THE
? TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
? FILE REFERENCE: 0800-0021
? CURRENT APPLICATION NUMBER: US/09/715,858
? CURRENT FILING DATE: 2000-11-14
? NUMBER OF SEQ ID NOS: 16
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 2
? LENGTH: 651
? TYPE: PR1
? ORGANISM: Homo sapiens
US-09-715-858-2

```

Query Match	7.6%	Score	71.5	DB	2	Length	651
Best Local Similarity	26.0%	Pred. No.	25				
Matches	34	Conservative	19	Mismatches	5	Indels	27
						Gaps	6

```

QY      29 SYSYKQMDLRKVIAPTLRIDY-----RSFLDK-----LMEAMFAEEFVGWSSKQMLGD 78
Db      35 SRECKLDLGM-----SFRADPSDNRRKGFEQWTRRLMBSGTYDMPVPSSINDISQD 89

QY      79 PLTRTOHFIIGTIRMEKVESEDEVIGYHQLRVPHQRKDTTWKEVTKMGAHSAHLHWYKKI 138
Db      90 WRLR--HFNGWWTYER---EVI-----LPERKTQDLRLRVRLRIGSAHSYALVWNGV 137

QY      139 DGVWKEFAGLKP 149
Db      138 DTLHEGGYLP 148

```

Search completed: December 5, 2006, 01:29:07  
Job time : 53 secs

RESULT 15  
US-09-715-858-2

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Best Local Similarity 100.0%; Pred. No. 1.2e-95;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSQVQKSDBITFSDYLGIMTCYEWADSDSKMDRLRKVIAPTLRIDYRSFLDKLWEA 60  
DB 1 MGSQVQKSDBITFSDYLGIMTCYEWADSDSKMDRLRKVIAPTLRIDYRSFLDKLWEA 60  
QY 61 MPABEEFVGWVSSKQMLGDPFLRTQHFIGGTRWEKVSDEVIQYHQLRVPHQRKDTTKE 120  
DB 61 MPABEEFVGWVSSKQMLGDPFLRTQHFIGGTRWEKVSDEVIQYHQLRVPHQRKDTTKE 120  
QY 121 VTMKGHAHSANLHWYKKIDGWKFAGLKPDIRWGEFDFRIFEDGRETFGDK 172  
DB 121 VTMKGHAHSANLHWYKKIDGWKFAGLKPDIRWGEFDFRIFEDGRETFGDK 172

## RESULT 2

ADCL6593  
ID ADC16593 standard; protein; 172 AA.

AC ADC16593;

XX 18-DEC-2003 (first entry)

XX Scytalone dehydrogenase #SEQ ID 4.

XX Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.

XX Magnaporthe grisea.

XX WO2003076628-A1.

XX 18-SEP-2003.

XX 24-FEB-2003; 2003WO-JP001980.

XX 12-MAR-2002; 2002JP-00066955.

XX (TSUB ) KUMIAI CHEM IND CO LTD.

XX Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

XX WPI; 2003-748394/70.

XX DR N-PSDB; ADC16592.

XX Gene encoding for scytalone dehydrogenase (SCDH), useful for screening

XX for SCDH inhibitors and evaluating sensitivity to them.

XX Claim 7; SEQ ID NO 4; 50pp; Japanese.

XX The invention relates to a gene encoding scytalone dehydrogenase (SCDH),

XX that functions in the presence of an inhibitor, comprising an optionally

XX disclosed is a method for evaluating rice blast fungus (Pyricularia

XX oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase

XX inhibitors. The gene is useful for screening for new SCDH inhibitors and

XX evaluating sensitivity to them. The current sequence represents the

XX Scytalone dehydrogenase amino acid sequence.

XX Sequence 172 AA;

XX Query Match 99.6%; Score 938; DB 7; Length 172;

XX Best Local Similarity 99.4%; Pred. No. 3.3e-95;

XX Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSQVQKSDBITFSDYLGIMTCYEWADSDSKMDRLRKVIAPTLRIDYRSFLDKLWEA 60  
DB 1 MGSQVQKSDBITFSDYLGIMTCYEWADSDSKMDRLRKVIAPTLRIDYRSFLDKLWEA 60  
QY 61 MPABEEFVGWVSSKQMLGDPFLRTQHFIGGTRWEKVSDEVIQYHQLRVPHQRKDTTKE 120  
DB 61 MPABEEFVGWVSSKQMLGDPFLRTQHFIGGTRWEKVSDEVIQYHQLRVPHQRKDTTKE 120

QY 121 VTMKGHAHSANLHWYKKIDGWKFAGLKPDIRWGEFDFRIFEDGRETFGDK 172  
DB 121 VTMKGHAHSANLHWYKKIDGWKFAGLKPDIRWGEFDFRIFEDGRETFGDK 172

## RESULT 3

ADA32883  
ID ADA32883 standard; protein; 153 AA.

XX ADA32883;

XX 20-NOV-2003 (first entry)

XX Acinetobacter baumannii protein #44.

XX Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;

XX plant biocontrol agent.

XX Acinetobacter baumannii.

XX US6562958-B1.

XX 13-MAY-2003.

XX 04-JUN-1999; 99US-00328352.

XX 09-JUN-1998; 98US-0088701P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton G, Bush D;

XX WPI; 2003-576092/54.

XX N-PSDB; ADA28757.

XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents

XX for diagnosing a bacterial disease, as components of antibacterial

XX vaccines, as targets for antibacterial drugs, or as biocontrol agents for

XX plants.

XX Example; SEQ ID NO 4170; 328pp; English.

XX The invention relates to isolated Acinetobacter baumannii nucleic acids.

XX The A. baumannii nucleic acids and polypeptides are useful as reagents

XX for diagnosing a bacterial disease, as components of antibacterial

XX vaccines, as targets for antibacterial drugs, to detect the presence of

XX A. baumannii and other Acinetobacter species in a sample, in screening

XX compounds for the ability to interfere with the A. baumannii life cycle

XX or to inhibit A. baumannii infection, and as biocontrol agents for

XX plants. The present sequence represents the amino acid sequence of an A.

XX baumannii protein.

XX Sequence 153 AA;

XX Query Match 10.0%; Score 94.5; DB 6; Length 153;

XX Best Local Similarity 23.0%; Pred. No. 0.062;

XX Matches 31; Conservative 28; Mismatches 59; Indels 17; Gaps 6;

QY 15 DYLGIMTCYEWADSDSKMDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGWVSSKO 74  
DB 13 DYRLIEVITRFQVLVDQKNWDAFDELLADQLEVIYLPQGRSPLCVSCHEYKG--SRQ 70  
QY 75 MGDPTLRTQHFIGGTRWEKVSDEVIQYHQLRVPHQRKDTTKEVTWKGAHSANLHW 134  
DB 71 ALSH--LRQHNLSP--LRIRIQDQ-----WECNYQIR-----FSENDYFHSGRXY 117  
QY 135 Y--KKIDGWKFAGL 147  
DB 118 FTLLAKQGGIMKITGI 132

## RESULT 4

AAB38266

ID AAE38266 standard; protein; 924 AA.  
 AC AAE38266;  
 DT 20-NOV-2003 (first entry)  
 DE Rice disease resistance protein, LOX1.  
 DE Rice disease resistance protein, LOX1.  
 KM Rice; abiotic stress tolerance; pathogen resistance; disease resistance;  
 KM grain quality; nutritional content; plant yield; LOX1; plant.  
 OS Oryza sativa.  
 PN MO2003048319-A2.  
 PD 12-JUN-2003.  
 XX 27-NOV-2002; 2002MO-US038359.  
 XX 30-NOV-2001; 2001US-0334501P.  
 XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 PA Sainz MB, Salmerson J, Weislo L;  
 PI WPI; 2003-505288/47.  
 DR N-PSDB; AAD57634.  
 XX  
 XX New nucleic acid from Oryza sativa, useful for altering abiotic stresses  
 PT tolerance, pathogen or disease resistance or the grain quality,  
 PT nutritional content or yield in a plant.  
 PS Claim 1; Page 133-137; 223pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules from rice encoding  
 CC proteins for abiotic stress tolerance, enhanced pathogen or disease  
 CC resistance and altered nutritional quality. The sequences of the  
 CC invention are useful for altering abiotic stress tolerance, pathogen or  
 CC disease resistance or the grain quality, nutritional content or yield in  
 CC a plant. The present sequence is rice disease resistance protein, LOX1  
 CC  
 XX  
 SQ Sequence 924 AA;  
 Query Match 9.2%; Score 87; DB 6; Length 924;  
 Best Local Similarity 23.0%; Pred. No. 4.7; Indels 54; Gaps 7;  
 Matches 34; Conservative 16; Mismatches 44;  
 QY 55 DKLM---EAMPABEEFVGVSSKQMLGDPTRLRTQHF-----GGRMEKV---95  
 DB 654 DKLMRPDTALPAD---LVRGMAEDPT--AEHGKLAIEDYPPANDGLIMDAIKTW 707  
 QY 96 -----SEBEVIGYHQLRVPHQRKYKDTTMEKVTMKGHANSANLHWYKIKDG-----140  
 DB 708 VQAYVAFYDADSVAGDEELQ-----AFWTEVATKGGHDKQAPWMPKLDSPESLA 759  
 QY 141 -----VWKFAGLKPDIRMGEPFDRIF 162  
 DB 760 HTLTITVVAALHAHAAVNFQGYDFGGIF 787  
 RESULT 5  
 AEB40857  
 ID AEB40857 standard; protein; 331 AA.  
 AC AEB40857;  
 DT 08-SEP-2005 (first entry)  
 DE L. pneumophila protein SEQ ID NO 5189.  
 DE detection; infection; Antibacterial; Vaccine.  
 KM Legionella pneumophila.  
 OS  
 XX

XX  
 PN MO2005049642-A2.  
 XX  
 PD 02-JUN-2005.  
 XX  
 XX 23-SEP-2004; 2004MO-IB003578.  
 XX  
 XX 21-NOV-2003; 2003FR-00013687.  
 XX  
 XX (INSP ) INST PASTEUR.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Buchrieser C, Tichit M, Etienne J, Ma L, Caralec C, Glaeser P;  
 PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;  
 PI Jarraud S;  
 DR WPI; 2005-388305/40.  
 XX  
 XX New genome of Legionella pneumophila Paris strain and derived  
 PT polypeptides, useful for detection or identification of the strain and  
 PT for treatment and prevention of infections.  
 PS Claim 3; SEQ ID NO 5189; 660pp; English.  
 XX  
 XX The invention relates to an isolated or purified nucleotide sequences (I)  
 CC from Legionella pneumophila Paris strain. (I), and their related  
 CC sequences or fragments, are useful as primers and probes for detection  
 CC and amplification, including differentiation between the Paris and  
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant  
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
 CC specific antibodies (Ab), also used for detection/identification of  
 CC Legionella, and some (II), specifically those involved in synthesis of  
 CC surface proteins, are targets for identification of inhibitors. (II), or  
 CC vectors that contain (II), are useful as vaccines and immunogenic  
 CC compositions, for treatment and prevention of infections by L.  
 CC pneumophila. The present sequence represents the amino acid sequence of a  
 CC L. pneumophila protein.  
 CC  
 XX  
 SQ Sequence 331 AA;  
 Query Match 9.2%; Score 86.5; DB 9; Length 331;  
 Best Local Similarity 22.8%; Pred. No. 1.3; Indels 17; Gaps 2;  
 Matches 26; Conservative 20; Mismatches 51;  
 QY 74 QMLGDPTRLRTQHFIGTR-----WEKVSDEVIGYHQLRVPHQRKY-----DT 116  
 DB 13 QILGDGACHSGSGSELGNALKIRSSAVWKKQINQINDLGIPIRIIPHQGYQLEKPLILDSNE 72  
 QY 117 TMKEVTMKGHANSANLHWYKIKIDGVWKFAGLKPDIRMGEPFDRIFEDGRFTFG 170  
 DB 73 ITKQLHSKGFSPFNLHFTSIDSTNRVLKDPSSSAVEICTCTEOTQGRGRFG 126  
 RESULT 6  
 AEB37544  
 ID AEB37544 standard; protein; 332 AA.  
 AC AEB37544;  
 DT 08-SEP-2005 (first entry)  
 DE L. pneumophila protein SEQ ID NO 1876.  
 DE detection; infection; Antibacterial; Vaccine.  
 KM Legionella pneumophila.  
 OS  
 PN MO2005049642-A2.  
 XX  
 XX 02-JUN-2005.  
 XX

PF 23-SEP-2004; 2004WO-IB003578.  
 XX  
 PR 21-NOV-2003; 2003FR-00013687.  
 XX  
 XX (INSP ) INST PASTEUR.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (ULY-) UNIV LYON 1 BERNARD CLAUDE.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P,  
 PI Renuik C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F,  
 PI Jarraud S;  
 DR WPI; 2005-388305/40.  
 XX  
 PT New genome of *Legionella pneumophila* Paris strain and derived  
 PT polypeptides, useful for detection or identification of the strain and  
 PT for treatment and prevention of infections.  
 XX  
 PS Claim 3; SEQ ID NO 1876; 660bp; English.  
 XX  
 CC The invention relates to an isolated or purified nucleotide sequences (I)  
 CC from *Legionella pneumophila* Paris strain. (I), and their related  
 CC sequences or fragments, are useful as primers and probes for detection  
 CC and amplification, including differentiation between the Paris and  
 CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant  
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
 CC specific antibodies (Ab), also used for detection/identification of  
 CC *Legionella*, and some (II), specifically those involved in synthesis of  
 CC surface proteins, are targets for identification of inhibitors. (II), or  
 CC vectors that contain (II), are useful as vaccines and immunogenic  
 CC compositions, for treatment and prevention of infections by *L.*  
 CC *pneumophila*. The present sequence represents the amino acid sequence of a  
 CC *L. pneumophila* protein.

```

XR 23-JUL-1997, 97US-00902615.
XX (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Kleantous H, Al-Garawi A, Miller C, Tomb J, Oomen RP;
XX
DR WPI, 1998-542293/46.
XX N-PSDB; AAX14439.
XX
XX New isolated Helicobacter polymucleotides - used to develop products for
PT the diagnosis, prevention and treatment of Helicobacter infections and
PT gastrointestinal diseases.
XX
XX Claim 8, Page 1521-1522; 2054dp; English.
XX
XX This sequence represents a Helicobacter pylori GHPD protein of the
CC invention. The polypeptides can be used for preventing or treating
CC Helicobacter infections, and gastroodnodal diseases associated with
CC these infections, including acute, chronic, and atrophic gastritis, and
CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
CC used for the production of antibodies. The products can also be used for
CC detection and diagnosis
XX
XX
SQ Sequence 265 AA;
XX
XX Query Match 9.0%; Score 85; DB 2; Length 265;
XX Best Local Similarity 22.4%; Pred. No. 1.5;
XX Matches 39; Conservative 28; Mismatches 57; Indels 50; Gaps 7
XX
XX 13 FSDYLALMTCYEMADSDYSKQMDLRLRYVIAPTLRIDYRSLDKL--WEAMPPEFVGWV 70
XX 102 FYQFVQ-----FSDSCNRRRRKRRKVCVLLPNESVDSLFLYRSANWSEREAYDMIGIV 154

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[illegible][illegible]

	RESULT 7
AAW98720	
ID	AAW98720 standard; protein; 265 AA.
XX	
AC	AAW98720;
XX	
DT	31-MAR-1999 (first entry)
XX	
DE	H. pylori GHPO 811 protein.
XX	
KM	GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis,
KW	peptic ulcer disease.
XX	
OS	Helicobacter pylori.
XX	
PN	MO9843478-A1.
XX	
PD	08-OCT-1998.
XX	
PF	01-APR-1998; 98MO-US006371.
XX	
PR	01-APR-1997; 97US-00833457.
PR	24-JUN-1997; 97US-00881227.

XX	
DE	Bacterial polypeptide #477.
XX	
KW	<i>Proteus mirabilis</i> infection; bacterial infection; antibacterial;
KW	immunostimulant.
XX	
OS	<i>Proteus mirabilis</i> .
XX	
PN	US6605709-B1.
XX	
PD	12-AUG-2003.
XX	
FP	05-APR-2000; 2000US-00543681.
XX	
PR	09-APR-1999; 99US-0128706P.
XX	
PA	(GENO-) GENOME THERAPEUTICS CORP.
XX	
P1	Bretton GL;
XX	
DR	WPI; 2003-895291/82.
XX	
DR	N-PSDB; ADP00192.
XX	

PT New Proteus mirabilis polypeptides and polynucleotides, useful as  
 PT reagents for diagnosis of bacterial disease, as components of  
 PT antibacterial vaccines, as targets for antibacterial drugs, or as  
 PT biocontrol agents for plants.

PS Disclosure; SEQ ID NO 4649; 870bp; English.

XX The invention relates to new Proteus mirabilis polypeptides and  
 CC polynucleotides. The invention also relates to antibodies against the  
 CC polypeptides, methods for producing the polypeptides, a method of  
 CC generating vaccines for immunising an individual against P. mirabilis, a  
 CC method for evaluating a compound for the ability to bind a P. mirabilis  
 CC polypeptide and a method for screening test compounds for anti-bacterial  
 CC activity. The polypeptides and polynucleotides are useful as molecular  
 CC targets for diagnosing, preventing and treating pathological conditions  
 CC resulting from bacterial infection, as reagents for diagnosis of  
 CC bacterial diseases, as components of antibacterial vaccines, as targets  
 CC for antibacterial drugs or as bio-control agents for plants. This  
 CC sequence represents a Proteus mirabilis polypeptide of the invention.

XX Sequence 338 AA;

Query Match 8.9%; Score 84; DB 7; Length 338;  
 Best Local Similarity 25.5%; Pred. No. 2.6;  
 Matches 39; Conservative 18; Mismatches 42; Indels 54; Gaps 10;

QY 35 WDLRLKVIATLADIRSFIDKIMEMPAEFPQMSKMDPTLR-TQHGIGRWE 93

Db 94 WDAQR-----EDVLDKMFETAP-OSFV-----MLADLCRGAKHTLQRTSW 135

QY 94 KVSDEVIQYHQR-----VPHORYKDTMTKEVTMGHNSANLHYKK--IDGVW 142

Db 136 GI---ETI--ERLKAQGRNVTFMVPHGMAVDVPAMLLAAGQMAAFHHQKDPVDTLM 190

QY 143 -----KPAGLKPDIR-----WGEP 156

Db 191 NKARYHFGRLHSREAGIKPFIETVSGFWGY 223

QY

RESULT 9  
 AAE12983  
 ID AAE12983 standard; protein; 349 AA.

XX AAE12983;

XX 28-JUN-2002 (first entry)

XX Murine Wnt-7B protein.

XX Mouse; Wnt-7B-like protein; gene therapy; hypotensive; neoplasia; cancer;

XX immunodisorder; inflammatory disorder; arthritis; haematopoiesis; allergy;

XX neurological disease; Alzheimer's disease; cardiovascular disorder; burn;

XX diabetes mellitus; periodontal disease; haemorrhage; multiple sclerosis;

XX rheumatoid arthritis; thrombocytopaenia; skin disorder; atherosclerosis;

XX lung fibrosis; skeletal disorder; platelet disorder; cell proliferation;

XX transplant rejection; acquired immune deficiency syndrome; AIDS; wound;

XX connective tissue disease; drug screening; ulcer; liver fibrosis.

XX Mus musculus.

XX WO200174856-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010679.

XX 03-APR-2000; 2000US-0194256P.

XX 26-JUL-2000; 2000US-00625634.

XX (CURA-) CURAGEN CORP.

XX Vernet CAM, Raetelli L, Herrmann JL;

XX WPI; 2001-626382/72.

PT New Wnt-7B-like polypeptides and polynucleotides for diagnosing,

PT preventing and treating broad range of pathological states such as

PT cancer, hematopoietic, inflammatory, skin, skeletal disorders and

PT atherosclerosis.

PS Claim 15; Fig 2B; 115bp; English.

XX The invention relates to human Wnt-7B-like protein and its cDNA molecule.  
 CC Human Wnt-7B-like proteins and their nucleic acids are useful for  
 CC treating and preventing Wnt-7B-like-associated disorders such as  
 CC neoplasia, cancer, e.g., colorectal carcinoma, prostate cancer, immune  
 CC disorder, autoimmune diseases, such as connective tissue disease,  
 CC multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis,  
 CC acquired immune deficiency syndrome (AIDS), transplant rejection,  
 CC allergy, infection, inflammatory disorder, arthritis, haematopoietic  
 CC disorder, skin disorder (keloid), restenosis, neurological disease,  
 CC Alzheimer's disease, trauma, wound, spinal cord injury, skeletal disorder  
 CC and cardiovascular disorders such as diabetes mellitus, atherosclerosis,  
 CC cerebral thrombosis or haemorrhage, and other diseases, including  
 CC hypertension, hypothyroidism, myeloid or lymphoid cell deficiencies and  
 CC various platelet disorders such as thrombocytopaenia. Wnt-7B-like protein  
 CC is also useful for cell proliferation, tissue repair and in the treatment  
 CC of burns, incisions and ulcers, periodontal disease and treatment of lung  
 CC or liver fibrosis. Wnt-7B-like protein plays an important role in  
 CC autocrine stimulation of tumour growth, chemoresistance, radiotherapy  
 CC resistance and also for screening drugs. Wnt-7B-like nucleic acids are  
 CC useful in gene therapy. The present sequence is murine Wnt-7B protein  
 CC related to the invention

XX Sequence 349 AA;

Query Match 8.9%; Score 84; DB 4; Length 349;  
 Best Local Similarity 31.1%; Pred. No. 2.7;  
 Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

QY 84 OHFIGTRW--EKVSDEVIQYHQLRPHQRKDTMTKEVTMGHNS-----ANLH- 133

Db 74 QHGFPRFRRNCSALGKTVFG--QELKVGSRBAFT--VAITAGVAHVATPAACSGCNLSN 130

QY 134 -----WYKKIDGVWKFAGLKPDIRMGEPDFDRIFEDGRE 167

Db 131 CGCDREKQGVYQABG-WKMGCSADVRYG-IDFSRRFVDARE 171

XX RESULT 10

XX ADS31850  
 ID ADS31850 standard; protein; 349 AA.

XX ADS31850;

XX 30-DEC-2004 (first entry)

XX Mouse wingless Wnt7b.

XX vulnerable; cell therapy; cartilage formation;

XX fibroblast growth factor 18; Fgf-18; sonic hedgehog; Shh; beta-catenin;

XX Wnt; tissue repair; tissue reconstruction; airway; trachea; bronchi; lung;

XX larynx; mouse; Wnt7b.

XX Mus musculus.

XX WO2004087055-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009264.

XX 27-MAR-2003; 2003US-0458224P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Whitsect JA;  
PI  
XX  
XX  
DR MPI: 2004-729163/71.  
XX N-PSDB; ADS31849.  
XX  
XX New pharmaceutical composition comprising a cartilage formation inducing  
PT protein, e.g., fibroblast growth factor (FGF)-18, sonic hedgehog (Shh),  
PT beta-catenin or Wnt proteins, useful in repairing tissues in a conducting  
PT airway.  
XX  
XX  
PS Disclosure; SEQ ID NO 14; 94bp; English.

XX  
XX The invention describes a new pharmaceutical composition comprises at  
CC least one cartilage formation inducing protein consisting of fibroblast  
CC growth factor (FGF)-18, sonic hedgehog (Shh), beta-catenin or Wnt  
CC proteins to induce cartilage formation. Also described are: inducing  
CC cartilage formation in an affected area of a patient requiring such  
CC treatment; an expression vector comprising at least one nucleotide  
CC sequence encoding at least one cartilage formation inducing protein  
CC consisting of FGF-18, Shh, beta-catenin or Wnt proteins; expressing FGF-  
CC 18 protein in a cell in vitro; treating a patient in need of cartilage  
CC formation in an affected area of the patient; a cell culture comprising  
CC cells, in a medium capable of sustaining cell growth, having an  
CC expression vector comprising at least one nucleotide sequence encoding at  
CC least one cartilage formation inducing protein consisting of FGF-18, Shh,  
CC beta-catenin or Wnt proteins; and preparing a cell culture comprising  
CC cells capable of inducing cartilage formation in vitro in a medium  
CC capable of sustaining cell growth. The pharmaceutical composition is  
CC useful in inducing cartilage formation for repairing and reconstructing  
CC various tissues in a conducting airway, e.g., trachea, bronchi, lung or  
CC larynx of a patient. This is the amino acid sequence of mouse Wnt7b.  
CC Note: The sequence listing of this specification was not finished upon  
CC filing resulting in the loss of SEQ ID NO 1 and the N-terminal end of SEQ  
CC ID NO 2.  
XX  
XX  
SQ Sequence 349 AA;

Query Match 8.9%; Score 84; DB 8; Length 349;  
Best Local Similarity 31.1%; Pred. No. 2.7;  
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

QY 84 QHFIGGTRN--EKVSEDEVIGYHQLRVPHQRYKDTMKVTKGHAHS-----ANLH- 133  
DB 74 QHQFRFGMNCSALGKVTGFG--QELRVGSRBAFT--YAITAGVAHVAVTAAACSGNLSN 130  
QY 134 -----WYKKIDGVKFKAGLKPDIRGGEFDPRIPEDEGR 167  
DB 131 CGCDREKOGYINQAEQ-WKMGCSADVRYG-IDFSRRFVDARE 171

RESULT 11  
ADU86486  
ID ADU86486 standard; protein; 349 AA.  
XX  
XX ADU86486;  
AC  
XX  
XX  
DT 24-FEB-2005 (first entry)  
DE  
XX

XX Mouse wingless-type protein, Wnt7B.  
XX  
XX Wnt; wingless-type protein; neurogenesis; spinal cord injury; injury;  
KW parkinsons disease; antiparkinsonian; neurological disease;  
KW motor neurone disease; neuroprotective; paralysis.  
XX  
XX

OS Mus musculus.  
XX  
XX WO2004103394-A2.  
XX  
XX 02-DEC-2004.  
XX  
XX 17-MAY-2004; 2004WO-US015264.  
XX

PR 15-MAY-2003; 2003US-0470913P.  
XX  
XX (UYCH-) UNIV CHICAGO.  
PA  
XX  
XX  
PI Zou Y;  
XX  
XX MPI: 2004-834171/82.  
DR N-PSDB; ADU86485.  
XX  
XX

PT Modulating growth of a neuron for treating spinal cord disorder or  
PT paralysis comprises contacting the neuron with a Wnt, a Wnt-like  
PT substance, and/or a chemical compound affecting a Wnt signaling pathway.  
XX  
XX  
PS Disclosure; SEQ ID NO 60; 248bp; English.

XX  
XX The invention relates to modulating growth of a neuron comprises  
CC contacting the neuron with a Wnt (wingless-type protein), a Wnt-like  
CC substance, and/or a chemical compound affecting a Wnt signaling pathway.  
CC Also included are a method for identifying a substance that modulates  
CC growth of a neuron, a pharmaceutical composition for modulating growth of  
CC a neuron in a mammal (comprising a Wnt, a Wnt-like substance, or a  
CC chemical compound affecting a Wnt signaling pathway and a pharmaceutical  
CC preparation suitable for delivery to the mammal) and a method of  
CC inhibiting growth of a neuron in a subject. The neuron is a neuron in a  
CC spinal cord that has been damaged by traumatic spinal cord injury.  
CC Inhibiting growth of a neuron in a subject comprises providing a  
CC composition (comprising a secreted frizzled-related protein (SFRP), SFRP-  
CC like substance, Ryk or Ryk-like substance and a pharmaceutical  
CC preparation suitable for delivery to the subject and administering the  
CC composition to the subject. SFRP and Ryk are both proteins that bind to  
CC block the activity of Wnt. The method is useful for modulating growth of  
CC a neuron for preparing a composition for treating spinal cord disorder,  
CC paralysis, Parkinson's disease and motor neurone disease. The present  
CC sequence represents a Wnt protein from human or mouse.  
XX  
XX  
SQ Sequence 349 AA;

Query Match 8.9%; Score 84; DB 8; Length 349;  
Best Local Similarity 31.1%; Pred. No. 2.7;  
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

QY 84 QHFIGGTRN--EKVSEDEVIGYHQLRVPHQRYKDTMKVTKGHAHS-----ANLH- 133  
DB 74 QHQFRFGMNCSALGKVTGFG--QELRVGSRBAFT--YAITAGVAHVAVTAAACSGNLSN 130  
QY 134 -----WYKKIDGVKFKAGLKPDIRGGEFDPRIPEDEGR 167  
DB 131 CGCDREKOGYINQAEQ-WKMGCSADVRYG-IDFSRRFVDARE 171

RESULT 12  
AED95375  
ID AED95375 standard; protein; 349 AA.  
XX  
XX AED95375;  
AC  
XX  
XX  
DT 26-JAN-2006 (first entry)  
DE  
XX

XX Mouse Wnt7B protein SEQ ID NO:46.  
XX  
XX cell proliferation; cell regeneration; Wnt signaling pathway; cardiac;  
KW antiarteriosclerotic; vasotrophic; cytosclerotic; myocardial infarction;  
KW atherosclerosis; coronary artery disease; myocardial disease;  
KW cardiac failure; heart disease; cancer; Wnt7B.  
XX  
XX

OS Mus musculus.  
XX  
XX US2005261189-A1.  
XX  
XX 24-NOV-2005.  
XX  
XX 18-APR-2005; 2005US-00108528.  
XX

PR 16-APR-2004; 2004US-0563137P.  
 PR 02-AUG-2004; 2004US-0598368P.  
 PA (HYDR-) HYDRA BIOSCIENCES INC.  
 XX  
 PI Larsen G, Marvin M, Li DY, Wang E, Chen CMA, Shamah SM,  
 XX  
 XX WPI; 2006-008454/01.  
 DR N-PSDB; AED95374.  
 DR GENBANK; NM\_009528.  
 XX  
 PT Promoting neonatal or adult cardiac cell proliferation or regeneration,  
 PT by contacting a cell with a composition comprising an agent that acts at  
 PT the cell surface to promote signaling via the canonical Wnt signaling  
 PT pathway.  
 XX  
 XX Disclosure; SEQ ID NO 46; 203bp; English.  
 PS  
 XX The invention relates to a method for promoting neonatal or adult cardiac  
 CC cell proliferation and/or regeneration. The method comprises contacting  
 CC the cell with a composition comprising an agent that acts at the cell  
 CC surface to promote signaling via the canonical Wnt signaling pathway,  
 CC where the cell is contacted with an amount of the composition to promote  
 CC neonatal or adult cardiac cell proliferation and/or regeneration. Also  
 CC described: (1) treating a condition having cardiac cell injury or death;  
 CC (2) treating a developmental disorder of cardiac cells; and (3) a  
 CC modified polypeptide comprising a Wnt-related polypeptide or bioactive  
 CC fragment, appended with one or more moieties to produce a modified Wnt-  
 CC related polypeptide or bioactive fragment, where the modified Wnt-related  
 CC polypeptide or bioactive fragment promotes Wnt signaling via the  
 CC canonical Wnt signaling pathway. The Wnt polypeptide or bioactive  
 CC fragment is useful in the manufacture of a medicament for promoting  
 CC cardiac cell proliferation and/or regeneration, where the Wnt  
 CC polypeptide, or bioactive fragment promotes Wnt signaling via the  
 CC canonical Wnt signaling pathway, and where the Wnt polypeptide or  
 CC bioactive fragment is modified with one or more moieties to produce a  
 CC modified Wnt polypeptide or bioactive fragment. The method is useful for  
 CC promoting neonatal or adult cardiac cell proliferation and/or  
 CC regeneration. The Wnt polypeptide is also useful for treating cardiac  
 CC cell injury or death, e.g. myocardial infarction, atherosclerosis,  
 CC coronary artery disease, obstructive vascular disease, dilated  
 CC cardiomyopathy, heart failure, myocardial necrosis, valvular heart  
 CC disease, non-compaction of the ventricular myocardium, hypertrophic  
 CC cardiomyopathy, cancer or cancer-related conditions such as structural  
 CC defects resulting from cancer or cancer treatments. The present sequence  
 CC represents mouse Wnt7B, which is used in the exemplification of the  
 CC present invention. Mouse Wnt7B is located on chromosome 15.  
 XX  
 XX Sequence 349 AA;  
 SQ  
 Query Match 8.9%; Score 84; DB 10; Length 349;  
 Best Local Similarity 31.1%; Pred. No. 2.7; Indels 24; Gaps 7;  
 Matches 32; Conservative 11; Mismatches 36;  
 QY 84 QHEIGGTRW--EKVSEDEVIGYHQLRVPHQRKYDTTKEVTMKGHASH-----ANTLH-133  
 DB 74 QHQFRRFRWMCNLSGKTVFG-QELRVGSRBAFT--YAITAGVNAHVAACSGNLSN 130  
 QY 134 -----WYKKIDGYWKFAGLKPDIRMGEPDFDRIFDEGGE 167  
 DB 131 CGCDREKGYNOAEG-WKMGCGSADVRG-IDFSRFRVDARE 171  
 RESULT 13  
 ADX933641  
 ID ADX93641 standard; protein; 411 AA.  
 XX  
 AC ADX93641;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 XX Plant full length insert polypeptide seqid 56305.  
 DE  
 XX

KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomanan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 PN US2004034888-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 28-APR-2003; 2003US-00425114.  
 XX  
 XX 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX  
 PA (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABAS/) TABASKA J E.  
 PA (CAO/) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX  
 XX WPI; 2004-180133/17.  
 DR  
 XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX  
 XX Claim 1; SEQ ID NO 56305; 15bp; English.  
 PS  
 XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomanan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 CC  
 XX Sequence 411 AA;  
 SQ  
 Query Match 8.9%; Score 84; DB 8; Length 411;  
 Best Local Similarity 25.2%; Pred. No. 3.4; Indels 56; Gaps 10;  
 Matches 35; Conservative 17; Mismatches 31;  
 QY 26 WADSYSKDW-PRKRVIAPTLRIDRSF-----LDK-----LW-EAMPAEEFVGAV 70  
 DB 171 WKDVFDSASWEDLIVXYIIPKRLALQDFQINPANOXKQDFWVWMTSALIPQLVWHN- 229  
 QY 71 SSKOMLGDPFLTRQHFIGSTRWEKXSEDEVIGYHQLRVPHQRKYDTTKEVTMKGHASHA 130  
 DB 230 -----LEVDFP---SKWQVYL-----YHMLCSNPDPNEL----- 256  
 QY 131 NHHWYKKIDGYWKFAGLKP 149  
 XX

```
DB      257 -MMWYKG---WK--GLFP 268
RESULT 14
AAE61136
ID      AAE61136 standard; protein; 923 AA.
XX
AC      AAE61136;
XX
DT      18-MAY-1995 (first entry)
XX
DE      Plant blight-specific resistance lipoxigenase.
XX
KW      Plant blight specific resistance lipoxigenase; chloroplast; resistant;
KW      blight; gene expression; recombinant production.
XX
OS      Oryza sativa.
XX
PN      JP06225774-A.
XX
PD      16-AUG-1994.
XX
PF      16-JUN-1992; 92JP-00180552.
XX
PR      16-JUN-1992; 92JP-00180552.
XX
PA      (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX
DR      MPI: 1994-298802/37.
XX
DR      N-PSDB; AAO68842.
XX
PT      Plant blight resistance-specific lipoxigenase gene - useful for
PT      expression of proteins in the chloroplast.
XX
PS      Claim 2; Page 5-11; 13pp; Japanese.
XX
CC      The CDNA encoding the blight resistance-specific lipoxigenase (See
CC      AAO68842) is useful for the elucidation of the mechanism of blight
CC      resistance in plants and makes possible the expression of various
CC      proteins in the chloroplast. The cDNA may also be expressed in bacterial,
CC      animal or plant cells to recombinantly produce the blight resistance-
CC      specific lipoxigenase
XX
SQ      Sequence 923 AA;
XX
Query Match      8.8%; Score 83; DB 2; Length 923;
Best Local Similarity 23.3%; Pred. No. 13;
Matches 34; Conservative 16; Mismatches 46; Indels 50; Gaps 7;
QY      55 DKLM---EAMPAEFVGVNVSKOMLGDPT-----LRTQHF---IGSTRWEKV----- 95
DB      653 DKLMREFDTEALPAD---LVRGMAESDPFAEQGLKLAIEDYFPANDGLIIMDAIKTWVQ 708
QY      96 -----SEDEVIGHOLRVPHQRKDTTMEKVTMKGHAHSLMWYKKIDG----- 140
DB      709 AYVARYPPDADSVAGDEIQ-----AFWTEVRTKGHDKKDAPMPKLDPSIESIAHT 760
QY      141 ----VWKFAGLKPDIRKGEFDPDIRIF 162
DB      761 LTNIVWVAHAHAANVNGOYDFGQYF 786
RESULT 15
AAE12982
ID      AAE12982 strand; protein; 349 AA.
XX
AC      AAE12982;
XX
DT      28-JAN-2002 (first entry)
XX
DE      Human Wnt-7B-like protein from clone 29518614.0.61.
XX
DE      Human; Wnt-7B-like protein; gene therapy; hypotensive; neoplasia; cancer;
KW
```

```
KW      tranquillizer; inflammatory disorder; arthritis; haematopoiesis; allergy;
KW      immune disorder; autoimmune disease; thyroiditis; restenosis; thrombosis;
KW      neurological disease; Alzheimer's disease; cardiovascular disorder; burn;
KW      diabetes mellitus; periodontal disease; haemorrhage; multiple sclerosis;
KW      rheumatoid arthritis; thrombocytopaenia; skin disorder; atherosclerosis;
KW      lung fibrosis; skeletal disorder; platelet disorder; cell proliferation;
KW      transplant rejection; acquired immune deficiency syndrome; AIDS; wound;
KW      connective tissue disease; drug screening; ulcer; liver fibrosis.
XX
OS      Homo sapiens.
XX
PN      WO200174856-A2.
XX
PD      11-OCT-2001.
XX
PF      03-APR-2001; 2001WO-US010679.
XX
PR      03-APR-2000; 2000US-0194256P.
XX
PR      26-JUL-2000; 2000US-00625634.
XX
PA      (CURA-) CURAGEN CORP.
XX
PI      Vernet CAM, Rascelli L, Herrmann JL;
XX
DR      MPI: 2001-626382/72.
XX
DR      N-PSDB; AAD20986.
XX
PT      New Wnt-7B-like polypeptides and polynucleotides for diagnosing,
PT      preventing and treating broad range of pathological states such as
PT      cancer, hematopoietic, inflammatory, skin, skeletal disorders and
PT      atherosclerosis.
XX
PS      Claim 12; Fig 2A; 115pp; English.
XX
CC      The invention relates to human Wnt-7B-like protein and its cDNA molecule.
CC      Human Wnt-7B-like proteins and their nucleic acids are useful for
CC      treating and preventing Wnt-7B-like-associated disorders such as
CC      neoplasia, cancer, e.g., colorectal carcinoma, prostate cancer, immune
CC      disorder, autoimmune diseases, such as connective tissue disease,
CC      multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis,
CC      acquired immune deficiency syndrome (AIDS), transplant rejection,
CC      allergy, infection, inflammatory disorder, arthritis, haematopoietic
CC      disorder, skin disorder (keloid), restenosis, neurological disease,
CC      Alzheimer's disease, trauma, wound, spinal cord injury, skeletal disorder
CC      and cardiovascular disorders such as diabetes mellitus, atherosclerosis,
CC      cerebral thrombosis or haemorrhage, and other diseases, including
CC      hypertension, hypothyroidism, myeloid or lymphoid cell deficiencies and
CC      various platelet disorders such as thrombocytopaenia. Wnt-7B-like protein
CC      is also useful for cell proliferation, tissue repair and in the treatment
CC      of burns, incisions and ulcers, periodontal disease and treatment of lung
CC      or liver fibrosis. Wnt-7B-like protein plays an important role in
CC      autocrine stimulation of tumour growth, chemoresistance, radiotherapy
CC      resistance and also for screening drugs. Wnt-7B-like nucleic acids are
CC      useful in gene therapy. The present sequence is human Wnt-7B-like protein
CC      which is obtained from clone 29518614.0.61
XX
SQ      Sequence 349 AA;
XX
Query Match      8.6%; Score 81; DB 4; Length 349;
Best Local Similarity 31.2%; Pred. No. 5.8;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;
QY      91 RW--EKVSEDEVIGHOLRVPHQRKDTTMEKVTMKGHAHSLMWYKKIDG-----ANLH----- 133
DB      81 RWNCGALGKTYFG--QELRVSGREAFT--VATTAAGVAHNTAAGSGNLSNCGDREX 137
QY      134 --WYKKIDGVWKFAGLKPDIRKGEFDPDIRIFPDGKE 167
DB      138 OGYYNQAGG-WKMGGCSADVRYG-IDFSRRFVDARE 171
```

Search completed: December 5, 2006, 01:22:15  
Job time : 202 secs





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OM protein - protein search, using sw model

Run on: December 5, 2006, 01:19:01 ; Search time 302 Seconds

(without alignments)  
526.830 Million cell updates/sec

Title: US-10-507-132-2

Perfect score: 942

Sequence: 1 MGSQVQKSDERFSDYLGIM.....WGSPDFRIFEDGRERFGDK 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	938	99.6	172	1	SCYD MAGGR
2	698	74.1	186	2	Q6XR11_9PEZI
3	686	72.8	188	1	SCYD GLCIA
4	686	72.8	216	2	Q9C4Z6_OPRFL
5	657	69.7	185	2	Q7ZBL5_9PLEO
6	627.5	66.6	174	2	Q7SBE1_NEUCR
7	550	58.4	122	2	Q8NJI6_9PEZI
8	548.5	58.2	150	2	Q2WEI4_SORMA
9	544	57.7	121	2	Q8NJI5_OPRFL
10	542	57.5	122	2	Q8NJI7_9PEZI
11	540	57.3	121	2	Q8NJI8_9PEZI
12	537	57.0	122	2	Q8NJI1_9PEZI
13	537	57.0	122	2	Q8NJI2_OPRFL
14	532	56.5	121	2	Q8NJI0_OPRFL
15	530	56.3	122	2	Q8NJI1_OPRFL
16	528	56.1	122	2	Q8NJI8_9PEZI
17	526	55.8	168	1	SCYD ASPFU
18	522	55.4	122	2	Q8NJI4_9PEZI
19	516	54.8	122	2	Q8NJI3_9PEZI
20	503	53.4	121	2	Q8NJI9_9PEZI
21	427	45.3	161	2	Q4I8I1_GIBZE
22	332	35.2	1201	2	Q5BH35_EMEVI
23	99.5	10.6	605	2	Q8ZSD9_ANASP
24	92	9.8	185	2	Q5YQ84_NOCFA
25	91	9.7	168	2	Q9RB47_9CLOT
26	90	9.6	318	2	Q7TDP4_9VIRU
27	89.5	9.5	583	2	Q6BVC7_DEBHA
28	88.5	9.4	530	2	Q2UUC3_ASPOR
29	88	9.3	166	1	BAIE_EUBSP
30	87.5	9.3	333	2	Q5WYB7_LEGPI
31	87	9.2	211	2	Q3IEB7_PSEHT

32	87	9.2	286	2	Q3G8U4_9FIRM	Q3G8U4 syntrophom
33	87	9.2	924	1	LOXC1_ORYSA	P38419 oryza sativ
34	87	9.2	941	1	LOXC2_ORYSA	P84YK8 oryza sativ
35	87	9.2	1277	2	Q2UEDE_ASPOR	Q2UEDE aspergillus
36	86.5	9.2	331	2	Q5X6W7_LEGPA	Q5X6W7 legionella
37	86.5	9.2	331	2	Q5X6W7_LEGPA	Q5X6W7 legionella
38	86	9.1	201	2	Q2IS89_RHOPA	Q2IS89 rhodosphe
39	84.5	9.0	380	2	Q26444_METHH	Q26444 methanobact
40	84	8.9	349	1	Q5NSW6_MOUSE	P28047 mus musculu
41	84	8.9	349	2	Q5NSW6_MOUSE	P28047 mus musculu
42	84	8.9	353	2	Q6NZR1_MOUSE	Q6NZR1 mus musculu
43	84	8.9	441	2	Q4IDL7_GIBZE	Q4IDL7 giardiala
44	84	8.9	1058	2	Q4X125_ASPFU	Q4X125 aspergillus
45	83.5	8.9	468	2	Q7R5D9_GIALA	Q7R5D9 giardia lam

#### ALIGNMENTS

RESULT 1  
SCYD\_MAGGR STANDARD; PRT: 172 AA.  
ID SCYD\_MAGGR  
AC P56221;  
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.  
DT 15-JUL-1998, sequence version 1.  
DT 07-FEB-2006, entry version 34.  
DE Scytalone dehydratase (EC 4.2.1.94).  
GN Name=Schl;  
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.  
OX NCBI\_Taxid=148305;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=9823280; PubMed=9571787;  
RA Motoyama T., Imanishi K., Yamaguchi I.;  
RT "CDNA cloning, expression, and mutagenesis of scytalone dehydratase  
RT needed for pathogenicity of the rice blast fungus, Pyricularia  
RT oryzae";  
RL Biosci. Biotechnol. Biochem. 62:564-566(1998).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=9517111; PubMed=7866745;  
RA Lundqvist T., Rice J., Hodge C.N., Basarab G.S., Pierce J.,  
RA Lundqvist Y.;  
RT "Crystal structure of scytalone dehydratase -- a disease determinant  
RT of the rice pathogen, Magnaporthe grisea.";  
RL Structure 2:937-944(1994).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RX MEDLINE=98332516; PubMed=9665698; DOI=10.1021/bj980321b;  
RA Nakasako M., Motoyama T., Kurahashi Y., Yamaguchi I.;  
RT "Cryogenic X-ray crystal structure analysis for the complex of  
RT scytalone dehydratase of a rice blast fungus and its tight-binding  
RT inhibitor, carpropamid: the structural basis of tight-binding  
RT inhibition.";  
RL Biochemistry 37:9931-9939(1998).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).  
RX MEDLINE=99119201; PubMed=9922139; DOI=10.1021/bj981848r;  
RA Chen J.M., Xu S.L., Wawrzak Z., Basarab G.S., Jordan D.B.;  
RT "Structure-based design of potent inhibitors of scytalone dehydratase:  
RT displacement of a water molecule from the active site.";  
RL Biochemistry 37:17735-17744(1998).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).  
RX MEDLINE=99310043; PubMed=10382670;  
DOI=10.1002/(SICI)1097-0134(19990601)35:4<425::AID-PROT6>3.0.CO;2-T;  
RA Wawrzak Z., Sandalova T., Steffens J.J., Basarab G.S., Lundqvist T.,  
RA Lundqvist Y., Jordan D.B.;  
RT "High-resolution structures of scytalone dehydratase-inhibitor  
RT complexes crystallized at physiological pH.";  
RL Proteins 35:425-439(1999).

```

CC -1- FUNCTION: Catalyzes two steps in melanin biosynthesis. From
CC scytalone they are two dehydration steps and one reduction step to
CC yield melanin.
CC -1- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +
CC H2O.
CC -1- PATHWAY: Fungal melanin biosynthesis; first step.
CC -1- SUBUNIT: Homotrimer. Each subunit contains an active site, located
CC in the central part of the hydrophobic core of the monomer, which
CC functions independently.
CC -----
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CC -----
DR EMBL; AB004741; BAA34046.1; -; mRNA.
DR PDB; 1IDP; X-ray; A/B/C=1-172.
DR PDB; 1STD; X-ray; @=1-172.
DR PDB; 2STD; X-ray; @=1-172.
DR PDB; 3STD; X-ray; A/B/C=10-172.
DR PDB; 4STD; X-ray; A/B/C=10-172.
DR PDB; 5STD; X-ray; A/B/C=10-172.
DR PDB; 6STD; X-ray; A/B/C=10-172.
DR PDB; 7STD; X-ray; A/B/C=10-172.
DR LinkHub; P56221; -.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
DR 3D-structure; Lyase; Melanin biosynthesis.
KM CHAIN 1 172 Scytalone dehydratase.
FT FT Scytalone dehydratase.
FT FT /FTId=PRO_0000097639.
FT HELIX 13 32
FT TURN 33 33
FT HELIX 35 39
FT TURN 40 41
FT STRAND 42 49
FT HELIX 51 54
FT STRAND 55 55
FT STRAND 57 62
FT HELIX 63 71
FT STRAND 72 72
FT TURN 73 76
FT TURN 79 80
FT STRAND 81 83
FT STRAND 86 96
FT TURN 97 98
FT STRAND 99 115
FT TURN 116 117
FT STRAND 121 138
FT TURN 139 140
FT STRAND 141 155
SQ SEQUENCE 172 AA; 20250 MW; 2FA56296D5EE00DC CRC64;

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Query Match 99.6%; Score 938; DB 1; Length 172;  
 Best Local Similarity 99.4%; Pred. No. 3e-77;  
 Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSQVQKSDIEFTSDYLGIMTCYVEWADSYDSKMDRLKVIAPTLRIDYRSFLDKLWBA 60
DB 1 MGSQVQKSDIEFTSDYLGIMTCYVEWADSYDSKMDRLKVIAPTLRIDYRSFLDKLWBA 60
QY 61 MPAEEFVGVSVSSKQWLGDPFLRTQHFIGGTRMEKVSDEDEVIQYHQLRVPHQRYKDTTKE 120
DB 61 MPAEEFVGVSVSSKQWLGDPFLRTQHFIGGTRMEKVSDEDEVIQYHQLRVPHQRYKDTTKE 120
QY 121 VTMKGHAHSAHLHWYKKIDGVWKEAGLKDIPRIGCEFDPRIFPDGRTGDK 172
DB 121 VTMKGHAHSAHLHWYKKIDGVWKEAGLKDIPRIGCEFDPRIFPDGRTGDK 172

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RESULT 2  
 ID Q6KRI1\_9PEZI PRELIMINARY; PRT; 186 AA.  
 AC Q6KRI1;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

```

DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Scytalone dehydratase I.
GN Name=SD1;
OS Ceratocystis resinifera.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC Ceratocystis.
OX NCBI_TaxID=95837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Loppnau P.A.;
RL Submitted (Jun-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY214004; AAO60167.1; -; Genomic_DNA.
DR SMR; Q6KRI1; 21-182.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
SQ SEQUENCE 186 AA; 21516 MW; FD947DBR2534005F CRC64;

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Query Match 74.1%; Score 698; DB 2; Length 186;  
 Best Local Similarity 72.8%; Pred. No. 2.4e-55;  
 Matches 118; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

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QY 11 ITFSDYLGIMTCYVEWADSYDSKMDRLKVIAPTLRIDYRSFLDKLWBAEPAEEFVGV 70
DB 21 ISFEDYGLMNTALVEWADSYDSKMDRLKVIAPTLRIDYRSFLDKLWBAEPAEEFVGM 80
QY 71 SSKQWLGDPFLRTQHFIGGTRMEKVSDEDEVIQYHQLRVPHQRYKDTTKEVTKGHA 130
DB 81 SDPNVLGDPFLRTQHFVGSASRMRYSDEDEVGMHQLRVPHQRYKDTTKEVTKGHA 140
QY 131 NLHWYKKIDGVWKEAGLKDIPRIGCEFDPRIFPDGRTGDK 172
DB 141 NKHWYKKIDGVWKEAGLKDIPRIGCEFDPRIFPDGRTGDK 182

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RESULT 3  
 ID SCYD\_GLOLA STANDARD; PRT; 188 AA.  
 AC Q00455;  
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE Scytalone dehydratase (EC 4.2.1.94).  
 GN Name=SCD1;  
 OS Glomerella lagenarium (Anthracnose fungus) (Colletotrichum lagenarium).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;  
 OC microsporid Phyllachoraceae; Colletotrichum.  
 OX NCBI\_TaxID=5462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RC STRAIN=104-T;  
 RX MEDLINE=97111971; PubMed=8953707;  
 RA Kubo Y., Takano Y., Endo N., Yasuda N., Tajima S., Furusawa I.;  
 RT Cloning and structural analysis of the melanin biosynthesis gene SCD1  
 RT encoding scytalone dehydratase in Colletotrichum lagenarium.";  
 RL Appl. Environ. Microbiol. 62:4340-4344(1996).  
 CC -1- FUNCTION: Catalyzes two steps in melanin biosynthesis. From  
 CC scytalone they are two dehydration steps and one reduction step to  
 CC yield melanin.  
 CC -1- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +  
 CC H<sub>2</sub>O.  
 CC -1- PATHWAY: Fungal melanin biosynthesis; first step.  
 CC -1- SUBUNIT: Homotrimer. Each subunit contains an active site, located

in the central part of the hydrophobic core of the monomer, which functions independently (By similarity).

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CC -----

DR EMBL; D86079; BAA13009.1; -; Genomic\_DNA.

DR HSSP; P56221; 1IDP.

DR SMC; Q00455; 6-167.

DR InterPro; IPR004235; Scytalone\_DH.

DR Pfam; PF02982; Scytalone\_dh; 1.

DR ProDom; PD022193; Scytalone\_dh; 1.

KM Lyase; Melanin biosynthesis.

FT CHAIN 1 188 Scytalone dehydratase.  
/Fttid=PRO\_0000097638.

SQ SEQUENCE 188 AA; 21687 MW; A58FB3B940321EFA CRC64;

Query Match 72.8%; Score 686; DB 1; Length 188;  
Best local Similarity 71.9%; Pred. No. 3e-54;  
Matches 115; Conservative 24; Mismatches 21; Indels 0; Gaps 0.

DY 11 ITFSFDYLGLMTCYEWADSYDSKDWRLRKVIAPTLRIDYSFLDKLTMEAMPAEFFVGV 70  
||| ||| ::||||||| |  
Dy ITTFEDYLGNALTEPMWSDSVSKMDRKRKCIAPELRIDNRSFLDKIMEAPEEFFIMI 67  
||| ||| ::||||||| |

DY 71 SSKMQLGDPILRTLOHFIIGTGRWEKVSEDEVIGYHOLRVPHQRKYDTMKVEYTMKGHANSA 130  
||| ||| ::||||||| |

DY 68 SDKSVLGNPLTKTOHFITGSRWKEKVSDEVIQHQLRPVHQKYTDASREVAVKGHANSHY 127  
||| ||| ::||||||| |

Dy 131 NLHWKKXIKDGVMKFAGLKPDRIWGEFPDDRIPEOGERHPFG 170  
||| ||| ::||||||| |

Dy 128 NMHWYRRKNVGWKFAGLNPETIRWSBYDPDAVPADGRDSYG 167  
||| ||| ::||||||| |

RESULT 4

OQC426.OPHFL PRELIMINARY; FRT; 216 AA.

ID OQC426.OPHFL

AC OQC426;

DT 01-JUN-2001, integrated into UniProtKB/TREMBL.

DT 01-JUN-2001, sequence version 1.

DT 07-FEB-2006, entry version 12.

DE Scytalone dehydratase.

GN Name=OSDL;

OS Ophiostoma floccosum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.

OX NCBI\_TaxId=104300;

[1]

RN NUCLEOTIDE SEQUENCE.

RA STRAIN=N387N;

RC MEDLINE=21473268; PubMed=11589570; DOI=10.1007/s004380100534;

RX Wang H.L., Kim S.H., Breuil C.;

RT "A scytalone dehydratase gene from Ophiostoma floccosum restores the melanization and pathogenicity phenotypes of a melanin-deficient Colletotrichum lagenarium mutant.";

RT Mol. Genet. Genomics 266:126-132(2001).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RA STRAIN=N387N;

RC Wang H., Breuil C.;

RL Submitted (Oct-2000) to the EMBL/GenBank/DDBJ databases.

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CC -----

DR EMBL; AF316575; AKK11296.1; -; Genomic\_DNA.

DR HSSP; P56221; 1IDP.

DR SMC; OQC426; 22-182.

DR GO; GO:0016836; F:hydro-lyase activity; IEA.

DR GO; GO:0006582; P:melanin metabolism; IEA.

DR InterPro; IPR004235; Scytalone\_DH.

DR Pfam; PF02982; Scytalone\_dh; 1.

DR ProDom; PD022193; Scytalone DH; 1

Seq	Sequence	216 AA;	24167 MW;	D349BF7ADDF3DAD CRC64;
Qy	Query Match	72.8%;	Score 686;	DB 2; Length 216;
Db	Best Local Similarity	71.4%;	Pred. No. 3.5e-54;	
	Matches 115;	Conservative 23;	Mismatches 23;	Indels 0; Gaps 0;
Qy	10 ETPSDVLGMTCVYEWADSYDSKDMQRLKVAIPTLRIDYRSPLDKLMEAMPABEFPYGM	69		
Db	22 DISIEDPMGLCSAAYEWADSYDSKDMQRLKCIPIRLIDYRSPLDKLMEAMPABEFPYGM	81		
Qy	70 VSSKOMLGDPTLRTQHPFISGTREWEKVSDEVTIGYHQLRVPHQRYKDTTMEKVGNAHS	129		
Db	82 ISDPVSVLGNPLLRHQHFFGASRMERISDTEVGVGHQLRVPHQRYVDTTLTQVAVKGAHS	141		
Qy	130 ANLHWYKKIDGVWKFAGLKPDIRKGEEDPDRIFEDGSEFTG	170		
Db	142 ANTHWYRKVDGVWKFAGLDPKIRWFEDYDFKVFASGRDQFG	182		
RESULT 5				
Q728L5_9PLEO	PRELIMINARY;	PRT;	185 AA.	
AC	Q728L5_9PLEO			
AC	Q728L5_9PLEO			
DT	01-OCT-2003, integrated into UniProtKB/TrEMBL.			
DT	01-OCT-2003, sequence version 1.			
DT	07-FEB-2006, entry version 9.			
DE	Scytalone dehydratase.			
GN	Name=SCD1;			
OS	Bipolaris oryzae.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;			
OC	Pileoporales; Pileoporaceae; mitosporic Cochlidiobolus; Bipolaris.			
OK	NCBI TaxID=331195;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=D9/F6-69;			
RX	PubMed=14716498; DOI=10.1007/s00294-003-0477-1;			
RA	Kihara J., Moriaki A., Ueno M., Tokunaga T., Arase S., Honda Y.;			
RT	"Cloning, functional analysis and expression of a scytalone			
RT	dehydratase gene ( SCD1) involved in melanin biosynthesis of the			
RL	phytopathogenic fungus Bipolaris oryzae.";			
RT	Curr. Genet. 45:197-204(2004).			
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	EMBL; AB100172; BAC79365.1; -; Genomic_DNA.			
DR	HSSP; P56221; 11DP.			
DR	SMR; Q728L5_10-168.			
DR	GO; GO:0016836; F:hydro-lyase activity, IEA.			
DR	GO; GO:0006582; P:melanin metabolism, IEA.			
DR	InterPro; IPR004235; Scytalone_DH.			
DR	Pfam; PF02982; Scytalone dh; 1.			
DR	Prodom; PD023193; Scytalone DH; 1.			
DR	SEQUENCE 185 AA; 21285 MW; BE9937DB661D5DCB CRC64;			
Qy	Query Match	69.7%;	Score 657;	DB 2; Length 185;
Db	Best Local Similarity	67.5%;	Pred. No. 1.3e-51;	
	Matches 112;	Conservative 22;	Mismatches 32;	Indels 0; Gaps 0;
Qy	6 QKSEITPDSYDLGAMTCVYEWADSYDSKDMQRLKVAIPTLRIDYRSPLDKLMEAMPABE	65		
Db	4 KKEIQPTFEEWGCOSACYEWADSYDSKDMQRLKCAVPTIKIDYRSPLDKLMEAMPABE	63		
Qy	66 FVGVVSSKOMLGDPTLRTQHPFISGTREWEKVSDEVTIGYHQLRVPHQRYKDTTMEKVGNAHS	125		
Db	64 FVMAASDPAYVGNPLTQHPHIGSTREWEKVADEITGHHQLRVPHQRTDSRATVAVAKG	123		
Qy	126 HAHSAHLHWYKKIDGVWKFAGLKPDIRKGEEDPDRIFEDGSEFTG	171		
Db	124 HAHSAHLHWYKKIDGVWKFAGLKPDIRKGEEDPDRIFEDGSEFTG	169		
RESULT 6				

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07SBE1 NEUCR
ID 07SBE1 NEUCR PRELIMINARY; PRT; 174 AA.
AC 07SBE1
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE 07-FEB-2006, entry version 11.
DE Hypothetical protein.
GN ORFNames=NCU07823.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Reiman B.,
RA Eklins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Brann E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamyssejls M.,
RA Mauceli E., Bielke C., Rudd S., Frishman D., Krysstofova S.,
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catchside D.E.A., Li W., Pratt R.J., Osman S.A.,
RA Desouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamm M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.V., Fretlag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC
DR EMBL, AABX01000169; EAA33708.1; -; Genomic_DNA.
DR HSSP, P56221; 1IDP.
DR SMR, Q7SBE1; 11-171.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro: IPR004235; Scytalone_DH.
DR Pfam: PF02982; Scytalone_dh; 1.
DR ProDom: PD022193; Scytalone_DH; 1.
DR Hypothetical protein.
SQ SEQUENCE 174 AA; 20156 MW; 9CDS927C2302FE9A CRC64;

Query Match 66.6%; Score 627.5; DB 2; Length 174;
Best Local Similarity 65.1%; Pred. No. 5.8e-49;
Matches 112; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 1 MGSQVOKSDIEITPSDYLGLMTQVYENADSYDSKQMDRLKRVIAPTLRIDYRSFLDKLWEA 60
DB 1 MANAANPEKRTIEEYVLCTEACFEWADSYDTKDQFLRKCIAPTLRIDYRSFLNKLWEA 60
QY 61 MPAAEFVGNVSSKQMLCDPLRTQHFQGG-TRWEEKSSEDEVIGYHQLRVPHQRYKQDTMK 119
DB 61 MPAAEFVGNVSSKQMLCDPLRTQHFQGG-TRWEEKSSEDEVIGYHQLRVPHQRYKQDTMK 120
QY 120 EYVMKGGHAGSANLHWYKKIDGVNKKFAGLTKPDIDMGSEDPFRIPEDDETFEGD 171
DB 120 EYVMKGGHAGSANLHWYKKIDGVNKKFAGLTKPDIDMGSEDPFRIPEDDETFEGD 172
DB 121 KVAVTGHAHSHNTHYKIKINGVKKFAGLNPDIRMTBDFVADRAGEELGE 172

RESULT 7
08NUJ6_9PEZI PRELIMINARY; PRT; 122 AA.
AC 08NUJ6;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

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DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma piceae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxId=61273;
OS [1]
RN NUCLEOTIDE SEQUENCE.
RP Flect C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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CC
DR EMBL, AY098656; AAM34802.1; -; Genomic_DNA.
DR HSSP, P56221; 1IDP.
DR SMR, Q8NUJ6; 1-122.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro: IPR004235; Scytalone_DH.
DR Pfam: PF02982; Scytalone_dh; 1.
DR ProDom: PD022193; Scytalone_DH; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14291 MW; 50E940509D85F8A4 CRC64;

Query Match 58.4%; Score 550; DB 2; Length 122;
Best Local Similarity 76.2%; Pred. No. 4.4e-42;
Matches 93; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 25 EWADSYDSKQMDRLKRVIAPTLRIDYRSFLDKLWEAEPVGNVSSKQMLGDPPLRTQ 84
DB 1 EWADSYDSKQMDRLKRVIAPTLRIDYRSFLDKLWEAEPVGNVSSKQMLGDPPLRTQ 60
QY 85 HFIGSTRWEKSEDEVIGYHQLRVPHQRYKDTMKVETMKGHAHGANLHWYKKIDGVNKF 144
DB 61 HFIGSTRWEKSEDEVIGYHQLRVPHQRYKDTMKVETMKGHAHGANLHWYKKIDGVNKF 120
QY 145 AG 146
DB 121 AG 122

RESULT 8
Q2WEI4_SORMA PRELIMINARY; PRT; 150 AA.
AC Q2WEI4;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Scytalone dehydrogenase homologue (Fragment).
GN Name=smu7823;
OS Sordaria macrospora.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Sordaria.
OX NCBI_TaxId=5147;
RN NUCLEOTIDE SEQUENCE.
RP Nowrousian M., Wuertz C., Poegele S., Kueck U.;
RC STRAIN=S48977; TISSUE=Mycelium;
RA Nowrousian M., Wuertz C., Poegele S., Kueck U.;
RT "Why sequencing of Sordaria macrospora will lead to an improved
RT annotation of the Neurospora crassa genome.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC
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CC
DR EMBL, AJ575152; CAB00795.1; -; Genomic_DNA.
FT NON_TER 150
SQ SEQUENCE 150 AA; 17348 MW; CB9B307F47C1D5A7 CRC64;

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Query Match      58.2%; Score 548.5; DB 2; Length 150;
Best Local Similarity 65.3%; Pred. No. 7.7e-42;
Matches 98; Conservative 21; Mismatches 30; Indels 1; Gaps 1;

QY 1 MSQVQKSDSDITSDTLGLMTCYEMADSDSKMDRLKRVIAPTLRIDRSFLDKLMEWA 60
DB 1 MANANPKRITREYVIGCTEACFEWADSDSKDPLRKICIAPTLRVDYRSFLDKLMEWA 60
QY 61 MPABEFGWVSSKMGDPTLRTOHFIGG-TRMEKXSESDVIGYHOLRVPHQRYKDTMK 119
DB 61 MPABEFTQWSDKVKVIGNPLRTQHFMSGSKWEKVSDEITIGYHOLRVPHQVYTDKSC 120
QY 120 EYTMKGHAHSANLHWYKKIDGVWKFAGLKP 149
DB 121 KVAVTGHAHSHNTHYKXVDGWKFKAGLNP 150

RESULT 9
Q8NJ15.OPHFL PRELIMINARY; PRT; 121 AA.
ID O8NJ15.OPHFL
AC O8NJ15;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma floccosum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxID=104300;
RN NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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CC -----
DE EMBL: AY098657; AAM34803.1; -; Genomic_DNA.
DR HSSP; P56221; 1IDP.
DR SMR; O8NJ15; 1-121.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 14234 MW; 1940509D85F0A42A CRC64;

Query Match      57.7%; Score 544; DB 2; Length 121;
Best Local Similarity 76.0%; Pred. No. 1.5e-41;
Matches 92; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 25 EWADSDSKMDRLKRVIAPTLRIDRSFLDKLMEAMPABEFGWVSSKMGDPTLRQ 84
DB 1 EWADRDSDKMDRLKRVIAPTLRIDRSFLDKLMEAMPABEFGWVSSKMGDPTLRQ 60
QY 85 HFTGTRWEKVSDEVIGYHOLRVPHQRYKDTMKWEVTKGHAHSANLHWYKKIDGVWKF 144
DB 61 HFTGASRWERISDTEVVGHQLRVPHQVYTDLTTLQVAVGHAHSANLTHYRVDGWKF 120
QY 145 A 145
DB 121 A 121

RESULT 10
Q8NJ17.9PEZI PRELIMINARY; PRT; 122 AA.
ID O8NJ17.9PEZI
AC O8NJ17;

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DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Scytalone dehydratase (Fragment).
OS Ceratocystis resinifera.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC Ceratocystis.
OX NCBI_TaxID=95837;
RN NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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CC -----
DE EMBL: AY098657; AAM34801.1; -; Genomic_DNA.
DR HSSP; P56221; 1IDP.
DR SMR; O8NJ17; 1-122.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14376 MW; D807589723063C91 CRC64;

Query Match      57.5%; Score 542; DB 2; Length 122;
Best Local Similarity 75.4%; Pred. No. 2.4e-41;
Matches 92; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 25 EWADSDSKMDRLKRVIAPTLRIDRSFLDKLMEAMPABEFGWVSSKMGDPTLRQ 84
DB 1 EWADRDSDKMDRLKRVIAPTLRIDRSFLDKLMEAMPABEFGWVSSKMGDPTLRQ 60
QY 85 HFTGTRWEKVSDEVIGYHOLRVPHQRYKDTMKWEVTKGHAHSANLHWYKKIDGVWKF 144
DB 61 HFTGASRWERISDTEVVGHQLRVPHQRYTDAIKTTVKVGHASHANKKHWKXVDGWKF 120
QY 145 AG 146
DB 121 AG 122

RESULT 11
Q8NJ18.9PEZI PRELIMINARY; PRT; 121 AA.
ID O8NJ18.9PEZI
AC O8NJ18;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ceratocystis dinicola.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC Ceratocystis.
OX NCBI_TaxID=72031;
RN NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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CC -----
DE EMBL: AY098654; AAM34800.1; -; Genomic_DNA.
DR HSSP; P56221; 1IDP.

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DR GO:0016836; F:hydro-lyase activity; IEA.  
 DR GO:0006582; P:melanin metabolism; IEA.  
 DR InterPro: IPR004235; Scytalone\_DH.  
 DR Pfam: PF02982; Scytalone\_dh; 1.  
 DR ProDom: PD022193; Scytalone\_DH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 121  
 SQ SEQUENCE 121 AA; 14394 MW; C183FA038FCF5820 CRC64;

Query Match 57.3%; Score 540; DB 2; Length 121;  
 Best Local Similarity 76.0%; Pred. No. 3.6e-41;  
 Matches 92; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 25 EWADSYDSKDWRLKRVIAPTLRIDYRSFLDKLMEAMPABEFGVAVSSKOMLGDPPLRTQ 84  
 DB 1 EWADSYDSKDWRLKRVIAPTLRIDYRSFLDKLMEAMPABEFGVAVSSKOMLGDPPLRTQ 60  
 QY 85 HFTGGRWEKVSDEVIGYHQLRVPHQRYKDTTMEKVTMKGHAHSAHLHWYKKIDGVWKF 144  
 DB 61 HFTGGRWEKVSDEVIGYHQLRVPHQRYKDTTMEKVTMKGHAHSAHLHWYKKIDGVWKF 120  
 QY 145 A 145  
 DB 121 A 121

## RESULT 12

Q8N1E1\_9PEZI PRELIMINARY; PRT; 122 AA.

AC Q8N1E1;  
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Scytalone dehydratase (Fragment).  
 OS Ophiostoma piceae.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
 RX NCBI\_TaxID=61273;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Fleet C., Breuil C.;  
 RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi.";  
 RL Mycol. Res. 106:1331-1339(2002).  
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CC  
 DR EMBL: AY098660; AAM34806.1; -; Genomic\_DNA.  
 DR EMBL: AY098661; AAM34807.1; -; Genomic\_DNA.  
 DR HSSP: P56221; IIDP.  
 DR SMR: Q8N1E1; 1-122.  
 DR GO:0016836; F:hydro-lyase activity; IEA.  
 DR GO:0006582; P:melanin metabolism; IEA.  
 DR InterPro: IPR004235; Scytalone\_DH.  
 DR Pfam: PF02982; Scytalone\_dh; 1.  
 DR ProDom: PD022193; Scytalone\_DH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 122  
 SQ SEQUENCE 122 AA; 14246 MW; A17A6DD02BD9C80A CRC64;

Query Match 57.0%; Score 537; DB 2; Length 122;  
 Best Local Similarity 75.4%; Pred. No. 6.8e-41;  
 Matches 92; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

QY 25 EWADSYDSKDWRLKRVIAPTLRIDYRSFLDKLMEAMPABEFGVAVSSKOMLGDPPLRTQ 84  
 DB 1 EWADSYDSKDWRLKRVIAPTLRIDYRSFLDKLMEAMPABEFGVAVSSKOMLGDPPLRTQ 60  
 QY 85 HFTGGRWEKVSDEVIGYHQLRVPHQRYKDTTMEKVTMKGHAHSAHLHWYKKIDGVWKF 144  
 DB 61 HFTGGRWEKVSDEVIGYHQLRVPHQRYKDTTMEKVTMKGHAHSAHLHWYKKIDGVWKF 120

QY 145 AG 146  
 DB 121 AG 122

## RESULT 13

Q8N12\_OPHPI PRELIMINARY; PRT; 122 AA.

AC Q8N12;  
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Scytalone dehydratase (Fragment).  
 OS Ophiostoma piliferum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
 RX NCBI\_TaxID=38032;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Fleet C., Breuil C.;  
 RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi.";  
 RL Mycol. Res. 106:1331-1339(2002).  
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CC  
 DR EMBL: AY098662; AAM34808.1; -; Genomic\_DNA.  
 DR HSSP: P56221; IIDP.  
 DR SMR: Q8N12; 1-122.  
 DR GO:0016836; F:hydro-lyase activity; IEA.  
 DR GO:0006582; P:melanin metabolism; IEA.  
 DR InterPro: IPR004235; Scytalone\_DH.  
 DR Pfam: PF02982; Scytalone\_dh; 1.  
 DR ProDom: PD022193; Scytalone\_DH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 122  
 SQ SEQUENCE 122 AA; 14221 MW; 7A99419E73E0735E CRC64;

Query Match 57.0%; Score 537; DB 2; Length 122;  
 Best Local Similarity 73.8%; Pred. No. 6.8e-41;  
 Matches 90; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 25 EWADSYDSKDWRLKRVIAPTLRIDYRSFLDKLMEAMPABEFGVAVSSKOMLGDPPLRTQ 84  
 DB 1 EWADSYDSKDWRLKRVIAPTLRIDYRSFLDKLMEAMPABEFGVAVSSKOMLGDPPLRTQ 60  
 QY 85 HFTGGRWEKVSDEVIGYHQLRVPHQRYKDTTMEKVTMKGHAHSAHLHWYKKIDGVWKF 144  
 DB 61 HFTGGRWEKVSDEVIGYHQLRVPHQRYKDTTMEKVTMKGHAHSAHLHWYKKIDGVWKF 120  
 QY 145 AG 146  
 DB 121 AG 122

## RESULT 14

Q8N10\_OPHPI PRELIMINARY; PRT; 121 AA.

AC Q8N10;  
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-OCT-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 10.  
 DE Scytalone dehydratase (Fragment).  
 OS Ophiostoma piliferum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
 RX NCBI\_TaxID=38032;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Fleet C., Breuil C.;  
 RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi.";

CC  
 DR EMBL: AY098663; AAM34809.1; -; Genomic\_DNA.  
 DR HSSP: P56221; IIDP.  
 DR SMR: Q8N10; 1-121.  
 DR GO:0016836; F:hydro-lyase activity; IEA.  
 DR GO:0006582; P:melanin metabolism; IEA.  
 DR InterPro: IPR004235; Scytalone\_DH.  
 DR Pfam: PF02982; Scytalone\_dh; 1.  
 DR ProDom: PD022193; Scytalone\_DH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 121  
 SQ SEQUENCE 121 AA; 14246 MW; A17A6DD02BD9C80A CRC64;



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RL Mycol. Res. 106:1331-1339(2002).
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CC -----
DR EMBL: AY098664; AAM34810.1; -; genomic_DNA.
DR HSSP: P56221; 1IDP.
DR SMR: Q8NJI10; 1-121.
DR GO: GO:0016836; F:hydro-lyase activity; IEA.
DR GO: GO:0006582; P:melanin metabolism; IEA.
DR InterPro: IPR004235; Scytalone_DH.
DR Pfam: PF02982; Scytalone_dh; 1.
DR ProDom: PD022193; Scytalone_DH; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 14150 MW; 1941990397735ELF CRC64;

Query Match 56.5%; Score 532; DB 2; Length 121;
Best Local Similarity 73.6%; Pred. No. 1.9e-40;
Matches 89; Conservative 17; Mismatches 15; Indels 0; Gaps 0;

QY 25 EWADSYDSKQMDRLRKVIAPTLRIDYRSFLDKLMEAMPDEFVGMVSSKQMLGDPPLRTQ 84
DB 1 EWADRYDSKQMDRLRKCIAPTLRIDYRSFLNKLMEAMPDEFIGMTSDPSVLGNPLRTQ 60
QY 85 HFIIGTRMEKVSDEVIYGHQLRVPHQRKYDPTMKKEVYTKGHAHSANLHMYKKIDGVWKF 144
DB 61 HFFGASRWERISDTEVVGHRQLRVPHQVYTDATLSQVAVKGHAHSANTHWYRKVDGVWKF 120
QY 145 A 145
DB 121 A 121

RESULT 15
Q8NJI1.OPHP1 PRELIMINARY; PRT; 122 AA.
AC Q8NJI1;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma piliiferum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetiales; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxID=38032;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuill C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
CC -----
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CC -----
DR EMBL: AY098663; AAM34809.1; -; Genomic_DNA.
DR HSSP: P56221; 1IDP.
DR SMR: Q8NJI1; 1-122.
DR GO: GO:0016836; F:hydro-lyase activity; IEA.
DR GO: GO:0006582; P:melanin metabolism; IEA.
DR InterPro: IPR004235; Scytalone_DH.
DR Pfam: PF02982; Scytalone_dh; 1.
DR ProDom: PD022193; Scytalone_DH; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14226 MW; 7A995CA5F045735E CRC64;

Query Match 56.3%; Score 530; DB 2; Length 122;
Best Local Similarity 73.0%; Pred. No. 2.9e-40;
Matches 89; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 25 EWADSYDSKQMDRLRKVIAPTLRIDYRSFLDKLMEAMPDEFVGMVSSKQMLGDPPLRTQ 84
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DB 1 EWADRYDSKQMDRLRKCIAPTLRIDYRSFLNKLMEAMPDEFIGMTSDPSVLGNPLRTQ 60
QY 85 HFIIGTRMEKVSDEVIYGHQLRVPHQRKYDPTMKKEVYTKGHAHSANLHMYKKIDGVWKF 144
DB 61 HFFGASRWERISDTEVVGHRQLRVPHQVYTDATLSQVAVKGHAHSANTHWYRKVDGVWKF 120
QY 145 AG 146
DB 121 AG 122
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Search completed: December 5, 2006, 01:27:22  
Job time : 304 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: December 5, 2006, 01:22:36 ; Search time 40 Seconds

(without alignments)  
413.732 Million cell updates/sec

Title: US-10-507-132-2

Sequence: 1 MGSQVQKSDIEITFSDYLGLM.....WGEFDFDRIFEDGRETGDK 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	932	98.9	172	2 JE0130	scytalone dehydrat
2	99.5	10.6	605	2 A12535	hypothetical prote
3	88	9.3	166	2 D37844	baile 19.5K protein
4	84.5	9.0	380	1 C69144	UDP-galactopyranos
5	84	8.9	349	2 H36470	Mnt-7b protein - m
6	83	8.8	266	2 F64677	NADH2 dehydrogenas
7	83	8.8	923	2 A51054	lipoygenase (EC 1
8	80	8.5	388	2 S57526	cellulase - Fibrob
9	79.5	8.4	614	2 T01121	probable beta-gluc
10	79.5	8.4	1239	1 A32579	neuroglian - fruit
11	79	8.4	265	2 D71838	nadh oxidoreductas
12	79	8.4	469	2 B96947	beta-glucosidase (
13	79	8.4	702	2 A75630	ribonucleoside-dip
14	78.5	8.3	380	2 A71716	chymosin (EC 3.4.2
15	77.5	8.2	299	2 T40437	phosphoribosylamid
16	77.5	8.2	356	2 G64937	isochlorismate synt
17	77.5	8.2	816	2 S54518	probable membrane
18	77	8.2	274	2 T51714	probable formamido
19	77	8.2	479	2 T26951	hypothetical prote
20	76.5	8.1	325	2 G84362	hypothetical prote
21	76.5	8.1	356	2 A91023	isochlorismate hydr
22	76.5	8.1	356	2 B85867	hypothetical prote
23	76	8.1	1150	2 T41260	hypothetical prote
24	75.5	8.0	315	2 JQ1250	coat protein - chr
25	75.5	8.0	591	2 S56202	probable glycerone
26	75	8.0	497	2 T27012	hypothetical prote
27	75	8.0	514	2 B64055	hypothetical prote
28	75	8.0	1405	2 T40607	periplasmic oligop
29	74.5	7.9	162	2 H69896	probable dna-direc
					hypothetical prote

30	74.5	7.9	259	2 E69811	hypothetical prote
31	74.5	7.9	436	2 D70693	probable ugpB lipo
32	74.5	7.9	667	2 AE2943	oxidoreductase Atu
33	74.5	7.9	667	2 E98339	probable oxidoredu
34	74	7.9	442	2 T50110	Mnt10a protein - 2
35	74	7.9	2692	1 I36344	clitin, cardiac mus
36	73.5	7.8	143	2 AB1701	hypothetical prote
37	73.5	7.8	313	2 H69984	conserved hypothet
38	73.5	7.8	482	2 S15748	nitrogenase (EC 1.
39	73.5	7.8	589	2 T42244	probable polypepti
40	73.5	7.8	763	2 S23457	polysulfide reduct
41	73.5	7.8	817	2 D86217	protein T27G7.8 (1
42	73.5	7.8	4859	2 S74173	ryanodine receptor
43	73	7.7	153	2 S53544	hypothetical prote
44	73	7.7	430	1 UYPVF1	nonstructural prote
45	72.5	7.7	97	2 A34291	pollen allergen Lo

#### ALIGNMENTS

RESULT 1  
JE0130  
scytalone dehydratase (EC 4.2.1.94) - Pyricularia oryzae  
C/Species: Pyricularia oryzae  
C/Date: 03-Jun-1998 #sequence\_revision 10-Jul-1998 #ext\_change 31-Dec-2004  
C/Accession: JE0130  
R/Motocyan, T.; Imanishi, K.; Yamaguchi, I.  
Biosci. Biotechnol. Biochem. 62, 564-566, 1998  
A/Title: cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for p  
A/Reference number: JE0130; MUID:98233280; PMID:9571787  
A/Accession: JE0130  
A/Molecule type: mRNA  
A/Residues: 1-172 <NOT>  
A/Cross-references: UNIPARC:UPI0000179D1F; DDBJ:AB004701  
C/Comment: The C-terminal protein of this enzyme is important in catalysis or/and structu  
C/Superfamily: scytalone dehydratase  
C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 98.9%; Score 932; DB 2; Length 172;  
Best Local Similarity 98.8%; Pred. No. 3.9e-79;  
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MGSQVQKSDIEITFSDYLGLMTCYEWADSYDSKMDRLKVIAPTRIDYRSLDLTMA	60
Db	1	MGSQVQKSDIEITFSDYLGLMTCYEWADSYDSKMDRLKVIAPTRIDYRSLDLTMA	60

Qy 61 MPAAEFVGVVSSKQMLGPTLRTQHFIGSTRMEKVSDEVIQYHQLRVPHQRKDTTKE 120  
Db 61 MPAAEFVGVVSSKQVLDGPTLRTQHFIGSTRMEKVSDEVIQYHQLRVPHQRKDTTKE 120

Qy 121 VTMKGHAHSANLHWYKIDGVWKFAGLKDIPWGEFDFPRIFEDGRETGDK 172  
Db 121 VTMKGHAHSANLHWYKIDGVWKFAGLKDIPWGEFDFPRIFEDGRETGDK 172

RESULT 2  
A12535  
hypothetical protein alr7572 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bet  
C/Species: Nostoc sp. PCC 7120  
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #ext\_change 09-Jul-2004  
C/Accession: A12535  
R/Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritaguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab  
A/Reference number: AB1807; MUID:21595285; PMID:11759840  
A/Accession: A12535  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-605 <KUR>  
A/Cross-references: UNIPROT:Q8ZSD9; UNIPARC:UPI00000CCD88; GB:AP003602; PIDN:BA07215.1;



```

Query Match 39: 8.8%; Score 83; DB 2; Length 266;
Best Local Similarity 22.4%; Pred. No. 3;
Matches 39; Conservative 28; Mismatches 57; Indels 50; Gaps 7;

QY 13 FSDYGLMTCVYEWADSYDSKDWRLRLRYAPTLRIDRSLDKL--WEAMPAEFVGMV 70
Db 103 FYQFEG-----FSDSCNRRRYRVKCVLLPNESVDSLFLYRSANMSEREADVMDGIV 155
QY 71 SSK-----QMGGDPLTRQHFICG--TRREKXSE-----DEVIGHQ----- 105
Db 156 FDKFHYLRLIMPHDWGHPHLRSTYPLKGDPAQYEVVDKIFGKEYRVRVGEKORDSARV 215
QY 106 -----LRVHORXKDTMKKEVYTMKGHAHSANLHWYKXIDGWWKFAGLRPDI 151
Db 216 DEKDTFNFAKIGVEGKGEBELKEVBEK-----HAKKKIPFYVDLHKIAPTI 261

RESULT 7
lipoxxygenase (EC 1.13.11.12) L-2 - rice
C:Species: Oryza sativa (rice)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 12-Mar-1999
C:Accession: A53054
R:Peng, Y.L.; Shitano, Y.; Ohta, H.; Hibino, T.; Tanaka, K.; Shibata, D.
J. Biol. Chem. 269, 3755-3761, 1994
A>Title: A novel lipoxxygenase from rice. Primary structure and specific expression upon
A:Reference number: A53054; MUID:94148883; PMID:7508918
A:Accession: A53054
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-923 <PEN>
A:Cross-references: UNIPARC:UPI000017524C
A:Experimental source: cv. Aichasahi, blast fungus-infected leaves
A>Note: Sequence extracted from NCBI backbone (NCBIN:143809, NCBI:P:143809)
A:Note: GB:DI4000: NID:g468491
C:Superfamily: lipoxxygenase
C:Keywords: oxidoreductase

Query Match 34: 8.8%; Score 83; DB 2; Length 923;
Best Local Similarity 23.3%; Pred. No. 14;
Matches 34; Conservative 16; Mismatches 46; Indels 50; Gaps 7;

QY 55 DKLW----EAMPAEFVGMVSSKQMLGDP-----LFTQH-----IGTWEKY----- 95
Db 653 DKLWRFPTDEALPAD-----LVRGMAEBDPTEAGKIKLAIEDYPPANDGLTIMDAIKTWVQ 708
QY 96 -----SEDEVIGYHOLRVPHORXKDTMKKEVYTMKGHAHSANLHWYKXIDG----- 140
Db 709 AYVAFRYDADSVAGDEELQ-----AFWTBVRTKSGDKDKDPMWPKLDSPESLAAT 760
QY 141 ----VWKFAGLKPDIRMGSEFDFDRIF 162
Db 761 LTNIVWVAALHAHAAVNFQGYDFGYYF 786

RESULT 8
S57526
cellulase - Fibrobacter succinogenes
C:Species: Fibrobacter succinogenes
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S57526
R:Ozcan, N.; Cunningham, C.; Harris, W.J.
submitted to the EMBL Data Library, June 1995
A:Description: Cloning of a cellulase gene from the rumen anaerobe fibrobacter succinogenes
A:Reference number: S57526
A:Accession: S57526
A:Molecule type: DNA
A:Residues: 1-388 <OZC>
A:Cross-references: UNIPROT:Q47929; UNIPARC:UPI00000B5944; EMBL:X88561; NID:9887439; PIR
C:Superfamily: Fibrobacter succinogenes cellulase

```

Query Match 34; Similarity 23.4%; Pred. No. 9; Matches 34; Conservative 23; Mismatches 54; Indels 34; Gaps 7;

8.5%; Score 80; DB 2; Length 388;

31 DSKMDRLRKVIAPTLRIDYRSFLDK---LW--EAMPAEE-FVGVNVSROMLGDPILRT 83

4 DNNDSGVATYSIGEGKFTIDLSKVYRDKGLYPMIKGLGEGKLYVGLINDG----GHDIKS 59

84 QHFGIGTWEKYSSEVEVGYHQLRVPHQRYKOTTKKEVTMKGAHSAANLHWYKKIDGVWK 143

60 QTKVGLNDWIKVSKD---WQLAKIPLKRFRTD-----KGAWDAN-----K 96

144 FAGLKPDIRMCGEFPDFRIPEDERET 168

97 SAEVAKDVKMTFRKKSASLSDWAKT 121

RESULT 9

701121

probable beta-glucosidase At2g32860 [imported] - Arabidopsis thaliana

N/Alternate names: chioglucosidase homolog T21L14.20

C/Species: Arabidopsis thaliana (mouse-ear cross)

C/Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #ext\_change 09-Jul-2004

C/Accession: T01121; D84738

R/Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, A.; Description: The EMBL Data Library, December 1997

A/Reference number: Z14209

A/Accession: T01121

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-614 <R0U>

A/Cross-references: UNIPROT:O48779; UNIPARC:UPI000009CB18; EMBL:AC003033; NID:g2702261; F

A/Experimental source: cultivar Columbia

M/Rlin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.; N

euss, D.; Niernan, W.C.; White, O.; Eilen, J.A.; Salberg, S.L.; Frazer, C.M.; Venter, J.

Nature 402, 761-769, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: D84738

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-614 <STO>

A/Cross-references: UNIPARC:UPI000009CB18; GB:AE002093; NID:g2702276; PIDN:AAB91979.1; GS

C/Genetics:

A/Gene: AT2g32860; T21L14.20

A/Map position: 2

A/Intons: 113/3; 137/1; 156/3; 182/1; 208/1; 237/2; 324/1; 362/2; 435/1; 481/1; 517/2

C/Superfamily: Agrobacterium beta-glucosidase

Query Match 34; Similarity 23.2%; Pred. No. 17; Matches 57; Conservative 29; Mismatches 61; Indels 99; Gaps 15;

8.4%; Score 79.5; DB 2; Length 614;

6 QKSDP-----ITFSDYLGIMTCVYEMADSYD-----SKMDRLRKVI 42

29 QPSDEDLGTLIGPHQTSFDDIEIGIYIPHAIVDDDEDIDMDGTTVGPOQTNLNDDGLGTLI 88

43 APTLRIDIRSLDKLMEAMPAAEFVG-WVSSKOMLGDPILRTOHFGIGTRW-----E 93

89 GPEFEIHKQDF-----PADFIQTSVSAQVQVE--AKGSGRGLTSWDEFTHMFPE 137

94 KVSF---DEVYIGHQLRVPHQRYKD--TTMSEVTTMKGAHSAANLHWYKKI 138

138 KVGQNGDSDDEVDV-----YTRYDDIKLMEELINTNGRFS--ISWTRILPFGITIKGV 189

139 --DGWVKP-----AGLKP-----DIRMGEPDFRIFEDGRE----- 167

190 NEEGV-KFYNDLINELANGIQPSVTLFPHWESPLALMEYGGFLNRIYEDFREFANFCF 248

168 -TFGDK 172

Db 249 KEGDR 254

RESULT 10

A32579

neuroglian - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: A32579

R:Bieber, A.J.; Snow, P.M.; Hortsch, M.; Patel, N.H.; Jacobs, J.R.; Traquina, Z.R.; Schi Cell 59, 447-460, 1989

A:Title: *Drosophila neuroglian*: a member of the immunoglobulin superfamily with extensiv

A:Reference number: A32579; MUID:90030418; PMID:2805067

C:Accession: A32579

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1239 <BIE>

A:Cross-references: UNIPROT:P20241; UNIPARC:UPI00001743A0; GB:M28231; NID:g157998; PINN: A:Note: the authors translated the codon TAT for residue 1234 as Thr and AAA for residue

C:Genetics:

A:Gene: FlyBase:FBgn0002968

A:Cross-references: FlyBase:FBgn0002968

C:Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; i

C:Keywords: alternative splicing; cell adhesion; duplication; membrane protein

F:353-412/Domain: immunoglobulin homology <IMM1>

F:446-502/Domain: immunoglobulin homology <IMM2>

F:535-596/Domain: immunoglobulin homology <IMM3>

Query Match 8.4%; Score 79.5; DB 1; Length 1239;

Best Local Similarity 27.6%; Pred. No. 41;

Matches 32; Conservative 20; Mismatches 51; Indels 13; Gaps 4;

Qy 34 DMDRLKRIA--PTL---RIDRSFLDKLEMPAEFEVGVSSKOMLGDPTLRTOHF- 87

Db 769 DMRONNVIADDPFTFKYLKIVAINDRGESNVAABEVGYSGEDRPLAPFTNFTMQTT 828

Qy 88 ----GSTRKVKSEDEVIGY---HQLRVPHQRKYDTTKEVTWKGAHSANLHWY 136

Db 829 SSTSGYMAWTPVSESVRGHPKGYKIQTWTENEGSELREIHVKGDTHNALVTQFK 884

RESULT 11

D71838

nadh oxidoreductase I - *Helicobacter pylori* (strain J99)

C:Species: *Helicobacter pylori*

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 31-Dec-2004

C:Accession: D71838

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: D71838

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-265 <ARN>

A:Cross-references: UNIPROT:Q9ZJW5; UNIPARC:UPI0000003707; GB:AE001545; GB:AE001439; NID

A:Experimental source: strain J99

C:Genetics:

A:Gene: nnc

A:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 30kD/nadh/nuc

Query Match 8.4%; Score 79; DB 2; Length 265;

Best Local Similarity 21.8%; Pred. No. 7;

Matches 38; Conservative 28; Mismatches 58; Indels 50; Gaps 7;

Qy 13 FSDYGLMTCYEWADSYDKMDRLKVIAPTLRIDYRSFLDKL--WEAMPAEEFVGWV 70

Db 102 FYQFV-----FSDSKNRVRVRVKVCLLPVESVDSLFLYRSANWSERAYDMLGIV 154

Qy 71 SSR-----QMLGDPFLTRTOHFIGS--TRREKVE-----DEVIGHQ----- 105

Db 155 FDKHPYLRLIMPHDWGHPLLRSYPLKDEFAQWYEVDKIFGKEYREVGKEQDSARV 214

Qy 106 -----LRVPHQRKYDTTKEVTWKGAHSANLHWYKKIDGYWFKAGLKPDI 151

Db 215 DEKTFNPAKIGYEGKGSEELKETEER-----HAFKKLPFKYKDLHKIAPTI 260

RESULT 12

B96947

beta-glucosidase [imported] - *Clostridium acetobutylicum*

C:Species: *Clostridium acetobutylicum*

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004

C:Accession: B96947

R:Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Dairy, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B96947

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-469 <KUR>

A:Cross-references: UNIPROT:Q97M15; UNIPARC:UPI00000C9554; GB:AE001437; PINN:AAK78365.1;

A:Experimental source: *Clostridium acetobutylicum* ATCC824

C:Genetics:

A:Gene: CAC0385

C:Superfamily: *Agrobacterium beta-glucosidase*

Query Match 8.4%; Score 79; DB 2; Length 469;

Best Local Similarity 19.2%; Pred. No. 14;

Matches 25; Conservative 28; Mismatches 39; Indels 38; Gaps 6;

Qy 45 TLRIYRFLDKLEMPAEFEVGVSSKOMLGDPTLR--TOHFIGSTRMEKSEDEVIGY 103

Db 334 TYKMDKTYTKKGEISPELSLIGLEKKEQYGDIKITYTENGGLDQ--DRIEIBLIDM 391

Qy 104 HQLRV--PHQR--YKDTTKEVTWKG-----HAHS----- 129

Db 392 PRKFRHMLRAIKERALSIRGLNKGYVMSYIDLTLWNLNGYKQGYFVYHKKHNLDRKK 451

Qy 130 -ANLHWYKKI 138

Db 452 KLSFYWKRV 461

RESULT 13

A75630

ribonucleoside-diphosphate reductase, alpha chain - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: A75630

R:White, O.; Eelsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Smith, H.O.; Venetier, J.C.; Frazer, C.M. Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75630

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-702 <WHI>

A:Cross-references: UNIPROT:Q9R2L7; UNIPARC:UPI00000D3B5A; GB:AE001826; NID:g6460827; PIL

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRB0108

A:Map position: megaplasmid

A:Genome: plasmid

A:Note: plasmid MPI

C:Superfamily: *Salmonella typhimurium* ribonucleoside-diphosphate reductase

Query Match 8.4%; Score 79; DB 2; Length 702;

Best Local Similarity 25.4%; Pred. No. 23;

Matches 32; Conservative 21; Mismatches 45; Indels 28; Gaps 8;



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;; CURRENT FILING DATE: 2004-09-10  
;; PRIOR APPLICATION NUMBER: JP 2002-66955  
;; PRIOR FILING DATE: 2002-03-12  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 4  
;; LENGTH: 172  
;; TYPE: PRP  
;; ORGANISM: Pyricularia oryzae  
US-10-507-132-4

Query Match 99.6%; Score 938; DB 6; Length 172;  
Best Local Similarity 99.4%; Pred. No. 1.2e-83;  
Matches 171; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQVQKSDIEITFSDYLGIMTCYEWADSYDSKMDRLKRVLAPTLRIDYRSLDKLMEA 60  
DB 1 MSQVQKSDIEITFSDYLGIMTCYEWADSYDSKMDRLKRVLAPTLRIDYRSLDKLMEA 60  
QY 61 MPAAEFVGVSSKQMLGDPFLTRQHFPGTRWEKVSSEDEVIGYHQLRPHQRKYDTTME 120  
DB 61 MPAAEFVGVSSKQVLDGDPFLTRQHFPGTRWEKVSSEDEVIGYHQLRPHQRKYDTTME 120  
QY 121 VTMKGHAHSANLHWYKKIDGWMKPAGLKPDIRWGEFDPRIEDGRETGDK 172  
DB 121 VTMKGHAHSANLHWYKKIDGWMKPAGLKPDIRWGEFDPRIEDGRETGDK 172

## RESULT 3

US-10-449-902-44748  
;; Sequence 44748, Application US/10449902  
;; Publication No. US20060123505A1  
;; GENERAL INFORMATION:  
;; APPLICANT: National Institute of Agricultural Sciences.  
;; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
;; APPLICANT: The Institute of Physical and Chemical Research.  
;; TITLE OF INVENTION: Foundation for Advancement of International Science.  
;; FILE REFERENCE: MOA-A0205Y1-US  
;; CURRENT APPLICATION NUMBER: US/10/449,902  
;; CURRENT FILING DATE: 2003-05-29  
;; PRIOR APPLICATION NUMBER: JP 2002-203269  
;; PRIOR FILING DATE: 2002-05-30  
;; PRIOR APPLICATION NUMBER: JP 2002-383870  
;; PRIOR FILING DATE: 2002-12-11  
;; NUMBER OF SEQ ID NOS: 56791  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 44748  
;; LENGTH: 941  
;; TYPE: PRP  
;; ORGANISM: Oryza sativa  
US-10-449-902-44748

Query Match 9.2%; Score 87; DB 6; Length 941;  
Best Local Similarity 23.0%; Pred. No. 3.9;  
Matches 34; Conservative 16; Mismatches 44; Indels 54; Gaps 7;

QY 55 DKLM-----EAMPAAEFVGVSSKQMLGDPFLTRQHF-----GTRWEKVS----- 95  
DB 671 DKLMRDMAALPAD-----LVRGMAEDPT--AEHGRLAIEDYPPRANGLLIWDALIKTW 724  
QY 96 -----SEDEVIGYHQLRPHQRKYDTTMEKVGHAHSANLHWYKKIDG----- 140  
DB 725 VQAVYARFYPDADSVAGDEBLQ-----AFWTEVRTGSHGDKQAPWPKLDSRESLA 776  
QY 141 -----VAKPAGLKPDIRWGEFDPRIE 162  
DB 777 HTLTITVWVAHAHAAVNFGQYDFGGYF 804

## RESULT 4

US-11-174-307B-3704  
;; Sequence 3704, Application US/11174307B

;; Publication No. US20060143729A1  
;; GENERAL INFORMATION:  
;; APPLICANT: ALEXANDROV, Nickolai  
;; APPLICANT: BROVER, Vyacheslav  
;; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
;; FILE REFERENCE: 2750-1601PUS2  
;; CURRENT APPLICATION NUMBER: US/11/174,307B  
;; CURRENT FILING DATE: 2005-06-30  
;; PRIOR APPLICATION NUMBER: 60/583,671  
;; PRIOR FILING DATE: 2004-06-30  
;; PRIOR APPLICATION NUMBER: 60/583,781  
;; PRIOR FILING DATE: 2004-06-30  
;; PRIOR APPLICATION NUMBER: 60/583,651  
;; PRIOR FILING DATE: 2004-06-30  
;; NUMBER OF SEQ ID NOS: 5544  
;; SEQ ID NO 3704  
;; LENGTH: 444  
;; TYPE: PRP  
;; ORGANISM: Triticum aestivum

;; NAME/KEY: misc\_feature  
;; LOCATION: P1am Name: HSP70; Pfam Description: Hsp70 protein  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION:  
;; OTHER INFORMATION: GI Number: 19813; NR Description: luminal binding protein  
;; OTHER INFORMATION: (BiP) [Nicotiana tabacum] >gi|100340|pir||S21880 dnak-type  
;; OTHER INFORMATION: molecular chaperone biP5 precursor - common tobacco  
;; OTHER INFORMATION: >gi|729623|sp|Q03685|BiP5\_TOBAC luminal binding homolog 5) (GRP  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION:  
;; OTHER INFORMATION: GI Number: 19811; NR Description: luminal binding protein  
;; OTHER INFORMATION: (BiP) [Nicotiana tabacum] >gi|100339|pir||S21879 dnak-type  
;; OTHER INFORMATION: molecular chaperone biP4 precursor - common tobacco  
;; OTHER INFORMATION: >gi|729620|sp|Q03684|BiP4\_TOBAC luminal binding homolog 4) (GRP  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION:  
;; OTHER INFORMATION: GI Number: 13398537; NR Description: BiP-isoform D [glycine max]  
;; OTHER INFORMATION:  
;; NAME/KEY: misc\_feature  
;; LOCATION:  
;; OTHER INFORMATION: GI Number: 2642238; NR Description: endoplasmic reticulum  
;; OTHER INFORMATION: Hsc70-cognate binding protein precursor [glycine max]  
;; OTHER INFORMATION: >gi|11277127|pir||T46574 dnak-type molecular chaperone BiP  
US-11-174-307B-3704

Query Match 8.5%; Score 80.5; DB 7; Length 444;  
Best Local Similarity 23.6%; Pred. No. 6.7;  
Matches 35; Conservative 25; Mismatches 45; Indels 43; Gaps 7;

QY 54 LDKLMEAPAAEFVGV-----VSSKQMLGDPFLTRQHFPGTRWEKVSSEDEVIGYHQLR 107  
DB 159 LAKLRES--AEAYLGRAIOEALIVTPOQYNDP-----SRYSMLRAAELAGLRVTR 206  
QY 108 V-----PHQRKYDT--TMKEVMTMKGHAHSANLHWYKKIDGWMKPAGLKPDIRWG 154  
DB 207 MDEPPTAAVAAGLHRKLDLBSGNVLVLHVGGSTDSASVMY--VDGVFEFGADEDPFPG 264  
QY 155 EFDPRIFED-----GRETFGDK 172  
DB 265 GQDFDQRIVDHFVELIRKKHGKDLNDK 292

## RESULT 5



```

? APPLICANT: National Institute of Agrobiological Sciences.
? APPLICANT: Bio-oriented Technology Research Advancement Institution.
? APPLICANT: The Institute of Physical and Chemical Research.
? APPLICANT: Foundation for Advancement of Interational Science.
? TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
? FILE REFERENCE: MOA-A0205Y1-US
? CURRENT APPLICATION NUMBER: US/10/449,902
? CURRENT FILING DATE: 2003-05-29
? PRIOR APPLICATION NUMBER: JP 2002-203269
? PRIOR FILING DATE: 2002-05-30
? PRIOR APPLICATION NUMBER: JP 2002-383870
? PRIOR FILING DATE: 2002-12-11
? NUMBER OF SEQ ID NOS: 56791
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 30829
? LENGTH: 436
? TYPE: PRT
? ORGANISM: Oryza sativa
? OS-10-449-902-30829

```

Query Match	8.2%	Score 77	DB 6	Length 436
Best Local Similarity	32.1%	Pred. No. 14		
Matches	25	Conservative	15	Mismatches 22; Indels 16; Gaps 4
QY	33	KDMRLKRV--AATPIR-----	DYSFLDKMAMAEAEFGVSSKMGIDPTLTQ	84
DB	243	KNDLFLKVMRLGCVRLAFTIGDGPYKSELKMFGEIPA-VFTGMQSEL-----	SSQ	294
QY	85	HFIGGTREKVSDEDAVIG	102	
DB	295	AYASGDVFMVPESEETLG	312	

```

RESULT 9
US-10-449-902-50460
; Sequence 50460, Application US/10449902
; Publication NO. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50460
; LENGTH: 436
; TYPE: PR1
; ORGANISM: Oryza sativa
; US-10-449-902-50460

```

Query Match	8.2%	Score 77 / DB 6,	Length 436,
Best Local Similarity	32.1%	Pred. No. 14,	
Matches	25;	Conservative 15;	Mismatches 22; Indels 16; Gaps 4

  

QY	33	KDMWRLRKVI--APLPTI-----DYRFLDKLTAMPAEELVGVVSSKQMLGDTPLTKRQ	84
Db	243	KNDDPLFKVMRLPGVRLAFTIGDGFYKSELEKMEFGMPA-VFTGMVQSEEL-----SQ	294
QY	85	HFIGGTREKVSDEDEVIQ	102
Db	295	AYASGDVFMPSSEETLG	312

RESULT 10  
US-10-449-902-52228

```

Sequence 52228, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52228
LENGTH: 844
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-52228

```

[illegible]

Oy 131 NLHMYKKIDGVMKEAGLKP 149  
 ::||| |||  
 Db 685 -MNMWYKG---WK--GLFP 696

```

RESULT 11
US-10-449-902-47097
; Sequence 47097, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47097
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-47097

```

Query Match 8.1%; Score 76.5; DB 6; Length 596;  
Best Local Similarity 22.5%, Pred. No. 23;  
Matches 36; Conservative 21; Mismatches 50; Indels 53; Gaps 9

Oy 26 WADSY--DSKDWDRIRKYIAPTLRIDYRSFDLKW-----AMPKEEPGVAVSSKKOM 75  
          :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|  
ob 85 WGHVSVDLDLNWALDTPALDPTSPD---ANGCMGSGATILPGALPAILVYGIDASKSQ 140

QY	76	L-----GPTLTQTFIGSTRREKKSDEEVIGYHOLRPHQKQYKDTTMMKVMKGH	126
Db	141	VQNVAFATKNSPELLR-----EKEKVAHPVIAL-PADVPQGDYFRDPSTA-----	184
QY	127	AHSANLHHYKKKIDGYWKFA-----GIKRDIDMGDEDPDR	160
Db	185	-----WLGR-DGLMKRVAVSAEVDVASTLYIRSKDFVRA	216

```

RESULT 12
US-10-449-902-41550
; Sequence 41550, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41550
; LENGTH: 827
; TYPE: prt
; ORGANISM: Oryza sativa
; US-10-449-902-41550

```

	Query Match	8.1%;	Score 76.5;	DB 6;	length 827;	
	Best Local Similarity	27.8%;	Pred. No. 35;			
	Matches	Conservative	9;	Mismatches	27;	Indels 29; Gaps 4;
OY	4 QVOKSD-----ETFSFDGLMTCVYE-----WADSYSKRW-----DR 37					
Dd	690 QUESDNCIMVGVELMESASATKTIDIAIVGLVLELLFMGDDPYFDHMTMSGLEVDIKAG 749					
OY	38 LRKYIAPFLR--IDYRSFLDKLEAMPAE 64					
Dd	750 LRPVIPDSRKQIFPEYITILMEKCWEALPAE 779					

```

RESULT 13
US-10-953-349-24962
: Sequence 24962, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERAY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 24962
: LENGTH: 537
: TYPE: PRT
: ORGANISM: Glycine max
: US-10-953-349-24962

```

```

Query Match 8.1%; Score 76; DB 6; Length 537;
Best Local Similarity 20.3%; Pred. No. 23;
Matches 28; Conservative 23; Mismatches 43; Indels 44; Gaps 77;

Qy 56 KLM-----EAMPAEEVGVAVSSKQMLGDPTRLQHTIGCTR-----WEKVS 96
    |||
    |||
Db 269 KLMRPMKSLPAD-----LIRRGAAVDDPSMPC-----GVKVIDVDPYAADGLIWSAIK 319
    |||
    |||

```

Oy	97 E-DEVTGTHQLRPHORYDITM-----KEVTMGAGHSANLHMYKKIDG-----146
Db	320 EMVESTVAHFYSDPSNVSDVELQAMREIKLKXGSDKQNEPMPMKDPTDEDLSGITTM 379
Oy	141 VMKFAKLKDIPMRGERDF 158
Db	380 IMTASGCHALINNGQIFP 397

```

RESULT 14
US-10-953-349-24961
; Sequence 24961, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2/50-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24961
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24961

```

Query Match	8.1%;	Score 76;	DB 6;	Length 634;
Best Local Similarity	20.3%;	Pred. No. 28;		
Matches	28;	Conservative	23;	Mismatches 43;
			Indels	44;
			Gaps	77;

  

QY	56	KLM----	EAMPABEFGVWSSKQMLGDTLTLTOHFIGTR-----	WEKYS	96
			::: ::	:	
			::: ::	:	
Db	366	KLMFDMESLPAD----	LIRGMAVDDPPSMPC-----	GVKLVIDYPYAADGLIMSAIK	416
			::: ::	:	
			::: ::	:	
QY	97	E-DEVIGYHQLRVNHQYKDTTM----	KEYTMKHAHSANLHMYKKIDG-----		140
			::: ::	:	
			::: ::	:	
Db	417	EWESYVAHFYSDNSNSTVDLEQAWREIKLKGHSKDKKEPMPWKLDTEKEDLSGILITM			476
			::: ::	:	
			::: ::	:	
QY	141	VMKFAGLKPDIRMGEPDF	158		
			::: ::	:	
			::: ::	:	
Db	477	IWIASGQHAALNFGQYFP	494		
			::: ::	:	
			::: ::	:	

```

RESULT 15
US-10-953-349-24960
: Sequence 24960, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCONDSED THERIY
: FILE REFERENCE: 2750-1579PU52
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 24960
: LENGTH: 664
: TYPE: PRT
: ORGANISM: Glycine max
US-10-953-349-24960

```

```

Query Match      8.1%; Score 76; DB 6; Length 664;
Best Local Similarity 20.3%; Pred. No. 30;
Matches 28; Conservative 23; Mismatches 43; Indels 44; Gaps 7;

Qy      56 KLV---EAMPAEFVGWSSKQMLGPTLTQHFGTGR-----WEVNS 96
          |||::|||::|
Db      396 KLMPEDNESLPAD---LIRGNAAVDPPSPMC---GVKLVIIDYDPYAADGLIWSAIK 446

```

Oy 97 E-DEVIGHQLRVPHQRYKDTM---KEVTMKGHAHSANLHWYKKIDG----- 140  
Db 447 EWVESYVAHFYSDDPNSVTSDVELQAWWREIKLKGHSDDKKNBPWWPKLDTREDLGILTTM 506  
Oy 141 VVKFAGLKPDIRWGEFDF 158  
Db 507 IWIASGQHAALNFGQYPF 524

Search completed: December 5, 2006, 01:45:21  
Job time : 46 secs

Wed Dec 6 12:28:21 2006

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:39:46 ; Search time 187 Seconds

(without alignments)  
426.059 Million cell updates/sec

Title: US-10-507-132-2

Perfect score: 942  
Sequence: 1 MGSQVQKSDRITFSDYLGLM.....WGFDPDRIFEDGRFTGDK 172

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	9.2	924	5	US-10-491-733-22
2	85	9.0	265	3	US-09-882-227-306
3	84	8.9	349	5	US-10-847-972-306
4	84	8.9	349	6	US-11-108-528-46
5	84	8.9	411	4	US-10-425-114-56305
6	84	8.9	411	4	US-10-425-115-21335
7	81	8.6	349	4	US-10-285-976-21
8	81	8.6	349	4	US-10-364-888-2
9	81	8.6	349	4	US-10-364-888-6
10	81	8.6	349	5	US-10-364-888-8
11	81	8.6	349	5	US-10-678-639-20
12	81	8.6	349	5	US-10-847-972-22
13	81	8.6	349	6	US-11-108-528-44
14	79.5	8.4	614	6	US-11-096-568A-28399
15	79.5	8.4	1239	6	US-11-097-143-1701
16	79.5	8.4	266	4	US-10-335-977-6427
17	79.5	8.4	702	4	US-10-369-493-23474
18	78.5	8.3	374	4	US-10-156-761-7674
19	78	8.3	424	4	US-10-424-589-782063
20	78	8.3	861	6	US-11-087-099-1420
21	78	8.3	861	6	US-11-188-298-12347
22	77.5	8.2	2195	4	US-10-437-963-181567
23	77.5	8.2	371	5	US-10-469-204-150
24	77.5	8.2	598	4	US-10-437-963-142051
25	77	8.2	375	6	US-11-096-568A-13512
26	77	8.2	436	4	US-10-437-963-178354
27	77	8.2	844	4	US-10-437-963-132118

28	76.5	8.1	834	5	US-10-481-032A-70	Sequence 70, Appl
29	76	8.1	227	4	US-10-314-657-51	Sequence 51, Appl
30	76	8.1	227	5	US-10-473-193-51	Sequence 51, Appl
31	76	8.1	583	4	US-10-289-757-79	Sequence 79, Appl
32	76	8.1	583	5	US-10-955-745-79	Sequence 79, Appl
33	76	8.1	1073	4	US-10-032-585-7157	Sequence 157, Appl
34	75.5	8.0	430	4	US-10-108-260A-4232	Sequence 4232, Ap
35	75.5	8.0	591	4	US-10-369-493-1784	Sequence 1784, Ap
36	75.5	8.0	36946	5	US-10-840-512-155	Sequence 155, App
37	75	8.0	463	4	US-10-437-963-154890	Sequence 154890,
38	75	8.0	497	4	US-10-179-766-9	Sequence 9, Appl1
39	75	8.0	767	6	US-11-188-298-12759	Sequence 12759, A
40	75	8.0	798	4	US-10-696-616-20	Sequence 20, Appl
41	75	8.0	1397	4	US-10-369-493-2413	Sequence 2413, Ap
42	74.5	7.9	438	4	US-10-437-963-136067	Sequence 136067,
43	74.5	7.9	436	4	US-10-282-122A-62311	Sequence 62311, A
44	74.5	7.9	436	4	US-10-282-122A-64780	Sequence 64780, A
45	74.5	7.9	437	3	US-09-996-634-136	Sequence 136, App

ALIGNMENTS

RESULT 1  
US-10-491-733-22  
Sequence 22, Application US/10491733  
Publication No. US20040219675A1  
GENERAL INFORMATION:  
APPLICANT: Syngenta Participations AG  
APPLICANT: Sainz, Manuel  
APPLICANT: Weislo, Laura J.  
TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic St  
FILE REFERENCE: 60127WOPT  
CURRENT APPLICATION NUMBER: US/10/491,733  
PRIORITY FILING DATE: 2004-04-05  
PRIOR APPLICATION NUMBER: 60/334,501  
PRIORITY FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 22  
LENGTH: 924  
TYPE: PRT  
ORGANISM: Oryza sativa  
US-10-491-733-22

Query Match  
Best local Similarity 23.0%; Pred. No. 8;  
Matches 34; Conservative 16; Mismatches 44; Indels 54; Gaps 7;

QY 55 DKLM---EMPRAEFVGVSSKMTADPTLRTOHFI-----GRTWEKV---95  
DB 654 DKLMREFTLEPAD---LVRRGMAEDPT--AEHGKLAIEDYPPANDLLIWDALIKTW 707  
QY 96 -----SEBEVIGYHQLRVHQRKYOTMKETVMGHASNLHWYKRTDG-----140  
DB 708 VQAVYARFYDPADSVAGDEELQ-----AFTEVTRTGHGDKKAPWPKIDSPESILA 759  
QY 141 -----VWKFAGLKPDIRWGEFDPDRIF 162  
DB 760 HTLTITVWAAAHAAVNFQGYDFGCVF 787

RESULT 2  
US-09-882-227-306  
Sequence 306, Application US/09882227  
Publication No. US20030158396A1  
GENERAL INFORMATION:  
APPLICANT: Kleantous, Harold  
APPLICANT: Al-Garawi, Amal  
APPLICANT: Miller, Charles  
APPLICANT: Tomb, Jean-Francois

```
/ APPLICANT: Ooomen, Raymond P.
/ TITLE OF INVENTION: Identification of Polynucleotides
/ TITLE OF INVENTION: Encoding No. US20030158396A1 Helicobacter Polypeptides in the
/ TITLE OF INVENTION: Genome
/ FILE REFERENCE: 06132/047002
/ CURRENT APPLICATION NUMBER: US/09/882,227
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: US 08/902,615
/ PRIOR FILING DATE: 1997-07-29
/ NUMBER OF SEQ ID NOS: 638
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 306
/ LENGTH: 265
/ TYPE: PRF
/ ORGANISM: Helicobacter pylori
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: 118
/ OTHER INFORMATION: Xaa = Any Amino Acid
US-09-882-227-306
```

```
Query Match          9.0%; Score 85; DB 3; Length 265;
Best Local Similarity 22.4%; Pred. No. 2.7;
Matches 39; Conservative 28; Mismatches 57; Indels 50; Gaps 7;
```

```
QY 13 FSDYLGMTCYEWADSYDSKMDRLKVIAPTLRIDYRSPDLK--WEAMPAEEFVGNY 70
DB 102 FQQFVG-----FSDSCKNRRKRVKCVLLPENSVDLSFLYRSANSEBAYDMIGIV 154
QY 71 SSK-----QMLGDPFLRTQHFIGG--TWREKYSE-----DEVIGYHQ----- 105
DB 165 FPKHFKYKRLIMPHDWGHPILRSYPLKQDEFAQMYEVDKI FCKRYREVVGEGDSARV 214
QY 106 -----LRVPHORYKDTTMEKVTMKGHAHSANLHWYKIDGVKKAGLKPDI 151
DB 215 DEKDTFNPFAKIGYEQCKGELKVEEK-----HAFKKIPFVDLKHIAPTI 260
```

```
RESULT 3
US-10-847-972-60
/ Sequence 60, Application US/10847972
/ Publication No. US20050049195A1
/ GENERAL INFORMATION:
/ APPLICANT: ZOU, YIMIN
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
/ FILE REFERENCE: ARCD:395US
/ CURRENT APPLICATION NUMBER: US/10/847,972
/ CURRENT FILING DATE: 2004-05-17
/ PRIOR APPLICATION NUMBER: 60/470,913
/ PRIOR FILING DATE: 2003-05-15
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 60
/ LENGTH: 349
/ TYPE: PRF
/ ORGANISM: Mus musculus
US-10-847-972-60
```

```
Query Match          8.9%; Score 84; DB 5; Length 349;
Best Local Similarity 31.1%; Pred. No. 4.8;
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;
```

```
QY 84 OHFIGGTRW--EKVSEDEVIGYHQLRVPHORYKDTTMEKVTMKGHAHS-----ANLH- 133
DB 74 OHQFRFRMNCALGEKTVFG-QELRVGSEAAFT--YAITAGVAHAATPAACSGNLN 130
QY 134 -----WYKKIDGVKKFAGLKPDIRWGEFDFDRIFEDGRE 167
DB 131 CGCDREKGYNYNAEG-WKMGCSADVRYG-IDFSRRFVDARE 171
```

```
RESULT 4
US-11-108-528-46
```

```
/ Sequence 46, Application US/11108528
/ Publication No. US20050261189A1
/ GENERAL INFORMATION:
/ APPLICANT: Larsen, Glenn
/ APPLICANT: Marvyn, Martha
/ APPLICANT: Li, Dean Y.
/ APPLICANT: Wang, Elizabeth
/ APPLICANT: Chen, C. M. Amy
/ APPLICANT: Shannah, Steven M.
/ TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
/ TITLE OF INVENTION: PROLIFERATION
/ FILE REFERENCE: HYDR-P01-041
/ CURRENT APPLICATION NUMBER: US/11/108,528
/ CURRENT FILING DATE: 2005-04-18
/ PRIOR APPLICATION NUMBER: US 60/563,137
/ PRIOR FILING DATE: 2004-04-16
/ PRIOR APPLICATION NUMBER: US 60/598,368
/ PRIOR FILING DATE: 2004-08-02
/ NUMBER OF SEQ ID NOS: 86
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 46
/ LENGTH: 349
/ TYPE: PRF
/ ORGANISM: Mouse
US-11-108-528-46
```

```
Query Match          8.9%; Score 84; DB 6; Length 349;
Best Local Similarity 31.1%; Pred. No. 4.8;
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;
```

```
QY 84 OHFIGGTRW--EKVSEDEVIGYHQLRVPHORYKDTTMEKVTMKGHAHS-----ANLH- 133
DB 74 OHQFRFRMNCALGEKTVFG-QELRVGSEAAFT--YAITAGVAHAATPAACSGNLN 130
QY 134 -----WYKKIDGVKKFAGLKPDIRWGEFDFDRIFEDGRE 167
DB 131 CGCDREKGYNYNAEG-WKMGCSADVRYG-IDFSRRFVDARE 171
```

```
RESULT 5
US-10-425-114-56305
/ Sequence 56305, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Tongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 56305
/ LENGTH: 411
/ TYPE: PRF
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: UC-ZWFLB73131C10_F1.1.pcp
US-10-425-114-56305
```

```
Query Match          8.9%; Score 84; DB 4; Length 411;
Best Local Similarity 25.2%; Pred. No. 5.9;
Matches 35; Conservative 17; Mismatches 31; Indels 56; Gaps 10;
```

```
QY 26 WADSYSKW--DRLKVIAPTLRIDYRSP-----LDK-----LW-EAMPAEEFVGNY 70
DB 171 WADVDSASWEDLIVRYIIPKRLALQDFQIPANOKDQFWMWNLMTSAIVQLMVHW- 229
QY 71 SSKOMLGDPFLRTQHFIGGTRWEKVSDEVIGYHQLRVPHORYKDTTMEKVTMKGHAHA 130
```



Db 230 -----LEVDF--SKMOQVL-----YHMLCSFMPDFNEI----- 256  
 QY 131 NLHWYKKIDGVWKFAGLKP 149  
 Db 257 -MMWYKG---WK--GLFP 268

RESULT 6

US-10-425-115-213325  
 ; Sequence 213325, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 213325  
 ; LENGTH: 411  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_126150C.1.pap  
 ; US-10-425-115-213325

Query Match 8.9%; Score 84; DB 4; Length 411;  
 Best Local Similarity 25.2%; Pred. No. 5.9;  
 Matches 35; Conservative 17; Mismatches 31; Indels 56; Gaps 10;

QY 26 WADSYDSKDM-DRLRKVTAFTLRIDYRSP-----LDK-----LM-EAMPAEEFYGV 70  
 Db 171 WADVDSASMEDLYRRIIPKRLALQDQINPANOKLDQFWWMLMTSAIVQLMVEN- 229  
 QY 71 SSKOMLGPFTLRTOHFGTMEKYSSEDEVIGYHQLRVPHQRKDTMTKEVTMKGHASHA 130  
 Db 230 -----LEVDF--SKMOQVL-----YHMLCSFMPDFNEI----- 256  
 QY 131 NLHWYKKIDGVWKFAGLKP 149  
 Db 257 -MMWYKG---WK--GLFP 268

RESULT 7

US-10-285-976-21  
 ; Sequence 21, Application US/10285976  
 ; Publication No. US20030165500A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rhee, Chae-Seo  
 ; APPLICANT: Malini, Sen  
 ; APPLICANT: Wu, Christina  
 ; APPLICANT: Leon, Lorenzo M.  
 ; APPLICANT: Corr, Maripac  
 ; APPLICANT: Carson, Dennis A.  
 ; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy  
 ; FILE REFERENCE: 023070-130320US  
 ; CURRENT APPLICATION NUMBER: US/10/285,976  
 ; CURRENT FILING DATE: 2002-11-01  
 ; PRIOR APPLICATION NUMBER: US 60/287,995  
 ; PRIOR FILING DATE: 2001-05-01  
 ; PRIOR APPLICATION NUMBER: WO PCT/US02/13802  
 ; NUMBER OF SEQ ID NOS: 232  
 ; SOFTWARE: Patent Ver. 2.1  
 ; SEQ ID NO 21  
 ; LENGTH: 349

; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: human wnt-7b  
 ; US-10-285-976-21

Query Match 8.6%; Score 81; DB 4; Length 349;  
 Best Local Similarity 31.2%; Pred. No. 10;  
 Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

QY 91 RW-EKVSDEVIGYHQLRVPHQRKDTMTKEVTMKGHASH-----ANLH----- 133  
 Db 81 RWNCSALGKTVFG-QELRVGSREAAFT--YAITAGVAHAHTAACSGNLSCGCDREK 137  
 QY 134 --WYKKIDGVWKFAGLKPDIRMGEFDPDRIFEDGEE 167  
 Db 138 QGYINQABG-WKMGCSADVRYG-IDFSRRFVDARE 171

RESULT 8

US-10-364-888-2  
 ; Sequence 2, Application US/10364888  
 ; Publication No. US20040023259A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Zhong, Haihong  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Gangolli, Esna  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Malyankar, Uriel  
 ; APPLICANT: Paturajan, Meera  
 ; APPLICANT: Pena, Carol  
 ; APPLICANT: Shinkens, Richard  
 ; APPLICANT: Spyrek, Kimberly  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Rieger, Daniel  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: Burgess, Catherine  
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
 ; FILE REFERENCE: 15966-744CIP  
 ; CURRENT APPLICATION NUMBER: US/10/364,888  
 ; CURRENT FILING DATE: 2003-02-12  
 ; PRIOR APPLICATION NUMBER: 60/356,375  
 ; PRIOR FILING DATE: 2002-02-12  
 ; PRIOR APPLICATION NUMBER: 60/387,082  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: 09/625,634  
 ; PRIOR FILING DATE: 2000-07-26  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: Curaseq1ist version 0.1  
 ; SEQ ID NO 2  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-364-888-2

Query Match 8.6%; Score 81; DB 4; Length 349;  
 Best Local Similarity 31.2%; Pred. No. 10;  
 Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

QY 91 RW-EKVSDEVIGYHQLRVPHQRKDTMTKEVTMKGHASH-----ANLH----- 133  
 Db 81 RWNCSALGKTVFG-QELRVGSREAAFT--YAITAGVAHAHTAACSGNLSCGCDREK 137  
 QY 134 --WYKKIDGVWKFAGLKPDIRMGEFDPDRIFEDGEE 167  
 Db 138 QGYINQABG-WKMGCSADVRYG-IDFSRRFVDARE 171

RESULT 9

US-10-364-888-6  
 ; Sequence 6, Application US/10364888  
 ; Publication No. US20040023259A1

```

GENERAL INFORMATION:
APPLICANT: Rastelli, Luca
APPLICANT: Zhong, Haihong
APPLICANT: Boldog, Ferenc
APPLICANT: Gangolli, Bsha
APPLICANT: Guo, Xiaojia
APPLICANT: Malyankar, Uriel
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Shimkete, Richard
APPLICANT: Spytek, Kimberly
APPLICANT: Vermet, Corine
APPLICANT: Rieger, Daniel
APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 15966-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
PRIOR FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Curoseq1st version 0.1
SEQ ID NO 6
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-364-888-6

Query Match      8.6%; Score 81; DB 4; Length 349;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

QY      91 RW--EKVSEDEVIGHOLRVPHQRYKDTMTKVMKHAHS-----ANLH----- 133
DB      81 RWNCSALGEKTVFG-QELRVGSREDAFT--YAITPAAGVAHAHTVATCSGAINLSNGCDREK 137
QY      134 --WYKIDGVWKFAGLKPDIRMGSEFDPDIRPEDGRE 167
DB      138 QGYINQAEQ-WKMGGCSADVRYG-IDFSRRFVDARE 171

RESULT 10
US-10-364-888-8
Sequence 8, Application US/10364888
Publication No. US20040023259A1
GENERAL INFORMATION:
APPLICANT: Rastelli, Luca
APPLICANT: Zhong, Haihong
APPLICANT: Boldog, Ferenc
APPLICANT: Gangolli, Bsha
APPLICANT: Guo, Xiaojia
APPLICANT: Malyankar, Uriel
APPLICANT: Patturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Shimkete, Richard
APPLICANT: Spytek, Kimberly
APPLICANT: Vermet, Corine
APPLICANT: Rieger, Daniel
APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 15966-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
PRIOR FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Curoseq1st version 0.1
SEQ ID NO 6
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-364-888-6

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```

PRIORITY APPLICATION NUMBER: 09/625,634
PRIORITY FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 8
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-364-888-8

Query Match      8.6%; Score 81; DB 4; Length 349;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

Qy      91 RW--EKVSEDEVIGYHQLRVPHQRKYKDTMTKKEVTMKGAHS-----ANLH----- 133
Db      81 RKNCSALGKTYVFG-QELRVGSRFAFT--YAIRAAGVAHAHVTAACSGNLNCGCDREK 137
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy      134 --WYKKIDGVWKFKAGLKPDIRMGSEFPDDRIFEDGRE 167
Db      138 QGYVNOAEG-WKWGCGSADVRYS-IDFSRRFVDARE 171
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 11
US-10-678-639-20
Sequence 20, Application US/10678639
Publication No. US20040247593A1
GENERAL INFORMATION:
APPLICANT: He, Biao
APPLICANT: You, Zhidong
APPLICANT: Xu, Zhidong
APPLICANT: Jablons, David M.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signaling
FILE REFERENCE: 023070-125630US
CURRENT APPLICATION NUMBER: US/10/678,639
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: US 10/264,825
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US 60/509,037
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US 60/491,350
PRIOR FILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human wingless-type 7B (Wnt-7B) peptide sequence
US-10-678-639-20

Query Match      8.6%; Score 81; DB 5; Length 349;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

Qy      91 RW--EKVSEDEVIGYHQLRVPHQRKYKDTMTKKEVTMKGAHS-----ANLH----- 133
Db      81 RKNCSALGKTYVFG-QELRVGSRFAFT--YAIRAAGVAHAHVTAACSGNLNCGCDREK 137
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Qy      134 --WYKKIDGVWKFKAGLKPDIRMGSEFPDDRIFEDGRE 167
Db      138 QGYVNOAEG-WKWGCGSADVRYS-IDFSRRFVDARE 171
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 12
US-10-847-972-22
Sequence 22, Application US/10847972
Publication No. US20050049195A1
GENERAL INFORMATION:
APPLICANT: ZOU, YIMIN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION

```

```
FILE REFERENCE: ARCD:395US
CURRENT APPLICATION NUMBER: US/10/847,972
CURRENT FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/470,913
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-847-972-22

Query Match
Best Local Similarity 31.2%; Score 81; DB 5; Length 349;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

QY 91 RW--EKVSEDEVGYHQLRPHQRYKDTMKVETMKGHAHS-----ANLH----- 133
DB 81 RWCASALGEKTVFG-QELRVGSRBAFT--YAITAGVAHAATTAACSGNLNCGCDREK 137
QY 134 --WYKKIDGVWKFAGLKPDIRMGEPFDRIFEDGRE 167
DB 138 QGYVNOAEG-WKMGCGSADVRYG-IDFSRRFVDARE 171

RESULT 13
US-11-108-528-44
Sequence 44, Application US/11/108528
Publication No. US20050261189A1
GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
APPLICANT: Marvin, Martha
APPLICANT: Li, Dean Y.
APPLICANT: Wang, Elizabeth
APPLICANT: Chen, C. M. Amy
APPLICANT: Shambh, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
FILE REFERENCE: HYDR-P01-041
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-11-108-528-44

Query Match
Best Local Similarity 31.2%; Score 81; DB 6; Length 349;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

QY 91 RW--EKVSEDEVGYHQLRPHQRYKDTMKVETMKGHAHS-----ANLH----- 133
DB 81 RWCASALGEKTVFG-QELRVGSRBAFT--YAITAGVAHAATTAACSGNLNCGCDREK 137
QY 134 --WYKKIDGVWKFAGLKPDIRMGEPFDRIFEDGRE 167
DB 138 QGYVNOAEG-WKMGCGSADVRYG-IDFSRRFVDARE 171

RESULT 14
US-11-096-568A-28399
Sequence 28399, Application US/11/096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
```

```
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 28399
LENGTH: 614
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(614)
OTHER INFORMATION: Ceres Seq. ID no. 2717494
US-11-096-568A-28399

Query Match
Best Local Similarity 23.2%; Score 79.5; DB 6; Length 614;
Matches 57; Conservative 29; Mismatches 61; Indels 99; Gaps 15;

QY 6 OKSDS-----ITPSDYLGIMTCVYEWADSYD-----SKMDRLRKVI 42
DB 29 QPSDEDLTTIGPHOTSFDDEIGVIGHATVDDDEDIMDGTGVPQTINLDDDLGII 88
QY 43 APTLRIDYRSPDLKLEMPAEFVG-WYSSKOMLGDEFTLRTOHFIGTRV-----E 93
DB 89 GPEFIHKQDF-----PADFIQTSVSAVQVEG--AKKGSGRGLTSWDEFTMPPE 137
QY 94 KISE---DEVYGHQLRPHQRYD--TMTKEVTMKGHAHSANLHWYKI----- 138
DB 138 KVOQNGDDEGVDF-----TYRYDKIKIMELNTNCFRS--ISWRIILPYGIKGV 189
QY 139 --DGVWKF-----AGLKP-----DIRMGEPFDRIFEDGRE----- 167
DB 190 NEEGV-KFYNDLINELNGLIOPSVTLPHWESPLALEWYGGFLNERIYEDFREPANCF 248
QY 168 -TFGDK 172
DB 249 KEFGDR 254

RESULT 15
US-11-097-143-1701
Sequence 1701, Application US/11/097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1701
```

; LENGTH: 1239  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-11-097-143-1701

Query Match 8.4%; Score 79.5; DB 6; Length 1239;  
Best Local Similarity 27.6%; Pred. No. 71;  
Matches 32; Conservative 20; Mismatches 51; Indels 13; Gaps 4;

QY 34 DMDRLKRVIA--PTL--RIDYRSFLDKLMEAMPAEFFVGMVSSKQMLGDPTRLRTOHFI- 87  
Db 769 DMRQNNIVLADQPTFVKYLIKVAINDRGESNVAABEVGSGEDRPLDAPTNFTWRQIT 828  
QY 88 ----GSTRWEKVSDEVIY--HOLRVPHQRYKDTTKEVTWKGAHGSANLHWYK 136  
Db 829 SSTSGYVWMTFVSESVRGHFKGKIKIQTWTENEGSGELRIHVKGDTNHALVTQFK 884

Search completed: December 5, 2006, 01:44:31  
Job time : 189 secb

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 4, 2006, 19:11:55 / Search time 4365 Seconds  
(without alignments)  
3305.198 Million cell updates/sec

Title: US-10-507-132-2  
Perfect score: 942  
Sequence: 1 MCSQVQKSDIEITFDYGLM.....WGEFEDRIEFDGRTFGDK 172

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 48236798 seqs, 27959665780 residues  
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame\_plus.p2n.model -DEV=x1h  
-Q=/abs/ABSSWEB.spool/US10507132/runat\_04122006\_143903\_11302/app\_query.fasta\_1  
-DB=EST -QFMT=faclap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORF=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes07  
-USER=US10507132.@CCN\_1.1.6323@runat\_04122006\_143903\_11302 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT\_DSPLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.\*  
1: gb\_est1.\*  
2: gb\_est3.\*  
3: gb\_est4.\*  
4: gb\_est5.\*  
5: gb\_est6.\*  
6: gb\_est7.\*  
7: gb\_est8.\*  
8: gb\_est9.\*  
9: gb\_est10.\*  
10: gb\_est11.\*  
11: gb\_est12.\*  
12: gb\_est13.\*  
13: gb\_est14.\*  
14: gb\_est15.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	938	99.6	619	3 BM863356 mgcm006xo
2	933	99.0	657	3 BM864194 mgcm008xj
3	932	98.9	664	3 BM863315 mgcm006xe
4	923	98.0	649	3 BM863340 mgcm006xk

5	861	91.4	593	3 BM863546	BM863546 mgcm006xf
6	859	90.2	571	3 BM863710	BM863710 mgcm007xe
7	853	90.6	599	3 BM864156	BM864156 mgcm008xd
8	833	88.4	643	3 BM864457	BM864457 mgcm010xh
9	785	82.3	523	3 BM863209	BM863209 mgcm005xd
10	772	82.0	602	3 BM863558	BM863558 mgcm006xh
11	748	79.4	486	3 BM863639	BM863639 mgcm007xc
12	715	75.9	781	3 BM864820	BM864820 mgap007xa
13	703	74.6	510	3 BM863374	BM863374 mgcm007xa
14	703	74.6	530	3 BM863357	BM863357 mgcm006xc
15	694	73.7	600	3 BM864472	BM864472 mgcm010xj
16	685	72.7	552	5 CD275566	CD275566 T143B0121
17	685	72.7	588	5 CD275905	CD275905 T143B0122
18	675	71.7	515	3 BM861796	BM861796 mgcm001x1
19	665	70.6	504	3 BM863499	BM863499 mgcm006xl
20	649.5	68.9	473	3 BM864018	BM864018 mgcm008xc
21	643	68.3	530	5 CD275940	CD275940 T143B0156
22	639	66.8	499	5 BP273332	CD273332 T143B0196
23	618	65.2	573	3 BQ109916	BQ109916 VP0100E09
24	605	64.2	507	5 CD275678	CD275678 T143B0071
25	596	63.3	430	4 CD028671	CD028671 mgcm007xh
26	564	59.9	366	3 BM864053	BM864053 mgcm008xm
27	560	59.4	429	5 CD274144	CD274144 T143B0403
28	548	58.2	541	4 CD036729	CD036729 mgau011xc
29	530.5	56.3	570	4 CD034317	CD034317 mgmt015xp
30	529	56.2	398	3 BM861952	BM861952 mgcm001xl
31	496	52.7	491	4 CD035038	CD035038 mgmt018xh
32	477	50.6	486	4 CD035120	CD035120 mgmt018xl
33	463	49.2	377	5 CD276416	CD276416 T143B0271
34	452	48.0	489	3 BM863213	BM863213 mgcm005xd
35	408	43.1	441	3 BM871833	BM871833 mgns015xb
36	387.5	41.1	476	2 BG280255	BG280255 cb06np.r
37	355	37.7	563	5 CK906746	CK906746 rhzma0_00
38	269.5	28.6	670	7 BE188285	BE188285 ps161f.in
39	265	28.1	363	3 BP100008	BP100008 BP100008
40	253	26.9	881	9 DN476575	DN476575 altc207x3
41	193.5	20.5	697	7 BE188286	BE188286 ps161r3.i
42	183	19.4	797	6 AB228194	AB228194 Aspergillus
43	142	15.1	495	8 CO151881	CO151881 EST8269314
44	123	13.1	295	3 BM863872	BM863872 mgcm007xl
45	110	11.7	146	5 CK434157	CK434157 rhzma0_00

## ALIGNMENTS

RESULT 1  
BM863356 619 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm006x003f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006x003 5', mRNA sequence.  
BM863356  
ACCESSION BM863356 GI:30391591  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE  
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatnager,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
JOURNAL  
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231038.

Contact: Ebbole D  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person:best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone

dehydratase >gi|1127197|pdb|1STRD|. . . 367 e-101  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm006 row: 0 column: 03  
 Seq primer: T3.

FEATURES  
 source

1..619  
 Location/Qualifiers  
 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm006x003"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
 /note="Vector: pBluescript-SK-; Site 1: EcoRI, Site 2:  
 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredphrap version 991019 and trimmed  
 according to phd files (0.05) and for vector segs."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,51e-105 Length: 619  
 Score: 938.00 Matches: 171  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 99.4% Mismatches: 0  
 Query Match: 99.6% Indels: 0  
 DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM65356 (1-619)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20  
 DB 53 ATGGGTTTCGAAATTCACAAAGACGATGATTAACCTTCCACATCACTGGGCTTCATG 112  
 QY 21 ThrCysValTyrGlnTyrPalaAspSerTyrAspSerTyrAspTyrPalaAspTyrLeuAGly 40  
 DB 113 ACTTGCGTCTATAGTCGGACGACAGCTACGATCCCAAGACCTGGATAGGCTGCCAAG 172  
 QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTyrGluAla 60  
 DB 173 GTCATTGCGGCTACTCGCGCATTTGACTACCGCTCTCTCCACAAAGCTCTGGAGGCA 212  
 QY 61 MetProAlaGlnLysPheValGlyMetValSerSerTyrGlnMetLeuGlyAspProThr 80  
 DB 233 ATGCCCGCCAGAGATTCGTGGCATGTCTTCAGCAAGAGGTGCTGGCGACCCACC 292  
 QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTyrGlyValSerGluAspGluVal 100  
 DB 293 CTCGCCACGACGACCTTCATCGCGCGGCACCGCTGGGAGAAAGTGTCCAGACGACAGTTC 352  
 QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120  
 DB 353 ATCGGCTACACACAGCTCGCGCTCCGACCAAGAGTACCAACATGAGAGAG 412  
 QY 121 ValThrMetLysGlyHisAlaHisSerAlaAspLeuHisThrPyrTyrLysLysIleAspGly 140  
 DB 413 GTCACCATGAGGAGCCACGCGCACTCGGCAAACTTCATCGTACCAAGAAAGATCGACGCGC 472  
 QY 141 ValTyrLysPheAlaGlyLeuLysProAspIleArgTyrPylGlyLysPheAspPheAspArg 160  
 DB 473 GTCGTGAAAGTTCGCGCGCTCCAAAGCCGACATCCGCTGGGGCCAGTTCCGATTTGACAGG 532  
 QY 161 IlePheGlnAspGlyArgGluThrPheGlyAspLys 172

DB 533 ATCTTGAGACGACGACGAGACCTTTGGCGCAAA 568

RESULT 2  
 LOCUS BM64194 657 bp mRNA linear EST 06-MAY-2003  
 DEFINITION mgcm006xJ12.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 grisea cDNA clone mgcm008xJ12 5', mRNA sequence.  
 ACCESSION BM64194  
 VERSION BM64194.2 GI:30390885  
 KEYWORDS EST.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
 1 (bases 1 to 657)  
 AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatterai,K. and Dean,R.A.  
 TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 JOURNAL Unpublished (2002)  
 COMMENT On Mar 7, 2002 this sequence version replaced gi:19231876.  
 CONTACT: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact  
 person/Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR\_Scytalone  
 dehydratase >gi|1127197|pdb|1STRD|. . . 365 e-100  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm008 row: J column: 12  
 Seq primer: T3.

FEATURES  
 source

1..657  
 Location/Qualifiers  
 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm008xJ12"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
 /note="Vector: pBluescript-SK-; Site 1: EcoRI, Site 2:  
 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredphrap version 991019 and trimmed  
 according to phd files (0.05) and for vector segs."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.47e-104 Length: 657  
 Score: 933.00 Matches: 170  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 99.4% Mismatches: 0  
 Query Match: 99.0% Indels: 0  
 DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM64194 (1-657)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20  
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Db 91 ATGGGTTCCGAAAGGTTCAAGAGGATGAGTAACTTCTCAGACTACCTGGGCTTCAG 150  
Qy 21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerIlyAspTrpAspArgLeuArgIys 40  
Db 151 ACTTGCGTCTATAGTGGGACAGAGCTACGACTCCAGAGACTGGGATAGGCTGCGAAG 210  
Qy 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspIlyLeuTrpGluAla 60  
Db 211 GTCATTGGCGCTACTGCGGCACTGACTACCGGCTCTCTCCAGACAAGCTCTGGAGGCA 270  
Qy 61 MetProAlaGluGluPheValGlyMetValSerSerIlyGlnMetLeuGlyAspProThr 80  
Db 271 ATGCCGCGCCAGAGAGTTCGTCCGCAAGTCTCCAGCAAGAGGTGCTGGCGGAGCCACC 330  
Qy 81 LeuArgTrpGlnHisPheIleGlyIleThrArgTrpGluIlyValSerGluAspGluVal 100  
Db 331 CTCGCAACGAGCACTTCATCGGCGGACCGCTGGGAGAAAGTGTCCGAGACAGAGTC 390  
Qy 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrIlyAspTrpThrMetIlyGlu 120  
Db 391 ATGGGCTACCAAGAGCTGGCGGCTCCGCAACAGAGTACAGAGACACCAATGAAAGAG 450  
Qy 121 ValThrMetIlyGlyHisAlaHisSerAlaAsnLeuHisTrpTyrIlyIlySylIleAspGly 140  
Db 451 GTCACCATGAAAGGCGCAGCGCCACTCGGCAAACTTCACGTTACAAAGAAAGATCGACGCG 510  
Qy 141 ValTrpIlyPheAlaGlyLeuIlyProAspIleArgTrpGlyIlyPheAspPheAspArg 160  
Db 511 GTCTGGAAGTTCGCGGCTCCAGAGCCGACATCCGCGGAGGAGTTCGACTTGACAGG 570  
Qy 161 IlePheGluAspGlyArgGluTrpPheGlyAsp 171  
Db 571 ATCTTGAGAGCGAGCGGAGACCTTTGGCGAC 603

RESULT 3 664 bp mRNA linear EST 06-MAY-2003  
BM663315  
LOCUS mgcm006kx21.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006kx21 5', mRNA sequence.  
ACCESSION BM663315.2 GI:30391622  
VERSION EST.  
KEYWORDS Magnaporthe grisea (anamorph: Pyricularia grisea)  
SOURCE Magnaporthe grisea  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 664)  
Bbbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19230997.  
Contact: Bbbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-bbbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person: best nr hit (Apr11, 22, 2003) sp|P56221|SCYD\_MAGR\_Scytalone  
dehydratase >gi|1127157|pdb|1STM|. . . 364 e-100  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: E column: 21  
Seq primer: T3.  
Location/Qualifiers  
1. .664  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"

/db xref="taxon:148305"  
/clone="mgcm006kx21"  
/sex="Male-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_1ib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI, Site 2:  
XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was tried  
according to the alignment, otherwise sequence quality was  
assessed using phredPhrap version 991019 and trimmed  
according to pnd files (0.05) and for vector seqs."

## ORIGIN

Alignment Scores:  
Pred. No.: 3 33e-104 Length: 664  
Score: 932.00 Matches: 170  
Percent Similarity: 99.4% Conservative: 1  
Best Local Similarity: 98.8% Mismatches: 1  
Query Match: 98.9% Indels: 0  
DB: 3 Gaps: 0  
US-10-507-132-2 (1-172) x BM663315 (1-664)

Qy 1 MetGlySerGlnValGlnIlySerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20  
Db 81 ATGGGTTCCGAAAGTTCAAAGAGCGATGAGTAACTTCTCAGACTACCTGGGCTTCAG 140  
Qy 21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerIlyAspTrpAspArgLeuArgIys 40  
Db 141 ACTTGCGTCTATAGTGGGACAGAGCTACGACTCCAGAGACTGGGATAGGCTGCGAAG 200  
Qy 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspIlyLeuTrpGluAla 60  
Db 201 GTCATTGGCGCTACTGCGGCACTGACTACCGGCTCTCTCCAGACAAGCTCTGGAGGCA 260  
Qy 61 MetProAlaGluGluPheValGlyMetValSerSerIlyGlnMetLeuGlyAspProThr 80  
Db 261 ATGCCGCGCGAGAGTTCGTCCGCAAGTCTCCAGAGACAGAGGTGCGGAGCCACC 320  
Qy 81 LeuArgTrpGlnHisPheIleGlyIleThrArgTrpGluIlyValSerGluAspGluVal 100  
Db 321 CTCGCAACGAGCACTTCATCGGCGGACGCGCTGGGAGAAAGTGTCCAGAGACAGGTC 380  
Qy 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrIlyAspTrpThrMetIlyGlu 120  
Db 381 ATGGGCTACCAAGAGCTGGCGGCTCCGCAACAGAGTACAGAGACACCAATGAAAGAG 440  
Qy 121 ValThrMetIlyGlyHisAlaHisSerAlaAsnLeuHisTrpTyrIlyIlySylIleAspGly 140  
Db 441 GTCACCATGAAAGGCGCAGCGCCACTCGGCAAACTTCACGTTACAAAGAAAGATCGACGCG 500  
Qy 141 ValTrpIlyPheAlaGlyLeuIlyProAspIleArgTrpGlyIlyPheAspPheAspArg 160  
Db 501 GTCTGGAAGTTCGCGGCTCCAGAGCCGACATCCGCGGAGAGTTCGACTTGACAGG 560  
Qy 161 IlePheGluAspGlyArgGluTrpPheGlyAsp 172  
Db 561 ATCTTGAGAGCGAGCGGAGACCTTTGGGCGACAAA 596

RESULT 4 649 bp mRNA linear EST 06-MAY-2003  
BM663340  
LOCUS mgcm006kx09.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006kx09 5', mRNA sequence.  
ACCESSION BM663340  
VERSION BM663340.2 GI:30391603  
KEYWORDS EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
 REFERENCE 1 (bases 1 to 649)  
 AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bacterial,K. and Dean,R.A.  
 TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 JOURNAL Unpublished (2002)  
 COMMENT On Mar 7, 2002 this sequence version replaced gi:19231022.  
 Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person.Best nr hit (April. 22, 2003) sp|P56221|SCYP\_MAGGR\_Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 361 5e-99  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm006 row: K column: 09  
 Seq primer: T3.  
 FEATURES  
 source  
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 Location/Qualifiers  
 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm006xK09"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_1fb="Magnaporthe grisea CM Uni-Zap XR library"  
 /note="Vector: pBluescriptSK-; Site.1: EcoRI; Site.2:  
 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phred/nap version 991019 and trimmed  
 according to pnd files (0.05) and for vector seqs."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4,18e-103 Length: 649  
 Score: 923.00 Matches: 169  
 Percent Similarity: 99.4% Conservative: 2  
 Best Local Similarity: 98.3% Mismatches: 1  
 Query Match: 98.0% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-507-132-2 (1-172) x BM65340 (1-649)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20  
 DB 84 ATGGGTTTCGAACTTCAAAAGACGATGAGATTAACCTTCACAGATCACTGGCGCTCAG 143  
 QY 21 ThrCValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuGlyLys 40  
 DB 144 ACTTGGCTTATGAGGGGACACACTACTACTCCAAAGACTGGGATAGGCTGCGAAG 203  
 QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60  
 DB 204 GTCATTGGCGCTACTCTGGCGCATTAACCGCTCTCTCTCGACAAAGCTCTGGAGGCA 263  
 QY 61 MetProAlaGluGluIubPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80

DB 264 ATGCCGCGCGAGAGATTGTCGCGCATGCTCGAACAAGACAGTGTCTGGCGCAACCCCAAC 323  
 QY 81 LeuArgThrGlnHisPheIleGlyValThrArgTrpGlyLysValSerGluAspGluVal 100  
 DB 324 CTCGCGACGACGACTTCAATCGCGCGACGCGCTGGAGAAAGTGTCCGAGGACAGAGTC 383  
 QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120  
 DB 384 ATCGGCTACACACACTCGGGGTCCCGCACAGAGGTACAAGACACACCATGAAGAG 443  
 QY 121 ValThrMetLysGlyHisIleHisSerAlaAsnLeuHisTyrTyrLysLysIleAspGly 140  
 DB 444 GTCACCATGAAGGGGACAGCCACATCGGCAAACTTTACTGTATCAAAAGATCAACGCGC 503  
 QY 141 ValThrLysPheAlaGlyLeuLysProAspIleArgTrpGlyLysIubAspPheAspArg 160  
 DB 504 GTCGAAAGTTGCGCGGCTCAAGCCGACATCCGCTGGGCGAGTTCGACTTGAACAGG 563  
 QY 161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172  
 DB 564 ATCTTTGAGACGACGAGGAGACCTTTGGCAGCAAA 599  
 RESULT 5  
 BM65346 593 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm006xK04.f.b Magnaporthe grisea CM Uni-Zap XR library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm006xK04 5', mRNA sequence.  
 ACCESSION BM65346.2 GI:30391437  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Magnaporthe grisea (anamorph: Pyricularia grisea)  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
 REFERENCE 1 (bases 1 to 593)  
 AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bacterial,K. and Dean,R.A.  
 TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 JOURNAL Unpublished (2002)  
 COMMENT On Mar 7, 2002 this sequence version replaced gi:19231228.  
 Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person.Best nr hit (April. 22, 2003) sp|P56221|SCYP\_MAGGR\_Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 322 2e-87  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm006 row: F column: 04  
 Seq primer: T3.  
 FEATURES  
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 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm006xK04"  
 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_1fb="Magnaporthe grisea CM Uni-Zap XR library"  
 /note="Vector: pBluescriptSK-; Site.1: EcoRI; Site.2:  
 XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,



150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the *M. grisea* genome was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

## ORIGIN

## Alignment Scores:

Pred. No.:	1,67e-95	Length:	593
Score:	861.00	Matches:	164
Percent Similarity:	95.9%	Conservative:	1
Best Local Similarity:	95.3%	Mismatches:	7
Query Match:	91.4%	Indels:	1
DB:	3	Gaps:	0

US-10-507-132-2 (1-172) x BM63546 (1-593)

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QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
DB 79 ATGGGTTCCGAACTTCAAAAGCGATGATTAACCTTCTCAGACTACCTGGGCTTCATG 138
QY 21 ThrCysValTyrGlnTrrPalaAspSerTyrAspSerTyrAspTrrPalaArgLeuArgLys 40
DB 139 ACTTGGCTCTATAGTGGCGAGACAGCTACGACTCCAGAGGAGCTGGGATGAGCTGGCAAG 198
QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrrPalaIle 60
DB 199 GTATTGGCTCTACTCTGGCGATTGACTACGCTCTCTCTCCAGCAAGCTCTGGGAGGCA 258
QY 61 MetProAlaGlnGlnLysPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
DB 259 ATGCGCGCGAGAGAGTTCTCGGCGATGCTTCCAGCAAGAGAGTGTGGGCGACCCCAACC 318
QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrrPalaLysValSerGlnAspGluVal 100
DB 319 CTCGCGACGAGACACTTCATCGCGCGACCGCTGAGAGAGAGTGTCCGAGGACGAGAGTTC 378
QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTrrLysAspThrThrMetLysGln 120
DB 379 ATGGGCTACACAGCGCTCGCGCGACGACAGAGTACAGAGACACCATGAAAGAG 438
QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrrTyrLysLysIleAspGly 140
DB 439 GTACACATGAGGGCCAGCGCCACTCGGCAAACTTTCACGTACAGAAAGATCGACGGC 498
QY 141 ValTrrLysPheAlaGlyLeuLysProAspTrrLysTrrPalaLysLeuPheAspArg 160
DB 499 GTCTGGAAGTTCGCGGCTCAGCCCGCATCCCGTGGGGGAGATTCCACTTAC-AGG 557
QY 161 IlePheGlnAspGlyArgGlnTrrPheGlyAspLys 172
DB 558 ATCTTTGAGGGCGAGCGAGACCTTTGGCGACAAA 593
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RESULT 6  
LOCUS BM63710 571 bp mRNA linear EST 06-MAY-2003  
DEFINITION mgcm007XE24.f.b Magnaporthe grisea CM Uni-Zap XR library Magnaporthe  
grisea cDNA clone mgcm007XE24 5', mRNA sequence.  
ACCESSION BM63710  
VERSION BM63710.2 GI:30391295  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea

REFERENCE  
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 571)  
Bbbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bacterial,K. and Dean,R.A.

TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea

JOURNAL Unpublished (2002)

COMMENT On Mar 7, 2002 this sequence version replaced gi:19231392.

Contact: Bbbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-bbbole@tamu.edu

Chromatogram file of this sequence is available, see contact  
person.Best nr hit (April, 22 2003) sp|P56321|SCVD\_MAGGR\_Scytalone  
dehydratase>gi|1127197|pdb|1stnd|. . . 336 1e-91

PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm007 row: E column: 24  
Seq primer: T3.

## FEATURES

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/strain="Guy11"

/db\_xref="taxon:148305"

/clone="mgcm007XE24"

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/cell\_type="mycelium"

/clone\_lib="Magnaporthe grisea CM Uni-Zap XR library"

/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:

XhoI. Unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI site of insert.

Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,

reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.

Where a full-length alignment to the *M. grisea* genome  
sequence was available, the EST sequence was trimmed

according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed

according to phd files (0.05) and for vector segs."

## ORIGIN

## Alignment Scores:

Pred. No.:	2,81e-95	Length:	571
Score:	859.00	Matches:	156
Percent Similarity:	98.8%	Conservative:	2
Best Local Similarity:	97.5%	Mismatches:	2
Query Match:	91.2%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-2 (1-172) x BM63710 (1-571)

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QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
DB 92 ATGGGTTCCGAACTTCAAAAGCGATGATTAACCTTCTCAGACTACCTGGGCTTCATG 151
QY 21 ThrCysValTyrGlnTrrPalaAspSerTyrAspSerTyrAspTrrPalaArgLeuArgLys 40
DB 152 ACTTGGCTCTATAGTGGCGAGACAGCTACGACTCCAGAGAGCTGGGATGAGCTGGCAAG 211
QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrrPalaIle 60
DB 212 GTCAATGGCCCTACTCTGGCGATTGACTACGCTCTCTCCAGCAAGCTCTGGGAGGGA 271
QY 61 MetProAlaGlnGlnLysPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
DB 272 ATGCGCGCGAGAGAGTTCTCGGCGATGCTCTGAGCAAGAGAGTGTGGGCGACCCCAACC 331
QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrrPalaLysValSerGlnAspGluVal 100
DB 332 CTCGCGACGACAGCACTTCATCGCGCGACCGCTGGGAGAAAGTGTCCGAGACGAGGTC 391
QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTrrLysAspThrThrMetLysGln 120
DB 392 ATCGGCTACACAGCTGCGGCTCCGCGACGAGAGTACAGAGACACCATGAAAGAG 451
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QY 121 ValThMeLySGlyHsAlaHisSerAlaAsnLeuHisTrpTyrlsLysIleAspGly 140  
 DB 452 GTCACCATGAAAGGCGACCGCCACTCGGGAACCTTCACGTGACAAAGATCGACGGG 511  
 QY 141 ValTrpLysPheAlaGlyLeuLysProAspIleAspTrpGlyGluPheAspPheAspArg 160  
 DB 512 GTTTGGAGATTTCCTCCGCTCTCAAGCCGACATCCGCTGGGGCGAGACTGATTTCGACAG 571

RESULT 7  
 BM664156 599 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm008xD02f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm008xD02 5', mRNA sequence.  
 ACCESSION BM664156  
 VERSION BM664156.2 GI:30390915  
 KEYWORDS EST.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
 1 (bases 1 to 599)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatterai,K. and Dean,R.A.  
 Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 TITLE Unpublished (2002)  
 JOURNAL On Mar 7, 2002 this sequence version replaced gi:19231838.  
 COMMENT Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person:best nr hit (Apr11. 22, 2003) sp|P56221|SCYD\_MAGGR\_Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 302 3e-87  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm008 row: D column: 02  
 Seq primer: T3.

FEATURES  
 source  
 Location/Qualifiers  
 1..599  
 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm008xD02"  
 /sex="Mati-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
 XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods,  
 where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredphrap version 991019 and trimmed  
 according to phd files (0.05) and for vector seqs."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.65e-94 Length: 599  
 Score: 853.00 Matches: 160  
 Percent Similarity: 94.2% Conservative: 3  
 Best Local Similarity: 92.5% Mismatches: 9  
 Query Match: 90.6% Indels: 1  
 DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM664156 (1-599)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTrpLeuGlyLeuMet 20  
 DB 79 ATGGGTTGGCAAGTTCAAAAGCGCATGATTAACCTTCTCAAGTACTGGGCTCATAG 138  
 QY 21 ThrCysValTYrGluTrpAlaAspSerTYrAspSerLysAspTrpAspArgLeuArgLys 40  
 DB 139 ACTTGCGTCTATGATGGGCGAGACGCTACGACTCCAAAGACTGGGATAGCGTGGAAAG 198  
 QY 41 ValIleAlaProThrLeuArgIleAspTYrArgSerPheLeuAspLysLeuTrpGluAla 60  
 DB 199 GTCATTGGCGCTCACTCGCGCATGTACTACCGCTCTTCCTGCACAACTCTGGGAGGCA 258  
 QY 61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80  
 DB 259 ATGCCGCGCCGAGAAATTGCTGGCAATGCTCTGCAGCAAGAGTCTGGCCGACCCACCC 318  
 QY 81 LeuArgTrnGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100  
 DB 319 CTCGCCACGACGACACTTCATCGCGCGGACGCCCTGGAGAGGTGTCCGAGGACGAGGTC 378  
 QY 101 IleGlyTYrHisGlnLeuArgValProHisGlnArgTYrLysAspThrThrMetLysGlu 120  
 DB 379 ATCGGCTACCAACCACTGCGCTCCGACCAAGAGTCAAGAGACACACCATGAAGAG 438  
 QY 121 ValThMeLySGlyHsAlaHisSerAlaAsnLeuHisTrpTyrlsLysIleAspGly 140  
 DB 439 GTCACCATGAAAGGCGACCGCCACTCGGGAACCTTCACGTGACAAAGATCGACGGG 498  
 QY 141 ValTrpLysPheAlaGlyLeuLysProAspIleAspTrpGlyGluPheAspPheAspArg 160  
 DB 499 GTTCTGAAGTTTCATAGAGCTTTACGCCCGGACAGCTGCTGGGCGAGTTTGACCG 558  
 QY 160 gTlePheGluAspGlyAraGgtThrPheGlyAspLys 172  
 DB 559 GAACCTTGACGACGACGACGACGACCTTTGGGAGACAA 595

RESULT 8  
 BM664467 643 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm010xH12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm010xH12 5', mRNA sequence.  
 ACCESSION BM664467  
 VERSION BM664467.2 GI:30390655  
 KEYWORDS EST.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
 1 (bases 1 to 643)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatterai,K. and Dean,R.A.  
 Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 TITLE Unpublished (2002)  
 JOURNAL On Mar 7, 2002 this sequence version replaced gi:19232149.  
 COMMENT Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person:best nr hit (Apr11. 22, 2003) sp|P56221|SCYD\_MAGGR\_Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 320 8e-87  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm010 row: H column: 12  
 Seq primer: T3.

## FEATURES

Location/Qualifiers

1. 643  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm010xh12"  
/sex="Matl-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

## ORIGIN

## Alignment Scores:

Pred. No.: 5.33e-92 Length: 643  
Score: 833.00 Matches: 160  
Percent Similarity: 96.4% Conservative: 2  
Best Local Similarity: 95.2% Mismatches: 3  
Query Match: 88.4% Indels: 3  
DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM864467 (1-643)

```

QY 1 MetG1SerGlnValGlnIlySerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
Db 145 ATGGGTTCCGCAAGTCAAAAGAGGATGAGATTAACCTTCTCAGACTCCGGGCTTCATG 204
QY 21 ThrCysValTyrGluTTPAlaAspSerTyrAspSerIlyAspTPAPAPCylLeuArgLys 40
Db 205 ACTTGCGTCATAGTGGGAGACAGCTTACGACTCCAGAGACTGGGATGAGCTGGCAAG 264
QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTyrGluVala 60
Db 265 GTCAATGCGCTACTCTCGCATTCAGCTACGCGCTTCCTCCAGCAAGCTCTGGAGGCA 324
QY 61 MetProAlaGluGluPheValGlyMetValSerSerIlyGlnIleGlyAspProThr 80
Db 325 ATCCCGCCGAGAGATTGCTGCGCATGTCTCGAGCAAGAGAGGCTGGGCGGACCCACC 384
QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTyrGluLysValSerGluAspGluVal 100
Db 385 CTCGCGACGAGCACTTCATGCGGAGCAGCGCTGGGAGAGGTCGAGAGACAGGTC 444
QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
Db 445 ATCGGCTACACACAGCGCGCGCTCCGCAACAGAGTACAGAGCAACACATGAGAGAG 504
QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTyrTyrLysLysIleAspGly 140
Db 505 GTCACCACTGAAGGCGCACCGCCACTTCGCAAACTTTCATGATCAAGAGATCGCGC 564
QY 141 ValTTrpLysPheAlaGlyLeuLysProAspIleArgTyrGluGluPheAspPheAsp 160
Db 565 GTTTGAGAGTTCCGCGGCCCCCAGACATCCGCTTGGGCGAGTTCCGACTTTTACA 624
QY 160 Tgile-PheGluAspGly 165
Db 625 GGATTCTTTGAGGACGGA 642

```

RESULT 9  
BM863209  
LOCUS

BM863209

523 bp

mRNA

linear

EST 06-MAY-2003

## DEFINITION

mgcm005xD02.f.b Magnaporthe grisea CM Uni-Zap XR library Magnaporthe grisea cDNA clone mgcm005xD02 5', mRNA sequence.

## ACCESSION

BM863209

## VERSION

BM863209.2

## KEYWORDS

GI:30391705

## SOURCE

EST.

## ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

## REFERENCE

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

## AUTHORS

1 (base 1 to 523)

## TITILE

Ebbold,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatteval,K. and Dean,R.A.

## JOURNAL

Expressed sequence tags from the rice blast fungus, Magnaporthe grisea

## COMMENT

Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19230891.  
Contact: Ebbold DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbold@tamu.edu  
Chromatogram file of this sequence is available, see contact person: Best nr hit (April. 22, 2003) sp|56221|SCYD\_MAGGR\_Scyalone dehydratase >gi|1127197|pdb|1STMD|. . . 308 3e-83  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm005 row: D column: 02  
Seq primer: T3.

## FEATURES

Location/Qualifiers

1. 523  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm005xD02"  
/sex="Matl-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.42e-86 Length: 523  
Score: 785.00 Matches: 144  
Percent Similarity: 99.3% Conservative: 1  
Best Local Similarity: 98.6% Mismatches: 1  
Query Match: 83.3% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM863209 (1-523)

```

QY 1 MetG1SerGlnValGlnIlySerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
Db 86 ATGGGTTCCGCAAGTCAAAAGAGGATGAGATTAACCTTCTCAGACTCCGGGCTTCATG 145
QY 21 ThrCysValTyrGluTTPAlaAspSerTyrAspSerIlyAspTPAPAPCylLeuArgLys 40
Db 146 ACTTGCGTCATAGTGGGAGACAGCTTACGACTCCAGAGACTGGGATGAGCTGGCAAG 205

```

Oy		41	VallilealPaProthLeuArgIleAspTyrSerPheLeuAspLysLeuTrgClnUla	60
Db		206	GTCATTGGGCTTAAGCTTCGCCATTTACTACCGCTCTTCTCCGCACAACTCTGGAGGCA	265
Oy		61	MecProLaGiugLuPhueValGlYMeVaiSerSerLySgmMetLeuGIYaSPProThr	80
Db		266	ATGCCGCGCCGAGAGGTTCGTCGGCATGTCTCTGCACAGCAGAGTGCTGGCGAACCCACC	325
Oy		81	LeuArgrThrGlnHisPheIleGLYGLYThrArgrTrgClyVsVaISerGIUnASpGIUnAl	100
Db		326	CTCCGCACGCGACACTTGATGGCGCGCACGGCTGGGAGGAAGTGCTCCGAGACACAGGTC	385
Oy		101	IleGIYTrHisGInLeuArgValProHISglNarGIYrLyaSPThrThrMetLysGIUn	120
Db		386	ATCCGCTTCCACACAGCTCGCGCTCCCGCACAGAGTACAAGACACCAACATGAAGAG	445
Oy		121	ValThrMetLysGIYHISAlaHisSerAlaLeuLeuHIstPrTYrLysLysILEaspGIY	140
Db		446	GTCACCAATGAAGAGGCGCACGCCACCTCGCAAACTTCACGTGTACAAGAAGATCGACGC	505
Oy		141	ValTrplysPheAlaGIY 146	
Db		506	GTCGGAAGTTCGCGCGC 523	
RESULT 10				
BMB63558		602 bp	mRNA	linear EST 06-MAY-2003
LOCUS				
DEFINITION			mgcm006kxH04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe	
ACCESSION			grisea cDNA clone mgcm006kxH04_5', mRNA sequence.	
VERSION			BMB63558	
KEYWORDS			BMB63558.2 GI:30391426	
SOURCE			EST.	
ORGANISM			Magnaporthe grisea (anamorph: Pyricularia grisea)	
REFERENCE			Magnaporthe grisea	
AUTHORS			Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 602) Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.	
TITLE			Expressed sequence tags from the rice blast fungus, Magnaporthe grisea	
JOURNAL			Unpublished (2002)	
COMMENT			On Mar 7, 2002 this sequence version replaced gi:19231240. Contact: Ebbole DJ Department of Plant Pathology & Microbiology Texas A&M University Peterson Bldg, MS2132, College Station, TX 77843-2132, USA Tel.: 979 845 4831 Fax: 979 845 6483 Email: d-ebbole@tamu.edu Chromotogram file of this sequence is available, see contact person, Beat nr hit (April. 22, 2003) sp P56221 SCFD_MAGE Scytalone dehydrogenase  g i1127197 pdb 1STD . . . 272 3e-72 PCR Primers FORWARD: T3 primer BACKWARD: T7 primer Plate: mgcm006 row: H column: 04 Seq primer: T3.	
FEATURES				
SOURCE			Location/Qualifiers	
			1..602	

reincubated into complete medium 24 h room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the *M. grisea* genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

ORIGIN	
Alignment Scores:	
Pred. No.:	1,66e-84
Score:	772.00
Percent Similarity:	93.5%
Best Local Similarity:	91.1%
Query Match:	82.0%
DB:	3
US-10-507-132-2 (1-172) x BM863558 (1-602)	
	Length: 602
	Matches: 154
	Conservative: 4
	Mismatches: 10
	Indels: 3
	Gaps: 0

QY	1	MecG1SerGlnValGlnTyrSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet	20
Db	95	ATGGTTTCGAAGTCCAAAAGAGGAGGAGATACCTTCTCAGACTACCTGGGCTCATG	154
QY	21	ThrCysValIyrgIuTrpAlaAspSerTyrAspSerIyAspTyrAspArgLeuArgLys	40
Db	155	ACTTGCGCTCATGATGATGGCGACAGCTACGACTCCAGAGACTGGGATAGCTCGAAAG	214
QY	41	ValIleLeuIaProthrlLeuArgIleAspTyrArgSerPheLeuAspIyLysLeuTrrpGluAla	60
Db	215	GTCATTGCGCTTACTCTGGCGCATTTGACTACCGCTCTTCCTCCAGCAAGCTCTGGGAGGCA	274
QY	61	MetProIaGluGluIupPheValGlyMetValSerSerIyGlnMetLeuGlyAspProThr	80
Db	275	ATGCGGGCCGAGAGATTCTGTCGGCAATGTTCTCAAGCAGAGAGTCTGGGCGACCCAC	334
QY	81	LeuArgThrGlnIhisPheIleGlyGlyIyThrArgTrrpGluLysValSerGluAspGluVal	100
Db	335	CTCCGACACGACGACTTCATCCGGCGGACGGCGCTGATGAGAGAGTGTCCGAGACGAGTCT	394
QY	101	IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrIyAspThrThrMetIyGlu	120
Db	395	ATCGGCTACACACAGAGTCCGCGCTCCGCGACACAGATGATCAAGGACACACCATGAAAGAA	454
QY	121	ValThrMetIySerGlyHisAlaHisSerSerAlaAspLeuHisTrrpTyrIyLysIleAspGly	140
Db	455	GTCACCAATGAA-GGGCACCGCCCACTCGGCACCAACCTTATCTTGACAAAGAGATCGACGCG	513
QY	141	-ValTrrpLysPheAlaGlyLeuLysProAspIleArgTrrpGlyGluPheAspPheAspArg	160
Db	514	GCGCTGAGAGTTCGGGGCTTAACCCGACTT-CGGTGGGGCGAGTTCCAAATTTTACAG	572
QY	160	GlePheGluAspGlyArgGluThr	168
Db	573	GGTTCCTTAGACGACGAGGAAACC	597
RESULT 11			
LOCUS	BM863639	486 bp	linear
DEFINITION	mgcm007xg13.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe		EST 06-MAY-2003
ACCESSION	BM863639		
VERSION	BM863639.2		
SOURCE	Magnaporthe grisea (anamorph: Pyricularia grisea)		
ORGANISM	Magnaporthe grisea		
REFERENCE	Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
AUTHORS	Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.		
TITLE	1 (bases 1 to 486)		
JOURNAL	Bohlool,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,		
	Expressed sequence tags from the rice blast fungus, Magnaporthe		
	grisea		
	Unpublished (2002)		

## COMMENT

On Mar 7, 2002 this sequence version replaced gi:19231321.  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person: Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 293 5e-79  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm007 row: G column: 13  
Seq primer: T3.

## FEATURES

## source

Location/Qualifiers  
1..486  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm007XA05"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="mycelium"  
/note="Vector: BluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

## ORIGIN

## Alignment Scores:

Pred. No.: 1,15e-81 Length: 486  
Score: 748.00 Matches: 140  
Percent Similarity: 97.9% Conservative: 1  
Best Local Similarity: 97.2% Mismatches: 3  
Query Match: 79.4% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM863639 (1-486)

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OY 1 MetGlySerGlnValGlnYSerAspGluIleThrPheSerAprrYrLeuGlyLeuMet 20
DB 55 ATGGGTTTCGAAAGTCAAAAGAGGATGATTAACCTTCACACTACCGGCGCTCATG 114
OY 21 ThrCyValTyrGlnTrrPalaAspSerTyrAspSerTyrAspTrrPalaArgLeuArgLys 40
DB 115 ACTTGCGTCTATAGTGGGCAAGACAGCTACGACTCCCAAGGACGGGATGAGCCAAAG 174
OY 41 ValIleAlaProThrIleuAlaGllLeaPrrYrArgSerPheLeuAplyLeuTrrGluAla 60
DB 175 GTATTGGCGGCTCTCTGCGCATTTGACTACCGCTCTCTCCGACAAAGCTCTGGAGGCA 234
OY MetPrrAlaGluGluPheValGlyMetValSerSerTyrGlnMetLeuGlyAspProThr 80
DB 235 ATGCCGGCCGAGAGTTTCGTCGCAATGCTTCAGACAAAGAGGTCGGGCGAACCACC 294
OY 81 LeuArgThrGlnHisPheIleGlyGlyTrrArgTrrPduLysValSerGluAspGluVal 100
DB 295 CTCGCGACGAGACCTTCATCGGCGGACGCGTGGGAGAAAGTGTCCGACGACGAGTTC 354
OY 101 IleGlyTrrHisGlnLeuAlaGValProHisGlnAlaGrrYrLysAspThrThrMetLysGlu 120
DB 355 ATCGGCTACCAACAGCTGCGCGTTCGCGACAGAGGTACAAAGACACCAACATGAAGAG 414
```

```
OY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrrYrLysLysIleAspGly 140
DB 415 GTCCACATGAAGAGGCCCGCCCACTGGCAAACTTCACTGTGACAAAGAAATCGACGGG 474
OY 141 ValTrrPlyAspPhe 144
DB 475 GTCTGGAAAGTTC 486
```

## RESULT 12

## BM864820/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19232502.  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person: Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 271 1e-71  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgap007 row: A column: 05  
Seq primer: T3.

## JOURNAL

## COMMENT

## FEATURES

## source

Location/Qualifiers  
1..781  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="70-15"  
/db\_xref="taxon:148305"  
/clone="mgap007XA05"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="Appressorium"  
/clone\_1b="Magnaporthe grisea Ap Uni-Zap XR Library"  
/note="Vector: BluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Appressorium library. Conidia were germ inocated on an  
inductive surface for 5-8 h. Sequences were processed by  
one of two methods. Where a full-length alignment to the  
M. grisea genome sequence was available, the EST sequence  
was trimmed according to the alignment, otherwise sequence  
quality was assessed using phredphrap version 991019 and  
trimmed according to phd files (0.05) and for vector  
segs."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,56e-77 Length: 781  
Score: 715.00 Matches: 143  
Percent Similarity: 88.4% Conservative: 9  
Best Local Similarity: 83.1% Mismatches: 19  
Query Match: 75.9% Indels: 4  
DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM64820 (1-781)

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QY      2 GlysSerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMetThr 21
Db      723 GGGTTGTCATTCACAAAAACGATTAAATACCTTGTCTCTGACTACTCTGGCTCAATGCT- 665
QY      22 CysValTyrGluTTPAlaAspSerTyrAspSerLysAspTTPAspArgLeuArg-LysVa 41
Db      664 TCCGCTGTATGAGTGGCA-GACAGTTACCGCTCCAGAGATGGGATAGGCTGAGAAAGGT 606
QY      41 ILeaIleProThrLeuArgTLeaAspTyrArgSerPheLeuAspLysLeuTyrGluAlaLe 61
Db      605 CATGGCGCATCTGTGGGCGATTGAATC-CGCTCCCTCCCTCGACCAAGTTTGGGAGCCAAAT 547
QY      61 tProIaIaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrIle 81
Db      546 GCCGACGAAGAGAGTTGCTGGCATGTTCTCGAGCAAGAGCGTGTGGGCGACCCACCTT 487
QY      81 uArgThrGlnHisPheIleGlyGlyThrArgTTPGluLysValSerGluAspGluValIle 101
Db      486 CCGCAGCGACGATTTTCATGGCGGACGCGCTGGGAGAAAGTGTCCGAGAGACGAGTCT 427
QY      101 eGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVa 121
Db      426 CGGCTACCAACCAAGCTGGCGCTCCCGCACAGAGTTCAGAGACACACCATGAGAGAGGT 367
QY      121 tThrMetLysGlyHisAlaHisSerLysAsnLeuHisTTPYrLysLysIleAspGlyVa 141
Db      366 CACCATGAAGGGCCACGCCACCTCGCAAACTTCCTGTCATCAAGAAATGACGCGCT 307
QY      141 tTTPYrPheIaIaGlyLeuLysProAspIleArgTTPGlyGluPheAspPheAspArgIle 161
Db      306 CTGGAAGTTCCGCGGCTCAAGCCGACATCCGCTGGGCGAGTTGCACTTTGACAGGAT 247
QY      161 ePheGluAspGlyArgGluThrPheGlyAspLys 172
Db      246 CTTTGAGGACGAGCGGAGACCTTTGGCGCAAAA 213

RESULT 13
BM63374 510 bp mRNA linear EST 06-MAY-2003
LOCUS mgcm006x010f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
DEFINITION grisea cDNA clone mgcm006x010 5', mRNA sequence.
ACCESSION BM63374
VERSION BM63374.2 GI:30391576
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 510)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bacterial,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
Unpublished (2002)
On Mar 7, 2002 this sequence version replaced gi:19231056.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person/blast nr hit (April. 22, 2003) sp|p56221|SCYD_MAGGR_Scytalone
dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Place: mgcm006 row: C column: 10
Seq primer: T3.

```

# FEATURES

source

```

Location/Qualifiers
1..510
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006x010"
/sex="Mati-2 hermaphrodite"
/cell_type="mycelium"
/clone_idb="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-, Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI site has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimmed
according to the alignment, otherwise sequence quality was
assessed using phredphrap version 991019 and trimmed
according to phd files (0.05) and for vector segs."

```

## ORIGIN

### Alignment Scores:

```

Pred. No.: 4,39e-76 Length: 510
Score: 703.00 Matches: 131
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.2% Mismatches: 0
Query Match: 74.6% Indels: 0
DB: 3 Gaps: 0

```

US-10-507-132-2 (1-172) x BM63374 (1-510)

```

QY      1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
Db      83 ATGGGTTGCAAGTTCAAAGAGCGATGATTAACCTTCTCAGACTACTGGGCTCATGTG 142
QY      21 ThrCysValTyrGluTTPAlaAspSerTyrAspSerLysAspTTPAspArgLeuArgLys 40
Db      143 ACTTGCGTCTATGAGTGGGACAGACGCTACGACTCCAGAGACTGGGATAGCTGGCAAAAG 202
QY      41 ValIleIaProThrLeuArgTLeaAspTyrArgSerPheLeuAspLysLeuTyrGluAla 60
Db      203 GTCATTGGGCGCTACTCTGCGATTGACTACGCTCTTCCTCGACAACTCTGGAGAGCA 262
QY      61 MetProIaIaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
Db      263 ATGCCGCGGAGAGATTGCTGGCAVGGTCTCGACCAAGCAGAGTGTGGGCGACCCACCC 322
QY      81 LeuArgThrGlnHisPheIleGlyGlyThrArgTTPGluLysValSerGluAspGluVal 100
Db      323 CTCGCCACGACGACATTTTCATCGCGGACGCGCTGGGAGAAAGTGTCCGAGACGAGTC 382
QY      101 tLeGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
Db      383 ATCGGCTACCAACCACTGCGCGTCCGACACGAGGTACAAGACACACCATGAAGAG 442
QY      121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
Db      443 GTCACCATGAAGGGCCAGCTCATCTGGCAAACTT 478

RESULT 14
BM63357 510 bp mRNA linear EST 06-MAY-2003
LOCUS mgcm006x005f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
DEFINITION grisea cDNA clone mgcm006x005 5', mRNA sequence.
ACCESSION BM63357
VERSION BM63357.1 GI:19231039
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

```

REFERENCE  
1 (bases 1 to 530)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 6483  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person.Best nr hit (April, 22, 2003) sp|P56221|SCYD\_MAGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: 0 column: 05  
Seq primer: T3

## FEATURES

source

Location/Qualifiers  
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/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm006X005"  
/sex="Mati-2 hermaphrodite"  
/cell\_type="mycelium"  
/note="Vector: pBluescriptSK-, Site 1: EcoRI; Site 2:  
XhoI, unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredPhrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.62e-76 Length: 530  
Score: 703.00 Matches: 131  
Percent Similarity: 100.0% Conservative: 1  
Best Local Similarity: 99.2% Mismatches: 0  
Query Match: 74.6% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM863357 (1-530)

QY 1 MetG|Serg|Val|Gln|Yss|Ser|Asp|Glu|Leu|Thr|Phe|Ser|Asp|Tyr|Leu|Glu|Met 20  
Db 83 ATGGGTTGCAAGTCAAAAGAGCGAGATACCTTCCACACTACCTGGGCGCTCCTCAG 142  
QY 21 ThCyValTyrG|u|Trr|Pa|Asp|Ser|Tyr|Asp|Ser|Leu|Asp|Trr|Pa|Arg|Leu|A|G|lys 40  
Db 143 ACTTGCGTCATAGTGGGAGACAGTACGACTCCAGAGACTGGGATAGGCTGGCGAAG 202  
QY 41 Val|Leu|Ala|Pro|Thr|Leu|Arg|Leu|Asp|Tyr|Arg|Ser|Phe|Leu|Asp|Lys|Leu|Trr|G|u|Ala 60  
Db 203 GTCAATGGCGCTACTCGCGCATGACTACCGCTCCTCTCCGACCAAGCTCTGGGAGGCA 262  
QY 61 MetPrr|Ala|Gln|Glu|Phe|Val|G|u|Met|Val|Ser|Ser|Lys|Gln|Met|Leu|G|u|Asp|Pro|Thr 80  
Db 263 ATCCCGGCGGAGAGTTCGTGGGATGCTCTCAAGACAGAGAGGAGGGGCGAGCCACC 322  
QY 81 Leu|Arg|Thr|Gln|His|Phe|Leu|G|u|G|y|G|y|Thr|Arg|Trr|G|u|Lys|Val|Ser|G|u|Asp|G|u|Val 100

Db 323 CTCGCGACGACACTTCATCGCGGACGCGCTGGAGAGAGGTGCCAGGACGAGTTC 382  
QY 101 |I|e|G|y|T|r|H|i|s|G|l|n|e|u|a|r|g|v|a|P|r|o|H|i|s|G|l|n|a|r|g|y|T|r|L|y|s|p|h|r|t|H|m|e|t|y|s|G|l|u 120  
Db 383 ATCGGCTACACCAAGTGGCGGTCCCGCACAGAGGTACAGACACCAATGAAGAG 442  
QY 121 ValTrrMetLysG|y|H|is|A|la|H|is|Ser|Ala|Asn|Leu 132  
Db 443 GTCACCATAGAGGCCACGCCCACTCGCGAACTT 478

RESULT 15  
BM864472 600 bp mRNA linear EST 06-MAY-2003  
LOCUS BM864472  
DEFINITION mgcm010XJ04.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
grisea cDNA clone mgcm010XJ04 5', mRNA sequence.  
ACCESSION BM864472 GI:30390651  
VERSION  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
REFERENCE  
AUTHORS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 600)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19232154.  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person.Best nr hit (April, 22, 2003) sp|P56221|SCYD\_MAGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 268 5e-71  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm010 row: J column: 04  
Seq primer: T3

## FEATURES

source

Location/Qualifiers  
1..600  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm010XJ04"  
/sex="Mati-2 hermaphrodite"  
/cell\_type="mycelium"  
/note="Vector: pBluescriptSK-, Site 1: EcoRI; Site 2:  
XhoI, unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredPhrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

## ORIGIN

Alignment Scores:  
Pred. No.: 7.04e-75 Length: 600  
Score: 694.00 Matches: 144  
Percent Similarity: 94.8% Conservative: 1



Best Local Similarity: 94.1% Mismatches: 8  
Query Match: 73.7% Indels: 4  
DB: 3 Gaps: 0

US-10-507-132-2 (1-172) x BM64472 (1-600)

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QY      1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
DB      145 ATGGGTTGGCAAGTTCAAAGAGCGATGAGATACCTTCTCAGACTACCTGGGCTCANTG 204
QY      21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
DB      205 ACTTCGCTCTATGAGTGGCGACAGCTACGACTCCAAAGACTGGGATAGCTGGCGAAAG 264
QY      41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
DB      265 GTCAATTGGCCCTACTCTGCGCAATGACTACCGCTCTCTCGACAAAGCTTGGAGGCA 324
QY      61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
DB      325 ATGCCGGCCGAGAGAGTTCGTGGGCATGCTCGAGCAAGCAGAGTGCTGGCGACCCCAAC 384
QY      81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
DB      385 CTCCGCACGACGACACTTCATCGCGCGCACGCGCTGGAGAGAGTGTCCGAGGACGAGGTC 444
QY      101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
DB      445 ATCGGCTACCACTGAGCGCGCTCCCGCACAGAGGACAGAGCACACCATGAAAGAG 504
QY      121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
DB      505 GTCACCATGAAAGGCGCAGCCCACTCGCAAAACCT-CATTGGAC-AAAGAAATCGACGCGC 562
QY      141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrp 153
DB      563 GTCTGAAGTTCGCCGC-CTCAAGCCGAC-ATCCGTTGG 599
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Search completed: December 4, 2006, 21:49:49  
Job time : 4367 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 4, 2006, 20:22:27 ; Search time 628 Seconds  
(without alignments)  
842.475 Million cell updates/sec

Title: US-10-507-132-2  
Perfect score: 942  
Sequence: 1 MSGQVQKSDIEITPSDYLGIM.....WGFDFDRIPEDGRETFGDX 172

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2931743 seqs, 102533816 residues  
Total number of hits satisfying chosen parameters: 5863486

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame\_plus.model -DEV=x1h  
-Q=/abs/mbssweb.epool/US10507132/rnatc\_04122006\_143935\_12137/app\_query.fasta.1  
-DB=Published.Applications.NA.New -QFMT=fastap -SUPFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blonum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs8604  
-USER=US10507132\_@CGN\_1\_1\_271\_@rnatc\_04122006\_143935\_12137 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA.New:  
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9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
11: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	942	100.0	516	6	US-10-507-132-1
2	938	99.6	516	6	US-10-507-132-3
3	938	99.6	600	6	US-10-507-132-13
4	938	99.6	610	6	US-10-507-132-16
5	921	97.8	538	6	US-10-507-132-15
6	921	97.8	545	6	US-10-507-132-14

7	872.5	92.6	729	6	US-10-507-132-18	Sequence 18, Appl
8	870	92.4	732	6	US-10-507-132-17	Sequence 17, Appl
9	87	9.2	3196	6	US-10-449-902-16327	Sequence 16327, A
10	80.5	8.5	1611	9	US-11-174-3078-3703	Sequence 3703, Ap
11	79.5	8.4	1845	9	US-11-056-3558-70677	Sequence 70677, A
12	79.5	8.4	1848	9	US-11-056-3558-78749	Sequence 78749, A
13	77.5	8.2	2451	8	US-11-217-529-78037	Sequence 78037, A
14	77	8.2	1116	8	US-11-266-7488-85042	Sequence 85042, A
15	77	8.2	1157	8	US-11-266-7488-137853	Sequence 137853, A
16	77	8.2	1517	9	US-11-056-3558-65438	Sequence 65438, A
17	77	8.2	1606	6	US-10-449-902-22084	Sequence 22084, A
18	77	8.2	1633	6	US-10-449-902-2362	Sequence 2362, Ap
19	77	8.2	2778	6	US-10-449-902-23861	Sequence 23861, A
20	76.5	8.1	2101	6	US-10-449-902-18695	Sequence 18695, A
21	76.5	8.1	2973	6	US-10-449-902-13104	Sequence 13104, A
22	76.5	8.1	40070	6	US-10-540-898-747	Sequence 747, App
23	76.5	8.1	200033	8	US-11-266-7488-23936	Sequence 23936, A
24	76	8.1	1510	8	US-11-266-7488-260498	Sequence 260498, A
25	76	8.1	1510	8	US-11-266-7488-279244	Sequence 279244, A
26	76	8.1	1510	8	US-11-266-7488-331015	Sequence 321015, A
27	76	8.1	2104	6	US-10-953-349-24959	Sequence 24959, A
28	76	8.1	3330	6	US-11-217-529-3074	Sequence 3074, Ap
29	76	8.1	6379	9	US-11-218-305-11588	Sequence 11588, A
30	76	8.1	1971884	10	US-11-184-236-70	Sequence 70, Appl
31	75.5	8.0	1206	8	US-11-266-7488-188284	Sequence 188284, A
32	75.5	8.0	1776	8	US-11-217-529-190925	Sequence 190925, A
33	75.5	8.0	2065	8	US-11-293-697-1789	Sequence 1789, Ap
34	75.5	8.0	1317241	10	US-11-184-236-73	Sequence 73, Appl
35	75	8.0	1600	8	US-11-216-545-4433	Sequence 4433, Ap
36	74.5	7.9	1391	6	US-10-953-349-22946	Sequence 22946, A
37	74.5	7.9	1578	9	US-11-348-413-18390	Sequence 18390, A
38	74	7.9	1908	8	US-11-216-545-1060	Sequence 1060, Ap
39	74	7.9	4894	8	US-11-266-7488-33577	Sequence 32577, A
40	74	7.9	82027	8	US-11-266-7488-29375	Sequence 29375, A
41	74	7.9	294540	8	US-11-266-7488-23953	Sequence 23953, A
42	73.5	7.8	1698	8	US-11-266-7488-188286	Sequence 188286, A
43	73.5	7.8	1698	8	US-11-266-7488-194649	Sequence 194649, A
44	73.5	7.8	1698	8	US-11-266-7488-242302	Sequence 242302, A
45	73.5	7.8	2668	9	US-11-056-3558-76446	Sequence 76446, A

## ALIGNMENTS

RESULT 1  
US-10-507-132-1  
Sequence 1, Application US/10507132  
Publication No. US20060223136A1  
GENERAL INFORMATION:  
APPLICANT: Koichiro KAKU et al.  
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO  
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT  
FILE REFERENCE: 1254-0258PUS1  
CURRENT APPLICATION NUMBER: US/10/507,132  
CURRENT FILING DATE: 2004-09-10  
PRIOR APPLICATION NUMBER: JP 2002-66955  
PRIOR FILING DATE: 2002-03-12  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 516  
TYPE: DNA  
ORGANISM: Pyricularia oryzae  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(516)  
US-10-507-132-1

Alignment Scores:  
Pred. No.: 7.47e-118  
Score: 942.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 100.0%  
Length: 516  
Matches: 172  
Conservative: 0  
Mismatch: 0  
Indels: 0

DB:	6	Gaps:	0
US-10-507-132-2 (1-172) x US-10-507-132-1 (1-516)			
QY	1 MetGlySerGlnValAlaGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20		
Db	1 ATGGGTTTCGAAGTTCAAAAGAGGAGTGAATACCTTCTCAAGCTACCTGGGCTCATG 60		
QY	21 ThrCyValTyrGluTTPAlaAspSerTyrAspSerLysAspTTPaAspArgLeuArgLys 40		
Db	61 ACTGGCGCTATAGTGTGGGAGACAGCTACCACTCCAAAGACCTGGGATAGCTGGCAAG 120		
QY	41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTTPGluAla 60		
Db	121 GTCAATGGCGCTACTCTGGCGCATTTACTACCGCTCTTCTTCGACAAAGCTCTGGAGGCA 180		
QY	61 MetProAlaGluGluPheValAlaMetValSerSerLysGlnMetLeuGlyAspProThr 80		
Db	181 ATGGCGGCGGAGAGGATGCTGGGATGGTCTCGAGCAAGCAGAGTCTGGGCGACCCACC 240		
QY	81 LeuArgThrGlnHisPheIleGlyGlyThrArgTTPGluLysValSerGluAspGluVal 100		
Db	241 CTCGGCAGCGCAGCACTTCATCGCGGAGCAGCGCTGGAGAAAGTGTCCGAGCAGAGTCTC 300		
QY	101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGln 120		
Db	301 ATGGGCTACCAACCAAGCTGGCGCTCCGACCAAGAGTACAAAGCACACCATGAAAGAG 360		
QY	121 ValThrMetLysGlnHisAlaHisSerSerAlaAsnLeuHisTPTyrLysLysIleAspGly 140		
Db	361 GTCAACATGAAGGCGCCACGCCCACTCGGCAAACTTCACTGGTACAAAGAGATCGACGCG 420		
QY	141 ValTTPlysPheAlaGlyLeuLysProAspIleArgTTPGlyGluPheAspPheAspArg 160		
Db	421 GTCTGGAAGTTTCGCCGGCTCATGACCCGATATCCGCTGGGGCGAGTTTCGACTTGAACAG 480		
QY	161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172		
Db	481 ATCTTTGAGACGAGCAGGAGACCTTTGGCGACAAA 516		
RESULT 2			
US-10-507-132-3			
Sequence 3, Application US/10507132			
Publication No. US20060223136A1			
GENERAL INFORMATION:			
APPLICANT: Koichiro KAKU et al.			
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO			
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT			
FILE REFERENCE: 1254-0258PUS1			
CURRENT APPLICATION NUMBER: US/10/507,132			
CURRENT FILING DATE: 2004-09-10			
PRIOR APPLICATION NUMBER: JP 2002-66955			
PRIOR FILING DATE: 2002-03-12			
NUMBER OF SEQ ID NOS: 19			
SOFTWARE: Patentin Ver. 2.1			
SEQ ID NO 3			
LENGTH: 516			
TYPE: DNA			
ORGANISM: Pyricularia oryzae			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1) .. (516)			
US-10-507-132-3			
Alignment Scores:			
Pred. No.:	2.6e-117	Length:	516
Score:	938.00	Matches:	171
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.4%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	6	Gaps:	0
US-10-507-132-2 (1-172) x US-10-507-132-3 (1-516)			

```

Oy 1 MergLysSerLInValGInLysSerAapGluLeThPhSeSerAapTryLeuGlyLeuMet 20
Db 1 ATGGGTTCCGAAAGTTCAAAAGACGATGAGATTAACCTTCTCGAGCTAACCTGGGCTCATG 60
Oy 21 ThcYsValTyrgLutRpLaAapSerTyAspSerLyAspTrpAspArgLeuArgLys 40
Db 61 ACTTGCGCTATATAGTGTGGCGACAGCTACGACTCCAGAGACTGGGATGGCTGGCAAAAG 120
Oy 41 ValLLaALaProThrLeuArgllLeaAspTryArgSerPheLeuAspLysLeuTrpGluAla 60
Db 121 GTCAATTCGGCTCACTCGCCGATTAACCTACCGCTCCTTCTCTCGACAAAGCTTGGGAGGCA 180
Oy 61 MetProAlaGluGluPheValGlyMetValSerSerLyGlnMetLeuGlyAaPProThr 80
Db 181 ATGCCGCCCGAAGAGATTCTCGCGCATGCTCTCAAGCAAGAGAGTGTGGGCGAACCCACCC 240
Oy 81 LeuArgThrglnHisPheIleGlygLyThrArgTrpGluLysValSerGluAapGluVal 100
Db 241 CTCGGCAGCAGGACCTCATTCGGCGGCGACGCGCTGGGAGAAAGGTGTCCGAGGACGAGTCT 300
Oy 101 lLeGlyYrthlsgLInLeuAagValProHlsglnAArgTyLlyAspPthrThrMetLysGlu 120
Db 301 ATCGGCTTACCAACGAGCTGCGCGCTCCGCAACAAGGTATCAAGGACACCAACAAGAGAG 360
Oy 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTryLysLysIleAspGly 140
Db 361 GTCCACATGAAGGGCCACGCGCCACTCGGCAAACTTCACTCGTATCAAGAAGATCGACGGC 420
Oy 141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspParg 160
Db 421 GTCTGAAGATTCCGCGGCTCAAGCCGATATCCGCTGGGGCGAGTTGCACTTTGACAG 480
Oy 161 lLePheGluAspGlyArgGluThrPheGlyAspLys 172
Db 481 ATCTTTGAGGACGAGACGGAGACCTTTGGGCAAAA 516

RESULT 3
US-10-507-132-13
; Sequence 13, Application US/10507132
; Publication No. US20060221361
; GENERAL INFORMATION:
; APPLICANT: KOJICHIRO KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
US-10-507-132-13

Alignment Scores:
Pred. No.: 3,24e-117 Length: 600
Score: 938.00 Matches: 171
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 99.4% Mismatches: 1
Query Match: 99.6% Indels: 0
DB: 6 Gaps: 0

US-10-507-132-2 (1-172) x US-10-507-132-13 (1-600)
Oy 1 MetGlySerGlnValGInLysSerAapGluLeThPhSeSerAapTryLeuGlyLeuMet 20
Db 81 ATGGGTTCCGAAAGTTCAAAAGACGATGAGATTAACCTTCTCGAGCTAACCTGGGCTCATG 140
Oy 21 ThcYsValTyrgLutRpLaAapSerTyAspSerLyAspTrpAspArgLeuArgLys 40

```

```
Db 141 ACTGCGTATAGTGGGACAGACTACGATCCAGAGGACTGGATAGGCTGGCAAG 200
Qy 41 Val11ealaprothrlleuarglleasprtyrarsersptheuaspysleutrpjua1a 60
Db 201 GTATTGCGCTACTCTGCGCATTTGACTACCGCTCTTCTTCGACAGAGCTCTGGAGGCA 260
Qy 61 MetProalaglulupheVal1glmetValserSerlysglmetleuglyaspProthr 80
Db 261 ATCCCGCGGAGAGATTCTCGGCAATGCTTCAGACAGAGAGTGTCTGGCGACCCACC 320
Qy 81 LeuargThrGlnhisPhe1le1eglylYtharYtrpGluYvalserGluaspGluval 100
Db 321 CTCGCGACGAGACCTTCATCGGCGACCGCTGGGAGAGAGTGTCCGAGACGAGGTC 380
Qy 101 11e1g1YrH1sg1nleuargVal1Proh1sg1nargYrlyaspThr1rhmety1sg1n 120
Db 381 ATCGGCTACACACAGTGTGCGGCTCCGACAGAGGTACAGAGACACCATGAGAGGAG 440
Qy 121 Val1ThrMetlysglyH1sAlah1sSerAlaasnLeuH1strYrlyslYs11easpgly 140
Db 441 GTACACCATAGAGGGCCACCGCCCATCGGCAACCTTCACTGTTACAGAGAGATCGAGGC 500
Qy 141 Val1TrpLysPheal1aglyLeuLysProasp1leaYtrpGlyglupheaspheasparg 160
Db 501 GTCTGGAAGTTCGCGGCGCTCAAGCCGATATCCGCTGGGGCGAGTTCCACTTGAACAG 560
Qy 161 11ephegluaspGlyArGluThrPheglYaspLys 172
Db 561 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAA 596
```

## RESULT 4

```
US-10-507-132-16
; Sequence 16, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTLONE DEHYDRATASE EXHIBITING RESISTANCE TO
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
US-10-507-132-16
```

```
Alignment Scores:
Pred. No.: 3,32e-117 Length: 610
Score: 938.00 Matches: 171
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.4% Mismatches: 0
Query Match: 99.6% Indels: 0
DB: Gaps: 0
```

US-10-507-132-2 (1-172) x US-10-507-132-16 (1-610)

```
Qy 1 MetGlySerGlnVal1GlnYsSerAspGlu1leThrPheSerAspTyrlenuglyleuMet 20
Db 81 ATGGGTTGCGAAGTTCAAAAGACGATGAGATTAACCTTCAAGACTACCTGGGCTTCATG 140
Qy 21 ThrCyVal1YrG1uTrpAlaaspSerTyraSpSerlyaspTrpAspArgleuAglYs 40
Db 141 ACTTGCGCTATAGTGGGACAGACACTACCTCAAGAGACGGATAGGCTGGCAAG 200
Qy 41 Val11ealaprothrlleuarglleasprtyrarsersptheuaspysleutrpjua1a 60
Db 201 GTATTGCGCTACTCTGCGCATTTGACTACCGCTCTTCTTCGACAGAGCTCTGGAGGCA 260
```

```
Qy 61 MetProalaglulupheVal1glmetValserSerlysglmetleuglyaspProthr 80
Db 261 ATCCCGCGGAGAGATTCTCGGCAATGCTTCAGACAGAGAGTGTCTGGCGACCCACC 320
Qy 81 LeuargThrGlnhisPhe1le1eglylYtharYtrpGluYvalserGluaspGluval 100
Db 321 CTCGCGACGAGACCTTCATCGGCGACCGCTGGGAGAGAGTGTCCGAGACGAGGTC 380
Qy 101 11e1g1YrH1sg1nleuargVal1Proh1sg1nargYrlyaspThr1rhmety1sg1n 120
Db 381 ATCGGCTACACACAGTGTGCGGCTCCGACAGAGGTACAGAGACACCATGAGAGGAG 440
Qy 121 Val1ThrMetlysglyH1sAlah1sSerAlaasnLeuH1strYrlyslYs11easpgly 140
Db 441 GTACACCATAGAGGGCCACCGCCCATCGGCAACCTTCACTGTTACAGAGAGATCGAGGC 500
Qy 141 Val1TrpLysPheal1aglyLeuLysProasp1leaYtrpGlyglupheaspheasparg 160
Db 501 GTCTGGAAGTTCGCGGCGCTCAAGCCGATATCCGCTGGGGCGAGTTCCACTTGAACAG 560
Qy 161 11ephegluaspGlyArGluThrPheglYaspLys 172
Db 561 ATCTTTGAGGACGAGCGGAGACCTTTGGCGACAA 596
```

## RESULT 5

```
US-10-507-132-15
; Sequence 15, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTLONE DEHYDRATASE EXHIBITING RESISTANCE TO
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
US-10-507-132-15
```

```
Alignment Scores:
Pred. No.: 5,58e-115 Length: 538
Score: 921.00 Matches: 168
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.4% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: Gaps: 0
```

US-10-507-132-2 (1-172) x US-10-507-132-15 (1-538)

```
Qy 1 MetGlySerGlnVal1GlnYsSerAspGlu1leThrPheSerAspTyrlenuglyleuMet 20
Db 31 ATGGGTTGCGAAGTTCAAAAGACGATGAGATTAACCTTCAAGACTACCTGGGCTTCATG 90
Qy 21 ThrCyVal1YrG1uTrpAlaaspSerTyraSpSerlyaspTrpAspArgleuAglYs 40
Db 91 ACTTGCGCTATAGTGGGACAGACACTACCTCAAGAGACGGATAGGCTGGCAAG 150
Qy 41 Val11ealaprothrlleuarglleasprtyrarsersptheuaspysleutrpjua1a 60
Db 151 GTATTGCGCTACTCTGCGCATTTGACTACCGCTCTTCTTCGACAGAGCTCTGGAGGCA 210
Qy 61 MetProalaglulupheVal1glmetValserSerlysglmetleuglyaspProthr 80
Db 211 ATCGGCGCGAGAGATTCTCGGCAATGCTTCAGACAGAGAGTGTCTGGCGACCCACC 270
Qy 81 LeuargThrGlnhisPhe1le1eglylYtharYtrpGluYvalserGluaspGluval 100
```

Db 271 CCCCCACCCACACATTCATCGCCGACGCCCTGGGAAAGGTGTCACGAGACGAGGTC 330  
Qy 101 IleglYrYHieGlnleuArValProHieGlnArYrYLeAspThrThrMetLysglu 120  
Db 331 ATCGGCTACCAACAGTGGCGCTCCGACCAAGGTTACAGACCAACCAATGAAAGG 390  
Qy 121 ValThrMetLysglYHieAlahieSerAlaAenLeuHieTrpYrYLeLysIleAspGly 140  
Db 391 GTACCATGAAAGGCGCACGCCCACTCGCAAACTTCATCGGTACAAAGAAATCGACG 450  
Qy 141 ValThrLysPheAlaGlyLeuLysProAspIleArGTrpGlyGluPheAspPheAspArg 160  
Db 451 GTCTGGAAGTTCGCGGCTCAAGCCGACATCCGCTGGGCGAGTTGCACTTTGACAG 510  
Qy 161 IlePheGluAspGlyArGgluThrPhe 169  
Db 511 ATCTTTGAGACGACGAGGAGACCTTT 537

## RESULT 6

US-10-507-132-14  
/ Sequence 14, Application US/10507132  
/ Publication No. US20060223136A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Koichiro KAKU et al.  
/ TITLE OF INVENTION: GENE CODING FOR SCYTLONE DEHYDRATASE EXHIBITING RESISTANCE TO  
/ FILE REFERENCE: 1254-0258PUS1  
/ CURRENT APPLICATION NUMBER: US/10/507,132  
/ PRIOR FILING DATE: 2004-09-10  
/ PRIOR APPLICATION NUMBER: JP 2002-66955  
/ NUMBER OF SEQ ID NOS: 19  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 14  
/ LENGTH: 545  
/ TYPE: DNA  
/ ORGANISM: Pyricularia oryzae  
US-10-507-132-14

## Alignment Scores:

Pred. No.:	5,69e-115	Length:	545
Score:	921.00	Matches:	168
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.4%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-2 (1-172) x US-10-507-132-14 (1-545)

Qy 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTrpLeuGlyLeuMet 20  
Db 38 ATGGGTTGCAAGTTCAAAGAGCGATGATGATTAACCTTCTCAGACTGAGCCCTCAG 97  
Qy 21 ThrCyValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40  
Db 98 ACTTCGCTATGAGTGGGCGACAGACTACCTCCAAAGAGCTGGATGAGCTGGCAAG 157  
Qy 41 ValIleAlaProThrLeuArgIleAspYrYrAspSerPheLeuAspLysLeuTrpGluAla 60  
Db 158 GTCAATGGCCCTACTCTGGCATGACTACCGCTCTTCTCGACAAAGCTCTGGAGGGA 217  
Qy 61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80  
Db 218 ATGCCGCGCGAGAGAGTTCTCGGCGATGCTCGAGCAACAGAGTGTGGCGACCCCA 277  
Qy 81 LeuArgThrGlnHiePheIleGlyYrYrArgTrpGluLysValSerGluAspGluVal 100  
Db 278 CTCGCGACGACACATTCATCGCGCGACGCGCTGGGAAAGGTGTCGAGACGAGGTC 337  
Qy 101 IleglYrYHieGlnleuArValProHieGlnArYrYLeAspThrThrMetLysglu 120  
Db 338 ATCGGCTACCAACAGTGGCGCTCCGACCAAGGTTACAGACCAACCAATGAAAGG 397

Qy 121 ValThrMetLysglYHieAlahieSerAlaAenLeuHieTrpYrYLeLysIleAspGly 140  
Db 398 GTACCAATGAAAGGCGCACGCCCACTCGGCAAACTTCATCGGTACAAAGAAATCGACG 457  
Qy 141 ValThrLysPheAlaGlyLeuLysProAspIleArGTrpGlyGluPheAspPheAspArg 160  
Db 458 GTCTGGAAGTTCGCGGCTCAAGCCGACATCCGCTGGGCGAGTTGCACTTTGACAG 517  
Qy 161 IlePheGluAspGlyArGgluThrPhe 169  
Db 518 ATCTTTGAGACGACGAGGAGACCTTT 544

## RESULT 7

US-10-507-132-18  
/ Sequence 18, Application US/10507132  
/ Publication No. US20060223136A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Koichiro KAKU et al.  
/ TITLE OF INVENTION: GENE CODING FOR SCYTLONE DEHYDRATASE EXHIBITING RESISTANCE TO  
/ FILE REFERENCE: 1254-0258PUS1  
/ CURRENT APPLICATION NUMBER: US/10/507,132  
/ PRIOR FILING DATE: 2004-09-10  
/ PRIOR APPLICATION NUMBER: JP 2002-66955  
/ NUMBER OF SEQ ID NOS: 19  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 18  
/ LENGTH: 729  
/ TYPE: DNA  
/ ORGANISM: Pyricularia oryzae  
US-10-507-132-18

## Alignment Scores:

Pred. No.:	3,26e-108	Length:	729
Score:	872.50	Matches:	171
Percent Similarity:	75.4%	Conservative:	1
Best Local Similarity:	75.0%	Mismatches:	0
Query Match:	92.6%	Indels:	56
DB:	6	Gaps:	2

US-10-507-132-2 (1-172) x US-10-507-132-18 (1-729)

Qy 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSer----- 14  
Db 48 ATGGGTTGCAAGTTCAAAGAGCGATGATGATTAACCTTCTCAGTGAACATTAATCCCC 107  
Qy 14 ----- 14  
Db 108 CTCCAAAAAGAAATAGCGGTGAAGCCACCAAGCAGATACCGCTGACCTTAATCCCT 167  
Qy 15 ---AspYrYrLeuGlyLeuMetThrCyValTyrGluTrpAlaAspSerTyrAspSerLys 33  
Db 168 CCAGCTACCTGGGCTTATGACTTGCTATGAGTGGGCGACAGACTACGACTCCAA 227  
Qy 34 AspTrpAspArgLeuArgLysValIleAlaProThrLeuArg----- 47  
Db 228 GACTGGGATAGGCTCGGAAGGTCAATTCGCTACTCGCGCGATATGTTCCGCGCTGCA 287  
Qy 47 ----- 47  
Db 288 TGTATTATTTTACTTTCCACACCAATCCAGACTTTAAACAGCGACGCAAAAAA 347  
Qy 48 -----IleAspYrYrAspSerPheLeuAspLysLeuTrpGluAlaMetProAlaGlu 65  
Db 348 AAAACAGATTGACTACCCCTCTCTTCTCGACAAAGCTCTGGAGGCAATGCGCGAGGA 407  
Qy 65 uPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHie 85  
Db 408 GTTCGCGGACATGCTGTCGACAGACAGAGTGTGGGCGACCCCAACCTCCGACGACAGA 467  
Qy 85 sPheIleGlyYrYrArgTrpGluLysValSerGluAspGluValIleGlyYrYHieGln 105

```

Db      468 CTTCATCGGCGGACCGCTGCGGAGAAAGGTGTCCGAGACGAGTCATCGCTACACCA 527
QY      105 nleuargValProHisGlnArgTyrIysAspThrThrMetIysGluValThrMetIysG 125
Db      528 GTCGCCGCTCCCGACCAAGGTACAAAGACACCACTGAAAGAGTCAACCTGAAAGGG 587
QY      125 yHisAlaHisSerAlaAsnLeuHisTrpTyrIysIysIleAspGlyValIleTyrIysPheAl 145
Db      588 CACGCCCACTCGGCAAACTTCACTGTGTACAAAGAAAGATGACGGCGCTCGAAGTTCCG 647
QY      145 agIleuIysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAspG 165
Db      648 CGGCGTCAAGCCCGACATCCGCTGGGGCGAGTTGCACTTGACAGATCTTTGAGGACGG 707
QY      165 yArgGluThrPheGlyAspIys 172
Db      708 ACGGAGACCTTTGGCGACAA 729

```

## RESULT 8

```

US-10-507-132-17
; Sequence 17, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
US-10-507-132-17

```

## Alignment Scores:

```

Pred. No.: 7.15e-108 Length: 732
Score: 870.00 Matches: 170
Percent Similarity: 74.7% Conservative: 1
Best Local Similarity: 74.2% Mismatches: 1
Query Match: 92.4% Indels: 58
DB: 6 Gaps: 2

```

US-10-507-132-2 (1-172) x US-10-507-132-17 (1-732)

```

QY      1 MetGlySerGlnValGlnIysSerAspGluIleThrPheSer----- 14
Db      47 ATGGGTTCCGAAGTTCAAAAGACGATGAGATAACCTTCTCAGGTAGCATTAATATCCCC 106
QY      14 ----- 14
Db      107 CTCCAAAAAGAAATAGCGGTGAAGCCACCAAGACAGTACCGCTGACCTTATTCCTC 166
QY      15 ---AspTyrIleuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerIys 33
Db      167 CCAGACTTACTCGGCGCTCATGACTGTGCTGTATGAGGGGCAAGACTGACTCCAG 226
QY      34 AspTrpAspArgLeuArgIysValIleAlaProThrLeu----- 46
Db      227 GACTGGGATAGGCTGGGAAGAGTATGGCGCTACTCTGCGCTATGTTCCGCCCTGCCA 286
QY      46 ----- 46
Db      287 TGTATTATTTTACCTTCCACACCAATCCAGCTTTACAGCGACGACCAAAAAA 346
QY      47 -----ArgIleAspTyrArgSerPheLeuAspIysLeuTrpGluAlaMetProAla 63
Db      347 AAAAAAACAGATT-GACTACCGCTCTCTCTCGACAAAGCTTGGGAGGCAATGCCGCC 405

```

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QY      64 GluGluPheValGlyMetValSerSerIysGlnMetLeuGlyAspProThrLeuArgThr 83
Db      406 GAGAGACTTGTGGCATGATGTTCTGACACAGACAGGTCTGGGACACCCCTCCGCAAG 465
QY      84 GlnHisPheIleGlyIleThrArgTrpGlyValSerGluAspGluValIleGlyTyr 103
Db      466 CAGCACTTATCATGGCGGACCGCGCTGGAGGAAGTGTCCGAGAGACGAGGTCACTCGCTAC 525
QY      104 HisGlnLeuArgValProHisGlnArgTyrIysAspThrThrMetIysGluValThrMet 123
Db      526 CACCACTTCGCGGTCCCGACAGGTACAGACACCAATGAAAGAGGTCAACATG 585
QY      124 LysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrIysIysIleAspGlyValIleTyrIys 143
Db      586 AAGGGCCACGCCCATCGGCAAACTTCACTGTGTACAAAGAAAGATGACGGCGCTCGAAG 645
QY      144 PheAlaGlyLeuIysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGlu 163
Db      646 TTCGCCGCGCTCAAGCCGACATCCGCTGGGCGAGTTGCACTTGACAGATCTTTGAG 705
QY      164 AspGlyArgGluThrPheGlyAspIys 172
Db      706 GACGACGGGAGACCTTTGGCGACAA 732

```

## RESULT 9

```

US-10-449-902-16327
; Sequence 16327, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16327
; LENGTH: 3196
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK066825
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-16327

```

## Alignment Scores:

```

Pred. No.: 0.85 Length: 3196
Score: 87.00 Matches: 34
Percent Similarity: 33.8% Conservative: 16
Best Local Similarity: 23.0% Mismatches: 44
Query Match: 9.2% Indels: 54
DB: 6 Gaps: 7

```

US-10-507-132-2 (1-172) x US-10-449-902-16327 (1-3196)

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QY      55 AspIysLeuTrp-----GluAlaMetProAlaGluGluPheValGlyMetVal 70
Db      2160 GACAAAGCTCTGGCGCTTCACATGAGAGGCGTCCCGCGCAC-----CTCGTC 2207
QY      71 SerSerIysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIle----- 87
Db      2208 CGCCGCGGATGCGCGAGAGGACCCACG-----GCGAGACACGCGCTCAGGTCCGC 2261
QY      88 -----GlyGlyThrArgTrpGluIysVal----- 95

```

Db 2262 ATCGAGACTACCCGTTCCCAACGAGCGCTCTTCATCTGGAGCCCATCAAGACTGG 2321  
QY 96 -----SerGIuAspGIuValIleGIyTrHISGIu 105  
Db 2322 GTCGAGCGCTAGCGCGCGGTTCTAACCCGACGCGGACAGCGTCCCGGACAGAGG 2381  
QY 106 LeuAAspGIuProHISGIuArgTrYIyAspTrHrThmetIyGIuValThrmetIyGIy 125  
Db 2382 CTCGAG-----GGCTTGTGACCGAGGTGGCAGCAAGGGG 2417  
QY 126 HIsAlAHISerAlAsnLeuHISTrpTrYIySbSIleAspGIy----- 140  
Db 2418 CACGGGACAGAGAGACCCCGTGTGTGCGGACAGTGTGACTCGCCGAGAGAGCTCGCC 2477  
QY 141 -----ValTrpIySbPheAlaGIyLeuIySbProAspIleArgTrpGIy 154  
Db 2478 CACAGCGCTACCACTCTGTGTGGTGGCGGCGGACCAAGCGCCGCTCACTTGGGG 2537  
QY 155 GIuPheAspPheAspArgIlePhe 162  
Db 2538 CAGTACGACTTCGGCGGCTACTTC 2561

## RESULT 10

US-11-174-307B-3703  
; Sequence 3703, Application US/11174307B  
; Publication No. US20060143729A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
; FILE REFERENCE: 2750-1601PUS2  
; CURRENT APPLICATION NUMBER: US/11/174,307B  
; PRIOR FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/583,671  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,781  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,651  
; PRIOR FILING DATE: 2004-06-30  
; NUMBER OF SEQ ID NOS: 5544  
; SEQ ID NO 3703  
; LENGTH: 1611  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1611)  
; OTHER INFORMATION: Ceres cDNA ID no. 21665863  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1611)  
; OTHER INFORMATION: Ceres CLONE ID no. 779290  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1611)  
; OTHER INFORMATION: as cited in SEQ ID NO 25088318  
US-11-174-307B-3703

## Alignment Scores:

Pred. No.:	2.39	Length:	1611
Score:	80.50	Matches:	35
Percent Similarity:	40.5%	Conservative:	25
Best Local Similarity:	23.6%	Mismatches:	45
Query Match:	8.5%	Indels:	43
DB:	9	Gaps:	7

US-10-507-132-2 (1-172) x US-11-174-307B-3703 (1-1611)

QY 54 LeuAAspIyLeuTrpGIuIaMetProAlaGIuGIuPheValGIy----- 68  
Db 568 TTGGCCAAAGCTCAGGAGTGG-----GCCGAGCGGTACTCGGCCGTGCATCCAGGAG 621

QY 69 ---MetValSerSerIyGIuMetLeuGIyAspProTrHrLeuArgTrHrHISheIle 87  
Db 622 GCCATGCTACCCGCTCCCGCAGACGATACAGATCCG----- 657  
QY 88 GIyGIyTrHrArgTrpGIuIyValSerGIuAspGIuValIleGIyTrHISGIuArg 107  
Db 658 -----TCAAGGTATTCAATGTGAGGCGCGGAGCTCGCGGCTCGCTCAGAGG 711  
QY 108 Val-----ProHISGIuArgTrYIyAsp 115  
Db 712 ATGATGACAGAGCCGACCGCGGCTCGCTCGCTACGCGCTTCACAGAGAGCTGGCGAC 771  
QY 116 Thr---ThrmetIyGIuValThrmetIySbIleAlAHISerAlAsnLeuHISTrp 134  
Db 772 GAGGGCAAGCTCTGCTCTCGCTCCAGCGCGGAGCTGACAGCGCGAGCTCATGTGCG 831  
QY 135 TrYIySbSIleAspGIuValTrpIySbPheAlaGIyLeuIySbProAspIleArgTrpGIy 154  
Db 832 TAT-----GTGAGCGGCGTCTTCAGTTCATGGAGCAGAGAGACCTTCTTGGGA 885  
QY 155 GIuPheAspPheAspArgIlePheGIuAsp----- 164  
Db 886 GAGCAGAGCTTCGACCAAGAGATCGTCAACCACTTGTGAGCTGATCAGAGAGAGCAG 945  
QY 165 GIyArgGIuTrHrPheGIyAspIyS 172  
Db 946 GCGAAGACCTGAGCAGACAGCAG 969

## RESULT 11

US-11-056-355B-70677  
; Sequence 70677, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: BROVER, Vyacheslav  
; APPLICANT: ALEXANDROV, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; PRIOR FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 70677  
; LENGTH: 1845  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1845)  
; OTHER INFORMATION: Ceres Seq. ID no. 2717493  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(1845)  
; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13600220  
; OTHER INFORMATION: as cited in SEQ ID NO 0  
US-11-056-355B-70677

## Alignment Scores:

Pred. No.:	3.98	Length:	1845
Score:	79.50	Matches:	57
Percent Similarity:	35.0%	Conservative:	29
Best Local Similarity:	23.2%	Mismatches:	61
Query Match:	8.4%	Indels:	99
DB:	9	Gaps:	15

US-10-507-132-2 (1-172) x US-11-056-355B-70677 (1-1845)

QY 6 GIuIySerAspGIu-----IleTrHrPheSerAsp 15  
Db 85 CAACCAAGTATGATGAGATCTTGATCATCATTTGAGACCTCATCAACATGACTTTCATGAC 144  
QY 16 TrYleuGIyLeuMetTrHrCySerValTrpIuIaAspSerTrYAsp----- 31

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Db      145 GAGATAGGATCGTGAATTGGACCAATGCGACCGTAGATGACGAAGACATGTGACATGGAC 204
      32 -----SerLysAspTrpAspArgLeuArgLysValIle 42
Qy      205 ATGGGACCAACCGTTGGACCGACGACCAACCTAAATGATGATATTTGGGACCATCATTT 264
Db      43 AlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetPro 62
      265 GGACCCGAGTTTGAGATCCCAAGCAAGATTTCC-----CCC 300
Qy      63 AlaGluLupheValGly--MetValSerSerLysGlnMetLeuGlyAspProThrLeu 81
      301 GCAGATTTCATATTGGAAATCATCTGTTCCGATATCAGATTGAAGGT-----GCT 351
Db      82 ArgThrGlnHisPheIleGlyGlyThrArgTrp-----Glu 93
      352 AAAAAGGGTTCTGGAGAGGCTTGACCTCAYGGAGCAATTTTACACATGTTTCTTGAG 411
Qy      94 LysValSerGlu-----AspGluValIleGlyTyrHisGlnLeuArgValPro 109
      412 AAGGTTCAACAATAATGGCCATGAGATGAGGAGTGCATCTC-----453
Db      110 HisGlnArgTyrLysAsp-----ThrThrmethylsGluValThrmethylsGlyHisAla 127
      454 TATACCCGTTACAGAGATGATATAAATTAATGAAAGAGTTGAACAAGATGGCTTCAGA 513
Qy      128 HisSerLysAsnLeuHisTrpTyrLysLysIle-----138
      514 TTTTCA-----ATCATGATGACCAAGATCTTGCTTATGAACTATTAAAAAGGTGA 567
Db      139 -----AspGlyValTrpLysPhe-----AlaGly 146
      568 AACGAGAGAGGGGGTG--AAGTTCTACACAGATCTTATAATGAACTTTAAAGTAATGGA 624
Qy      147 LeuLysPro-----AspIleArgTrp 153
      625 ATTCAGCCTTCGGTTACTCTCTTTCACCTGGGAATCTCCACTTGCTGTAGAAATGAGATAC 684
Db      154 GlyLupheAspPheAspArgIlePheGluAspGlyArgGlu-----167
      685 GAGAGTTTCTTAACCAAGAGATAGTAGAGATTTCCGTGAGTTTGCAAACTTTTGCTTC 744
Qy      168 ---ThrPheGlyAspLys 172
      745 AAGGAATTTGAGATNAG 762
Db

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RESULT 12

US-11-056-355B-78749

; Sequence 78749, Application US/11056355B

; Publication No. US20060150283A1

GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nikolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEO ID NO 78749

LENGTH: 1848

TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)-(1848)

OTHER INFORMATION: Ceres Seq. ID no. 12644995

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)-(1848)

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; OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13600220
; OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-78749

Alignment Scores:
Pred. No.: 3.99 Length: 1848
Score: 79.50 Matches: 57
Percent Similarity: 35.0% Conservative: 29
Best Local Similarity: 23.2% Mismatches: 61
Query Match: 8.4% Indels: 99
DB: 9 Gaps: 15

US-10-507-132-2 (1-172) x US-11-056-355B-78749 (1-1848)

Qy      6 GlnLysSerAspGlu-----IleThrPheSerAsp 15
      85 CAACCAAGTATGATGAGATTTGGTACCATCATTTGACCTTCATCAAACTGATTCGATGAC 144
Db      16 TyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAsp-----31
      145 GAGATAGGATGATGATTTGGACCAATGCGACCGTAGATGACGAAGACATGTGACATGGAC 204
Qy      32 -----SerLysAspTrpAspArgLeuArgLysValIle 42
      205 ATGGGACCAACCGTTGGACCGACGACCAACCTAAATGATGATATTTGGGACCATCATTT 264
Db      43 AlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetPro 62
      265 GGACCCGAGTTTGAGATCCCAAGCAAGATTTCC-----CCC 300
Qy      63 AlaGluLupheValGly--MetValSerSerLysGlnMetLeuGlyAspProThrLeu 81
      301 GCAGATTTCATATTGGAAATCATCTGTTCCGATATCAGATTGAAGGT-----GCT 351
Db      82 ArgThrGlnHisPheIleGlyGlyThrArgTrp-----Glu 93
      352 AAAAAGGGTTCTGGAGAGGCTTGACCTCAYGGAGCAATTTTACACATGTTTCTTGAG 411
Qy      94 LysValSerGlu-----AspGluValIleGlyTyrHisGlnLeuArgValPro 109
      412 AAGGTTCAACAATAATGGCCATGAGATGAGGAGTGCATCTC-----453
Db      110 HisGlnArgTyrLysAsp-----ThrThrmethylsGluValThrmethylsGlyHisAla 127
      454 TATACCCGTTACAGAGATGATATAAATTAATGAAAGAGTTGAACAAGATGGCTTCAGA 513
Qy      128 HisSerLysAsnLeuHisTrpTyrLysLysIle-----138
      514 TTTTCA-----ATCATGATGACCAAGATCTTGCTTATGAACTATTAAAAAGGTGA 567
Db      139 -----AspGlyValTrpLysPhe-----AlaGly 146
      568 AACGAGAGAGGGGGTG--AAGTTCTACACAGATCTTATAATGAACTTTAAAGTAATGGA 624
Qy      147 LeuLysPro-----AspIleArgTrp 153
      625 ATTCAGCCTTCGGTTACTCTCTTTCACCTGGGAATCTCCACTTGCTGTAGAAATGAGATAC 684
Db      154 GlyLupheAspPheAspArgIlePheGluAspGlyArgGlu-----167
      685 GAGAGTTTCTTAACCAAGAGATAGTAGAGATTTCCGTGAGTTTGCAAACTTTTGCTTC 744
Qy      168 ---ThrPheGlyAspLys 172
      745 AAGGAATTTGAGATNAG 762
Db

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RESULT 13

US-11-217-529-78037

; Sequence 78037, Application US/11217529

; Publication No. US20060099612A1

GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAO, YOSHIIHIRO



[illegible]

```

APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 85042
LENGTH: 1116
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (119)..(119)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-85042

Alignment Scores:
Pred. No: 4.18 Length: 1116
Score: 77.00 Matches: 31
Percent Similarity: 35.8% Conservative: 22
Best Local Similarity: 20.9% Mismatches: 37
Query Match: 8.2% Indels: 58
DB: 8 Gaps: 6

US-10-507-132-2 (1-172) x US-11-266-748A-85042 (1-1116)
QY 57 LeuTtRGUAlAme-ProhlaGluGluPheValGlyMeCValSerSerLySGlMetLeu 76
||||| :||||| :||||| :|||||
DB 512 CTGTGAATTCATTCATCAT-----GACTCCAGAGCCCAAGTCTCCTTTA 556
77 GlyAspProThrLeuArgThrGln----- 84
||| ||| |||
DB 557 GGGCGACCTGAGAGCTTGCTCCAGCTAATACCTGATGCTCCTTGACACCTGTACC 616
85 -----His 85
DB 617 TCCGTTATGCCAATGCTCAGGGCAGCAATTTGTGATGAGAAATTTGCTGTAGGAGTACC 676
QY 86 PheIleGlyGlyThrArgTrpGluValSerGluSerGluValIleGlyTyrHisGln 105
677 CTTCAGCCAGAAACCAAGTTTGTCAAAACCACTGAGAGATGAA----- 718
106 LeuArgValProHisGlnArgTyrGlyAspArgThrThrMetLySGluValIlePheGly 125
719 -----AAATACAGAAATGTACAGTG--GAGTCCAGACACAAAGCT 757
QY 126 HisAlaHisSerAlaAsnLeuHisTrpTyrLySValIleArgGlyValTrpLyPheAla 145
758 CAAATTCAATGTGGGGAAACTGATTTGGTTCCAAAGAAAGAAAGAGATTTGGCTTGCCCT 817
QY 146 GlyLeuLeuProAspArgLeuArgTrpGluGluPheAspArgValIlePheGlu----- 163
818 GGGCTTAAGGCG-----GACAGCTGGGAGTGGAAATCCCGCGAGATTAAGTGCACC 865

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	9.2	2775	9	US-10-491-733-21
					Sequence 21, Appl

2	85	9.0	864	3	US-09-882-227-305	Sequence 305, App
3	84	8.9	850	3	US-09-964-238-8	Sequence 8, Appl1
4	84	8.9	1454	8	US-10-425-113-31125	Sequence 31125, A
5	84	8.9	1454	9	US-10-425-113-28662	Sequence 28662, A
6	84	8.9	3154	10	US-10-847-972-59	Sequence 59, Appl
7	84	8.9	3154	15	US-11-108-528-45	Sequence 45, Appl
8	82.5	8.8	88232	6	US-10-087-192-1699	Sequence 1699, Ap
9	81.5	8.7	1473	8	US-10-335-977-2219	Sequence 2219, Ap
10	81	8.6	1447	8	US-10-364-888-1	Sequence 1, Appl1
11	81	8.6	1070	7	US-10-305-810-1	Sequence 1, Appl1
12	81	8.6	1070	8	US-10-364-888-5	Sequence 5, Appl1
13	81	8.6	2160	8	US-10-364-888-7	Sequence 7, Appl1
14	81	8.6	2250	7	US-10-285-976-22	Sequence 22, Appl
15	81	8.6	2250	10	US-10-847-972-21	Sequence 21, Appl
16	81	8.6	2250	15	US-11-108-528-43	Sequence 43, Appl
17	80.5	8.5	2280	10	US-10-469-204-36	Sequence 36, Appl
18	80.5	8.5	2503	10	US-10-481-032A-69	Sequence 69, Appl
19	79.5	8.4	1845	16	US-11-096-568A-28398	Sequence 28398, A
20	79.5	8.4	2623	8	US-10-437-963-61451	Sequence 61451, A
21	79.5	8.4	4041	13	US-11-097-143-1700	Sequence 1700, Ap
22	79.5	8.4	20510	13	US-11-097-143-1699	Sequence 1699, Ap
23	79	8.4	801	8	US-10-335-977-1665	Sequence 1665, Ap
24	79	8.4	2109	7	US-10-369-493-47161	Sequence 47161, A
25	79	8.4	6588	8	US-10-437-963-79084	Sequence 79084, A
26	79	8.4	11096	7	US-10-149-736-4	Sequence 4, Appl1
27	79	8.4	11096	10	US-10-964-536-4	Sequence 4, Appl1
28	79	8.4	2256646	8	US-10-470-555-1	Sequence 1, Appl1
29	78.5	8.3	1122	7	US-10-156-761-124	Sequence 124, App
30	78.5	8.3	13734	8	US-10-287-226-303	Sequence 303, App
31	78.5	8.3	9025608	7	US-10-156-761-1	Sequence 1, Appl1
32	78	8.3	1400	16	US-11-136-557-4457	Sequence 4457, Ap
33	78	8.3	1462	8	US-10-424-599-139221	Sequence 139221, Ap
34	78	8.3	1947	8	US-10-152-312A-2121	Sequence 2121, Ap
35	78	8.3	1947	10	US-10-486-706-279	Sequence 279, App
36	78	8.3	1947	16	US-11-136-527-361	Sequence 361, App
37	78	8.3	1947	16	US-11-036-196-2121	Sequence 2121, Ap
38	78	8.3	2163	8	US-10-335-977-2753	Sequence 2753, Ap
39	78	8.3	2355	8	US-10-335-977-2754	Sequence 2754, Ap
40	78	8.3	2594	3	US-09-815-242-7512	Sequence 7512, Ap
41	78	8.3	2694	8	US-10-335-977-2755	Sequence 2755, Ap
42	77.5	8.2	4647	13	US-11-097-143-34924	Sequence 34924, A
43	77.5	8.2	719	7	US-10-027-633-18936	Sequence 18936, A
44	77.5	8.2	719	7	US-10-027-633-18936	Sequence 18936, A
45	77.5	8.2	1116	10	US-10-469-204-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1  
US-10-491-733-21  
; Sequence 21, Application US/10491733  
; Publication No. US20040219675A1  
; GENERAL INFORMATION:  
; APPLICANT: Syngenta Participations AG  
; APPLICANT: Sainz, Manuel  
; APPLICANT: Salmeron, John  
; APPLICANT: Weislo, Laura J.  
; TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic Str  
; FILE REFERENCE: 60127WOPCT  
; CURRENT APPLICATION NUMBER: US/10/491, 733  
; CURRENT FILING DATE: 2004-04-05  
; PRIOR APPLICATION NUMBER: 60/334, 501  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 2775  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-10-491-733-21  
Alignment Scores:

Pred. No.: 2.63 Length: 2775  
Score: 87.00 Matches: 34  
Percent Similarity: 33.8% Conservative: 16  
Best Local Similarity: 23.0% Mismatches: 44  
Query Match: 9.2% Indels: 54  
DB: 9 Gaps: 7

US-10-507-132-2 (1-172) x US-10-491-733-21 (1-2775)

```
OY 55 AaplyVleuTrp-----GluAlaMetProAlaGluGluPheValGlyMetVal 70
DB 1960 GACAACTCTGGCGCTTCGACACGAGGCGCTCCCGCGAC-----CTCGTC 2007
OY 71 SerSerLygIleMetLeuGlyAspProThrLeuArgThrGlnHisPheIle----- 87
DB 2008 CCGCGCGGATGGCCGAGAGAGACCCCAAG-----GCGAGACAGGCGCTCAAGCTCGCC 2061
OY 88 -----GlyGlyThrArgTrpGluLysVal----- 95
DB 2062 ATCGAGACTACCCGTCGCCCAACGAGCGCTCTCATCTGGGAGCGCATCAAGACTGG 2121
OY 96 -----SerGluAspGluValIleGlyTrpHisGln 105
DB 2122 GTCCAGCGCTACGTCGCGGTTTACCCCGACGCGCGCTCGCGCGACAGAG 2181
OY 106 LeuArgValProHisGlnArgTrpLysAspThrThrMetLysGluValThrMetLysGly 125
DB 2182 CTCGAG-----GCGTTTGACCGAGGTGGCGACCAAGGG 2217
OY 126 HsAlaHisSerAlaLeuLeuHisTrpTrpLysLysIleAspGly----- 140
DB 2218 CACGGCGACAGAGAGACGCGCGCTGTGGCGGAGATTGAGACTCGCGGAGAGACTCGCC 2277
OY 141 -----ValTrpLysPheAlaGlyLeuLysPheAspTrpLys 154
DB 2278 CACACGCTGACCACTTCGCTGGGTGGCGGCGCACACCGCGCGCTCACTTCGG 2337
OY 155 GluPheAspPheAspArgIlePhe 162
DB 2338 CAGTAGACTTCGCGCGCTACTTC 2361
```

RESULT 2  
US-09-882-227-305

```
; Sequence 305, Application US/09882227
; Publication No. US20030158396A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20030158396A1 Helicobacter Polypeptides in the
; FILE OF INVENTION: Genome
; FILE REFERENCE: 06132/047002
; CURRENT APPLICATION NUMBER: US/09/882,227
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/902,615
; PRIOR FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 618
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; NAME/KEY: CDS
; LOCATION: (37)...(831)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 388
; OTHER INFORMATION: n = A,T,C or G
; US-09-882-227-305
```

Alignment Scores:

Pred. No.: 0.964 Length: 864  
Score: 85.00 Matches: 43  
Percent Similarity: 41.1% Conservative: 31  
Best Local Similarity: 23.9% Mismatches: 54  
Query Match: 9.0% Indels: 54  
DB: 3 Gaps: 8

US-10-507-132-2 (1-172) x US-09-882-227-305 (1-864)

```
OY 18 GlyLeuMetThrCysValTrpGlu-----TrpAlaAspSerTrpAspSerLysAsp 34
DB 326 GGCATTGTGAATGTTT-TATCAGTTCGTGGGCTTTACGATAGCTGCAAGAACCGCGT 384
OY 35 TrpAspArgLeuArgLysValIleAlaProThrLeuAlaSerTrpArgSerPheLeu 54
DB 385 AGCNTGCGCGTGAAGTGGCTTTGTGCTTAATGAGACCGTGAATCTTGAAGTTT 444
OY 55 AaplyVleu-----TrpGluAlaMetProAlaGluGluPheValGlyMetValSerSer 72
DB 445 TACCATGGCTAATTGAGAGGAAAGGAGCGTATGACATGCTGTATTGTGTAC 504
OY 73 Lys-----GlnMetLeuGlyAspProThrLeu 81
DB 505 AAACACCCCTATTGAAACGCTTATTATGCCGATGATGGGTAGGCCACCATATTATG 564
OY 82 ArgThrGlnHisPheIleGlyGly-----ThrArgTrpGluLysValSerGlu----- 97
DB 565 CGCTCTTACCGCGCTCAAGAGCGATGAATTCGCCCAATGATGAAGTGAATTAATTTT 624
OY 98 -----AspGluValIleGlyTrpHisGln----- 105
DB 625 GGTAAAGAAATACCGAAGATGCTGGTAAAGACGAGAGACAGCGCAAGACTGATGA 684
OY 106 -----LeuArgValProHisGlnArgTrpLysAspThrThrMetLys 119
DB 685 AAAGACACTTTCATTTTGCAAAATTTGGCTATGAACAGGCGAAGCGAAGATTAA 744
OY 120 GluValThrMetLysGlyHisAlaHisSerAlaLeuLeuHisTrpTrpLysLysIleAsp 139
DB 745 GAAGTAGAAGAAAG-----CATGCGTTAAAGAAATCCCT 780
OY 140 GlyValTrpLysPheAlaGlyLeuLysProAsp-----IleArgTrp 153
DB 781 TTGTGTCA-AGATTGGACAAATATGCCCCCACTATTCTTAAGAGAGCTATTAAATGG 839
```

RESULT 3

US-09-964-238-8  
; Sequence 8, Application US/09964238  
; Patent No. US20020035246A1

```
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie
; TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
; FILE REFERENCE: 2676-423205
; CURRENT APPLICATION NUMBER: US/09/964,238
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/449,285
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: PCT/EP98/03193
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 97201645.5
; PRIOR FILING DATE: 1997-06-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-964-238-8
```

Alignment Scores:

Pred. No.: 1.29 Length: 850

Score: 84.00 Matches: 32  
 Percent Similarity: 41.7% Conservative: 11  
 Best Local Similarity: 31.1% Mismatches: 36  
 Query Match: 8.9% Indels: 24  
 DB: 3 Gaps: 7

US-10-507-132-2 (1-172) x US-09-964-238-8 (1-850)

QY 84 GlnHisPheIleGlyThrArgTrp-----GlnIleValSerGluAspGluValIle 101  
 DB 536 CACGACCAAGTTCGGATTCGGCCCTGGAACTGCTCCGCCCTGGGCAAGAACCGCTTC 555  
 QY 102 GtYrThiSglLeuValProHisGlnArgTyrLeuAspThrThiMetCysGluVal 121  
 DB 596 GGG---CAAGAACTCCGAGTAGGAGTGCAGAGAGCTGCCTTACCC-----TAGGCATC 646  
 QY 122 ThMetLysGlyHisAlaHisSer-----AlaAsnLeuHis--- 133  
 DB 647 ACGGCGCGGCGCTGCGCGCATCTGTCAACGCTGCCTGCAGCCAGGCGCAATCTGACCAAT 706  
 QY 134 -----TrpTyrLeuValLeuAspGlyValTrpLysPhe 144  
 DB 707 TGTGCTGTGACCGGAGAGAACGACTACTACACCGCGGAGGC---TGAAGTGG 763  
 QY 145 AlaGlyLeuLysProAspIleArgTyrGluPheAspPheAspArgIlePheGluAsp 164  
 DB 764 GGGGGCTGCTCAGCGGACGCTCCGCTACGCGC---ATGCATTTTCTGTGCTTGTGGAT 820  
 QY 165 GlyArgGlu 167  
 DB 821 GCCCGTGAG 829

# RESULT 4

US-10-425-114-31125  
 / Sequence 31125, Application US/10425114  
 / Publication No. US20040034888A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Liu, Jingdong  
 / APPLICANT: Zhou, Yihua  
 / APPLICANT: Kovalic, David K.  
 / APPLICANT: Screen, Steven E  
 / APPLICANT: Tabaska, Jack E  
 / APPLICANT: Cao, Yongwei  
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 / FILE REFERENCE: 38-21(5313)B  
 / CURRENT APPLICATION NUMBER: US/10/425,114  
 / CURRENT FILING DATE: 2003-04-28  
 / NUMBER OF SEQ ID NOS: 73128  
 / SEQ ID NO 31125  
 / LENGTH: 1454  
 / TYPE: DNA  
 / ORGANISM: Zea mays  
 / FEATURE:  
 / OTHER INFORMATION: Clone ID: UC-ZMFLB73131C10\_FLI  
 US-10-425-114-31125

## Alignment Scores:

Pred. No.: 2.74 Length: 1454  
 Score: 84.00 Matches: 35  
 Percent Similarity: 37.4% Conservative: 17  
 Best Local Similarity: 25.2% Mismatches: 31  
 Query Match: 8.9% Indels: 56  
 DB: 8 Gaps: 10

US-10-507-132-2 (1-172) x US-10-425-114-31125 (1-1454)

QY 26 TrpAlaAspSerTyrAspSerLysAspTrp---AspArgLeuArgLysValIleAlaPro 44  
 DB 512 TGGAAAGACGTGTTGATTCGGCAAGCTGTGGAAGACCTGATTTGGCGGTATTCATTTCT 571  
 QY 45 ThrLeuArgIleAspTyrArgSerPhe-----LeuAspLys 56  
 DB 45 ThrLeuArgIleAspTyrArgSerPhe-----LeuAspLys 56

DB 572 AAACGAGATTGGCGTTGCAAGACTTTTCAGATCAACCCAGAAACGAGCTCGATCAG 631  
 QY 57 -----LeuTrp---GlnAlaMetProAlaGluGluPheValGlyMetVal 70  
 DB 632 TTCACCTGGGTGATGTTGTGGACATCTGCATTCACGATCAGCTATGGATCATGTG--- 688  
 QY 71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyLys 90  
 DB 689 -----TTGGAAGTCGATTTCTTC-----ACG 709

QY 91 ArgTyrGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis 110  
 DB 710 AAGTGGCACAGACTTCTT-----TACCAGTGTGTGTCTCACCAAAAT 751  
 QY 111 GlnArgTyrLysAspThrThiMetCysGluValThiMetLysGlyHisAlaHisSerAla 130  
 DB 752 CCTGATTTCAATGAGATA----- 769

QY 131 AsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysPro 149  
 DB 770 ---ATGAACGTGATATAGGGA-----TGAAG-----GGCTTTTCCA 805

## RESULT 5

US-10-425-115-28662  
 / Sequence 28662, Application US/10425115  
 / Publication No. US20040214272A1  
 / GENERAL INFORMATION:  
 / APPLICANT: La Rosa, Thomas J.  
 / APPLICANT: Kovalic, David K.  
 / APPLICANT: Zhou, Yihua  
 / APPLICANT: Cao, Yongwei  
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 / FILE REFERENCE: 38-21(5322)B  
 / CURRENT APPLICATION NUMBER: US/10/425,115  
 / CURRENT FILING DATE: 2003-04-28  
 / NUMBER OF SEQ ID NOS: 369326  
 / SEQ ID NO 28662  
 / LENGTH: 1454  
 / TYPE: DNA  
 / ORGANISM: Zea mays  
 / FEATURE:  
 / OTHER INFORMATION: Clone ID: MRT4577\_126150C.1  
 US-10-425-115-28662

## Alignment Scores:

Pred. No.: 2.74 Length: 1454  
 Score: 84.00 Matches: 35  
 Percent Similarity: 37.4% Conservative: 17  
 Best Local Similarity: 25.2% Mismatches: 31  
 Query Match: 8.9% Indels: 56  
 DB: 9 Gaps: 10

US-10-507-132-2 (1-172) x US-10-425-115-28662 (1-1454)

QY 26 TrpAlaAspSerTyrAspSerLysAspTrp---AspArgLeuArgLysValIleAlaPro 44  
 DB 512 TGGAAAGACGTGTTGATTCGGCAAGCTGTGGAAGACCTGATTTGGCGGTATTCATTTCT 571  
 QY 45 ThrLeuArgIleAspTyrArgSerPhe-----LeuAspLys 56  
 DB 572 AAACGAGATTGGCGTTGCAAGACTTTTCAGATCAACCCAGAAACGAGCTCGATCAG 631  
 QY 57 -----LeuTrp---GlnAlaMetProAlaGluGluPheValGlyMetVal 70  
 DB 632 TTCACCTGGGTGATGTTGTGGACATCTGCATTCACGATCAGCTATGGATCATGTG--- 688  
 QY 71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyLys 90  
 DB 689 -----TTGGAAGTCGATTTCTTC-----ACG 709  
 QY 91 ArgTyrGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis 110  
 DB 91 ArgTyrGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis 110

```
Db 710 AAGTGCAGCAGGTTCTT-----TACCACCTGTTGCTCACCACAAAT 751
Qy 111 GlnArgTyrLeuAspThrThrmethylValThrmethylYhiAlaHisSerAla 130
Db 752 CCTGATTCAATGAGATA----- 769
Qy 131 AsnLeuHisTyrTyrLeuYhiLeuAspGlyValTrrPhePheAlaGlyLeuYspPro 149
Db 770 ---ATGAACCTGGATATAGGGA-----TGAAG-----GGCCTTTTCCCA 805

RESULT 6
US-10-847-972-59
; Sequence 59, Application US/10847972
; Publication No. US20050049195A1
; GENERAL INFORMATION:
; APPLICANT: ZOU, YIMIN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
; FILE REFERENCE: ARCD:395US
; CURRENT APPLICATION NUMBER: US/10/847,972
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/470,913
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 59
; LENGTH: 3154
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(1182)
US-10-847-972-59

Alignment Scores:
Pred. No.: 8.12 Length: 3154
Score: 84.00 Matches: 32
Percent Similarity: 41.7% Conservative: 11
Best Local Similarity: 31.1% Mismatches: 36
Query Match: 8.9% Indels: 24
DB: 10 Gaps: 7

US-10-507-132-2 (1-172) x US-10-847-972-59 (1-3154)
Qy 84 GlnHisPheIleGlyGlyThrArgTrp-----GlnYsValSerGluAspGluValIle 101
Db 352 CAGCAGCAGTTCCGATTCCGCGCGCTGGAACCTGCCCTGGCGGAGAAAGACCGCTTTC 411
Qy 102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLeuAspThrThrmethylVal 121
Db 412 GGG---CAAGAACTCCGAGTAGGAGAGTGAAGAGCTGCCTTCACC-----TATGCCATC 462
Qy 122 ThrMetLeuGlyYhiAlaHisSer-----AlaAsnLeuHis--- 133
Db 463 ACCGCGCGCGGCGGTGCGCATGCTGCACCGCTGCTGCAGCCAGGCGCAATCTGACCAAT 522
Qy 134 -----TrrYrYsYhiLeuAspGlyValTrrPhePhe 144
Db 523 TGTGCTGTGACCGGAGAAAGCAAGGCTACTACAAACAGCGGAGAGC---TGAAGTGG 579
Qy 145 AlaGlyLeuYspProAspIleArgTrrPglYgluPheAspPheAspArgIlePheGluAsp 164
Db 580 GGGGGCTGCTCAGCGGAGCGTCCGCTACGGC---ATCGACTTTTCTCGCTTGTGGAT 636
Qy 165 GlyArgGlu 167
Db 637 GCCCGTGGAG 645

RESULT 7
US-11-108-528-45
; Sequence 45, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
```

```
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 3154
; TYPE: DNA
; ORGANISM: Mouse
US-11-108-528-45

Alignment Scores:
Pred. No.: 8.12 Length: 3154
Score: 84.00 Matches: 32
Percent Similarity: 41.7% Conservative: 11
Best Local Similarity: 31.1% Mismatches: 36
Query Match: 8.9% Indels: 24
DB: 15 Gaps: 7

US-10-507-132-2 (1-172) x US-11-108-528-45 (1-3154)
Qy 84 GlnHisPheIleGlyGlyThrArgTrp-----GlnYsValSerGluAspGluValIle 101
Db 352 CAGCAGCAGTTCCGATTCCGCGCGCTGGAACCTGCCCTGGCGGAGAAAGACCGCTTTC 411
Qy 102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLeuAspThrThrmethylVal 121
Db 412 GGG---CAAGAACTCCGAGTAGGAGAGTGAAGAGCTGCCTTCACC-----TATGCCATC 462
Qy 122 ThrMetLeuGlyYhiAlaHisSer-----AlaAsnLeuHis--- 133
Db 463 ACCGCGCGCGGCGGTGCGCATGCTGCACCGCTGCTGCAGCCAGGCGCAATCTGACCAAT 522
Qy 134 -----TrrYrYsYhiLeuAspGlyValTrrPhePhe 144
Db 523 TGTGCTGTGACCGGAGAAAGCAAGGCTACTACAAACAGCGGAGAGC---TGAAGTGG 579
Qy 145 AlaGlyLeuYspProAspIleArgTrrPglYgluPheAspPheAspArgIlePheGluAsp 164
Db 580 GGGGGCTGCTCAGCGGAGCGTCCGCTACGGC---ATCGACTTTTCTCGCTTGTGGAT 636
Qy 165 GlyArgGlu 167
Db 637 GCCCGTGGAG 645

RESULT 8
US-10-087-192-1699
; Sequence 1699, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
```

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1699
; LENGTH: 88232
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (88232)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1699

Alignment Scores:
Pred. No.: 1.39e+03 Length: 88232
Score: 82.50 Matches: 28
Percent Similarity: 37.7% Conservative: 12
Best Local Similarity: 26.4% Mismatches: 45
Query Match: 8.8% Indels: 21
DB: 6 Gaps: 4

US-10-507-132-2 (1-172) x US-10-087-192-1699 (1-88232)
QY 22 CysValTyrGluThrPalaAspSerTyrAspSerLysAspThrAspArgLeuArg----- 39
DB 26290 TGTGTATATGATTGGATTCTTATTTTCCTCCCTAAGTACATGACGAGCGTTGAATTTCTGG 26349
QY 40 -----LysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
DB 26350 CCACCTTCAGAGACTTCCTATATGTCTCCACTTGAACGTGACAGCAGCTGCTGCTC 26409
QY 55 AspLeuLeuTyrGluAlaMetProAlaGluGluPheValGly-----MetVal 70
DB 26410 TCCACACTTTGGAGACTCTCCCTCCCAATGCTCTTAAGACTTATTTTGGTA 26469
QY 71 SerSerLysGluMetLeuGlyAspProThrLeuArgThrGlnHisHelleglyGlyThr 90
DB 26470 GGTATATAACAAACAAACAAACAAACAAACCTGCTGACCTTGAATGATTT--GAATAT 26526
QY 91 ArgTyrGluLysVal-----SerGluAspGluValIle 101
DB 26527 CAACGTGAGGTGGTTTGAATCTGGCACTCATTTTCTAAGACTCAGAGCAGGAGCTGTGG 26586
QY 102 GlyTyrHisGlnLeuArg 107
DB 26587 GGATACACACGCGCAGA 26604

RESULT 9
US-10-335-977-2219
; Sequence 2219, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
```

```
ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 2219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1473
; SEQUENCE DESCRIPTION: SEQ ID NO: 2219:
US-10-335-977-2219

Alignment Scores:
Pred. No.: 6.15 Length: 1473
Score: 81.50 Matches: 35
Percent Similarity: 44.1% Conservative: 25
Best Local Similarity: 25.7% Mismatches: 68
Query Match: 8.7% Indels: 8
DB: 4 Gaps: 4

US-10-507-132-2 (1-172) x US-10-335-977-2219 (1-1473)
QY 23 ValTyrGluThrPalaAspSerTyrAspSerLysAspThrAspArgLeuArgLysValIle 42
DB 106 GCTATGTAATTCGCGGAAACGCAATTGAATTTAGCCGATGTATTAAACCCCTTTC 165
QY 43 AlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTyrGluAlaMetPro 62
DB 166 AATTTAGGCTTATGTGTAATAAAACGACTTTTGGATAGATAGCATAGATTTTA 225
QY 63 AlaGluGluPheValGlyMetValSerLysGlnMetLeuGlyAspProThrLeuArg 82
DB 226 GCCGAAGAGTTTCATTGAATAATTTCTGTCAAAACACCTTAGAAGA-----TTTGA 279
QY 83 ThrGlnHisPheIleGlyGlyThrArgTyrGluLysValSerGluAspGluValIleGly 102
DB 280 GTAGAAGAGTCTAGAGGGGTGAATAAAAGAGCGCCCTGTGGTTACTATCATGGGG 339
QY 103 TyrHisGln-LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValTh 122
DB 340 CATGTTGATCATGTAATCTCTACTGACTGATTAATATCCGATAGAGAGTCCGCCAC 399
QY 122 rMetLys-----GlyHisAlaHisSerLysAsnLeuHisTyrLysValIle---As 139
DB 400 ACTGAAGCCGGGGGAGTACTCAGACACATGTGGCTTACATGCTGGAATAAATAACAA 459
QY 139 pGlyValTyrLysPheAla-----GlyLeuLysProAspIleArg 152
DB 460 TGGGTGTCTTTCATTGACACCCAGGGCATGGAAGCTTCAGCCAGA 505

RESULT 10
US-10-364-888-1
; Sequence 1, Application US/10364888
; Publication No. US20040023259A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Zhong, Haihong
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gangoli, Esma
; APPLICANT: Guo, Xiaojia
; APPLICANT: Malyankar, Uriel
```





```

APPLICANT: Malyankar, Uriel
APPLICANT: Paturajan, Meera
APPLICANT: Pena, Carol
APPLICANT: Shimkets, Richard
APPLICANT: Spytek, Kimberly
APPLICANT: Vernet, Corine
APPLICANT: Rieger, Daniel
APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE
FILE REFERENCE: 15966-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/387,082
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Curoseqqlist version 0.1
SEQ ID NO 5
LENGTH: 1070
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1047)
US-10-364-888-5

```

[illegible]

US-10-507-132-2 (1-172) x US-10-364-888-5 (1-1070)

[illegible]

RESULT 13  
US-10-364-886-7  
Sequence 7, Application US/10364888  
Publication No. US2004002359A1  
GENERAL INFORMATION:  
APPLICANT: Rastelli, Luca  
APPLICANT: Zhong, Haibong  
APPLICANT: Boldog, Ferenc  
APPLICANT: Ganggoli, Esha  
APPLICANT: Guo, Xiaojia  
APPLICANT: Malysankar, Uriel  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol

```

APPLICANT: Shimkets, Richard
APPLICANT: Spytek, Kimberly
APPLICANT: Vermet, Corine
APPLICANT: Rieger, Daniel
APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 15966-744CIP
CURRENT FILING DATE: 2003-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/387,082
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Curaseqlist version 0.1
SEQ ID NO 7
LENGTH: 2160
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (6)..(1052)
US-10-364-888-7

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Alignment Scores:	
Pred. No.:	12.3
Score:	81.00
Percent Similarity:	42.7%
Best Local Similarity:	31.2%
Query Match:	8.6%
DB:	8
Length:	2160
Matches:	30
Conservative:	11
Mismatches:	31
Indels:	24
Gaps:	7

US-10-507-132-2 (1-172) x US-10-364-888-7 (1-2160)

QY	ArgTTP-----GlnbValSerGluAspGluValIleGlyTyrThrIsglnLeuArgVal	108
Db	CcGTGAACTGCTCTGCTCCCTCGGCGAAGAACCGCTTCGGG---CAAGAGCTCGAGTA	302
QY	ProHsIslaArgTyrIlyAspThrThrMetIySgluValIThrMetIySglYHsIslaHs	128
	:::	
Db	GGAGCCGTGAGGCTGCTTCACG-----TACGCCATCACCGCGGCTGGCGTGGCCAC	358
QY	129 Ser-----AlaIstLeuHs-----	133
	:::	
Db	GCCGTACCGCTGCTCGACGCCAAGGAACTGAGCAACTGCGGCTGGACCGCGAAG	418
QY	134 -----TrpTyrIlybSglIleAspGlyValITrpIlybSphalaglYLeuIySProaspIle	151
	:::	
Db	CAGGCTACTACCAACCAACCGAGGGC---TGGAAGTGGCGGCGCTGCTGGCGGACGTG	473
QY	152 ArgTTrpGlyGluIuAspSphAspArgIleIleMetIuAspGlyIYAArgIu	167
Db	CGTTAGCGC---ATGACATTTCTCCGGCGGCTTCGTGACGCTCGGAGAG	518

RESULT 14  
 US-10-285-976-22  
 ; Sequence 22, Application US/10285976  
 ; Publication No. US20030165500A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rhee, Chae-Seo  
 ; APPLICANT: Malini, Sen  
 ; APPLICANT: Wu, Christina  
 ; APPLICANT: Leonl, Lorenzo M.  
 ; APPLICANT: Corr, Maripat  
 ; APPLICANT: Carson, Dennis A.  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy  
 ; TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas  
 ; FILE REFERENCE: 023070-130320US  
 ; CURRENT APPLICATION NUMBER: US/10/285,976

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/ CURRENT FILING DATE: 2002-11-01
/ PRIOR APPLICATION NUMBER: US 60/287,995
/ PRIOR FILING DATE: 2001-05-01
/ PRIOR APPLICATION NUMBER: WO PCT/US02/13802
/ NUMBER OF SEQ ID NOS: 232
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 2250
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human wnt-7b
US-10-285-976-22

Alignment Scores:
Pred. No.: 13          Length: 2250
Score: 81.00          Matches: 30
Percent Similarity: 42.7%      Conservative: 11
Best Local Similarity: 31.2%   Mismatches: 31
Query Match: 8.6%           Indels: 24
DB: 7                     Gaps: 7

US-10-507-132-2 (1-172) x US-10-285-976-22 (1-2250)
QY 91 ArgTTP-----GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
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Db 336 CGCTGAACTGCTGCTGCCCTCGGCGAAGAACCGCTTCGGG---CAAGAGCTCCGAGTA 392

QY 109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlnHis 128
   ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 393 GGGAGCCGTGAGGCTGCTTCACG-----TACGCCATCACCGCGCTGCGTGGCGCAC 446

QY 129 Ser-----AlaAsnLeuHis----- 133
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Db 447 GCCGTACCGCTGCTGCGCAAGCAAGGAACTGAGCACTGCGGCTGCGACCGCGAAG 506

QY 134 -----TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
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Db 507 CAGGCGTACTACAAACCAAGCCGAGGGC---TGGAACTGGGGCGGCTCGGCGGACGTG 563

QY 152 ArgTTPGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 564 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGACGCTCGGAG 608

RESULT 15
US-10-847-972-21
/ Sequence 21, Application US/10847972
/ Publication No. US20050049195A1
/ GENERAL INFORMATION:
/ APPLICANT: ZOU, YIMIN
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
/ FILE REFERENCE: ARCD:395US
/ CURRENT APPLICATION NUMBER: US/10/847,972
/ CURRENT FILING DATE: 2004-05-17
/ PRIOR APPLICATION NUMBER: 60/470,913
/ PRIOR FILING DATE: 2003-05-15
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 21
/ LENGTH: 2250
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (96)..(1145)
US-10-847-972-21

Alignment Scores:
Pred. No.: 13          Length: 2250
Score: 81.00          Matches: 30
Percent Similarity: 42.7%      Conservative: 11
Best Local Similarity: 31.2%   Mismatches: 31
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Query Match: 8.6%          Indels: 24
DB: 10                     Gaps: 7

US-10-507-132-2 (1-172) x US-10-847-972-21 (1-2250)
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Db 336 CGCTGAACTGCTGCTGCCCTCGGCGAAGAACCGCTTCGGG---CAAGAGCTCCGAGTA 392

QY 109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlnHis 128
   ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 393 GGGAGCCGTGAGGCTGCTTCACG-----TACGCCATCACCGCGCTGCGTGGCGCAC 446

QY 129 Ser-----AlaAsnLeuHis----- 133
   ::|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 447 GCCGTACCGCTGCTGCGCAAGCAAGGAACTGAGCACTGCGGCTGCGACCGCGAAG 506

QY 134 -----TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
   ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||  ::|||
Db 507 CAGGCGTACTACAAACCAAGCCGAGGGC---TGGAACTGGGGCGGCTCGGCGGACGTG 563

QY 152 ArgTTPGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 564 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGACGCTCGGAG 608
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Search completed: December 4, 2006, 20:27:11  
Job time : 912 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 4, 2006, 19:19:24 ; Search time 143 Seconds  
(without alignments)  
3375.847 Million cell updates/sec

Title: US-10-507-132-2  
Perfect score: 942  
Sequence: 1 MCSQVQKSDIRFSDVYGLM.....WGFDFDRIFEDQRETFDQK 172

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Ygapop 10.0 , Ygapext 0.5  
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Delop 6.0 , Delext 7.0

Searched: 1403666 segs, 93554401 residues  
Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/abs/ABSSWEB.spool/US10507132/runat\_04122006\_143910\_11443/app\_query.fasta\_1  
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-LIST=45 -DOCALLIGN=100 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORMext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-HOST=abs06h -USER=US10507132@CCN\_1\_1\_152 -runat\_04122006\_143910\_11443  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents NA:\*
- 1: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/1\_COMB.seq:\*
  - 2: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/5\_COMB.seq:\*
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  - 5: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/7\_COMB.seq:\*
  - 6: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/H\_COMB.seq:\*
  - 7: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/PCTUS\_COMB.seq:\*
  - 8: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/PP\_COMB.seq:\*
  - 9: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/RE\_COMB.seq:\*
  - 10: /EMC\_Celerra\_SIDS3/ptocdata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	94.5	10.0	462	US-09-328-352-44	Sequence 44, Appl
2	84	8.9	850	US-09-449-285A-8	Sequence 8, Appl
3	84	8.9	850	US-09-964-238-8	Sequence 8, Appl
4	84	8.9	1017	US-09-543-681A-477	Sequence 477, App
5	81	8.6	1070	US-09-625-634A-1	Sequence 1, Appl
6	79	8.4	11096	US-10-149-736-4	Sequence 4, Appl
7	77	8.2	687	US-09-252-991A-12976	Sequence 12976, A
8	77	8.2	2103	US-09-252-991A-12501	Sequence 12501, A

C	9	77	8.2	3045	3	US-09-252-991A-13297	Sequence 13297, A
	10	76.5	8.1	24070	3	US-09-949-016-16153	Sequence 16153, A
	11	76	8.1	1806	3	US-09-248-796A-1708	Sequence 1708, Ap
	12	75.5	8.0	1776	3	US-09-614-221A-97	Sequence 97, Appl
C	13	75	8.0	1830121	3	US-09-557-884-1	Sequence 1, Appl
C	14	75	8.0	1830121	3	US-09-643-990A-1	Sequence 1, Appl
C	15	75	8.0	1830121	3	US-10-158-865-1	Sequence 1, Appl
	16	74.5	7.9	1382	3	US-09-477-135A-122	Sequence 122, Appl
	17	74.5	7.9	48318	3	US-09-949-016-15717	Sequence 15717, A
C	18	74.5	7.9	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C	19	74.5	7.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl
	20	74	7.9	882	5	US-09-974-300-2748	Sequence 2748, Ap
	21	74	7.9	2307	3	US-09-489-039A-3960	Sequence 3960, Ap
	22	73.5	7.8	1839	3	US-09-540-236-1428	Sequence 1428, Ap
	23	73.5	7.8	66986	3	US-09-596-002-29	Sequence 29, Appl
C	24	73.5	7.8	325791	3	US-09-768-185A-1	Sequence 1, Appl
C	25	73	7.7	8961	3	US-09-949-016-15910	Sequence 15910, A
	26	72.5	7.7	1249	5	US-09-984-429-401	Sequence 401, App
	27	72.5	7.7	1557	3	US-09-489-039A-1236	Sequence 1236, Ap
	28	72.5	7.7	2498	2	US-07-943-843-3	Sequence 3, Appl
	29	72.5	7.7	2498	2	US-08-347-003-3	Sequence 3, Appl
	30	72.5	7.7	49931	3	US-09-949-016-13727	Sequence 13727, A
	31	72.5	7.7	49931	3	US-09-949-016-13728	Sequence 13728, A
	32	72.5	7.7	49931	3	US-09-949-016-13729	Sequence 13729, A
	33	72.5	7.7	92344	3	US-09-949-016-16802	Sequence 16802, A
	34	72	7.6	781	5	US-09-974-300-90	Sequence 90, Appl
	35	72	7.6	1191	3	US-09-328-352-3721	Sequence 3721, Ap
	36	72	7.6	1209	5	US-09-974-300-4488	Sequence 4488, Ap
	37	72	7.6	4282	3	US-09-976-594-799	Sequence 799, App
	38	72	7.6	6474	3	US-09-949-016-1717	Sequence 1717, Ap
	39	71.5	7.6	1503	3	US-09-949-016-15826	Sequence 5826, Ap
	40	71.5	7.6	1956	3	US-09-715-858-1	Sequence 1, Appl
	41	71.5	7.6	2191	3	US-09-039-555B-12	Sequence 12, Appl
	42	71.5	7.6	2312	5	US-09-984-429-371	Sequence 371, Appl
	43	71.5	7.6	3816	3	US-09-540-236-1620	Sequence 1620, Ap
	44	71.5	7.6	5140	3	US-10-098-600B-14	Sequence 14, Appl
	45	71.5	7.6	5140	3	US-10-098-600B-15	Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
US-09-328-352-44  
; Sequence 44, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 44  
; LENGTH: 462  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
; US-09-328-352-44

Alignment Scores:  
Pred. No.: 0.00957 Length: 462  
Score: 94.50 Matches: 31  
Percent Similarity: 43.7% Conservative: 28  
Best Local Similarity: 23.0% Mismatches: 59  
Query Match: 10.0% Indels: 17  
DB: Gaps: 6

US-10-507-132-2 (1-172) x US-09-328-352-44 (1-462)  
QY 15 AAPPYTLLEGLYLeumethrCysvalYrGtUTPAlaAspSerTyRAspSerlysaap 34  
DB 37 GACTACACACGATATTATTAGAGTCATTTACGCGCTTTTCAATGTTTTCACCAAGAAAT 96

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QY 35 TTPAARGLEuArgLySValIleAlaProThrLeuArgIleAspTYrZarSerPheLeu 54
DB 97 TCGGATGCCGTTGATGAGTTGTTAGCCGATCACTTGAGGTGACATTTTGAGATTAA 156
QY 55 AspLYsLeuTPrgLInALeMeCProAlaGluGluPheValGlyMeValSerSerlySglIn 74
DB 157 GGGAGACCTTTTATGTGTGGTGTCTGTGCATGATATMAAGT-----TCACGGCAACAA 210
QY 75 MeLeuGlyAspProThrLeuArgTrhGlnHisPheIleGlyGlyThraArgTrpGluLYs 94
DB 211 GCTTTGTCACT-----TTGGGGCTACAGCACAAATTATAGCAATCTT---CTTATTCCG 261
QY 95 ValSerGluAspGluValIleGlyTrhISglInLeuArgValProHisGlnArgTYrLYs 114
DB 262 ATTGAACAGATCAAGCA-----TGCTTGAAATGTAATTATCAAAATTATTCGT 309
QY 115 AspTrhThMeLySgluValThrMeLySglYhIALHisSerAlaLeuHisTrp 134
DB 310 -----TTTTCGAAATGATATTATTTTCATTTCTTGTGCTGCTATTAT 351
QY 135 TYr-----LYeLYsIleAspGlyValTTrpLYsPheAlaGlyLeu 147
DB 352 TTTACTTGGCAAAACAAACAGGCGCATATGAAAAATTATCCGGAATT 396

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## RESULT 2

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US-09-449-285A-8
; Sequence 8, Application US/09449285A
; Patent No. 6313280
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie
; TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
; FILE REFERENCE: 2676-4232US
; CURRENT APPLICATION NUMBER: US/09/449,285A
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: PCT/EP98/03193
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 97201645.5
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-449-285A-8

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## Alignment Scores:

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Pred. No.: 0.479      Length: 850
Score: 84.00      Matches: 32
Percent Similarity: 41.7%      Conservative: 11
Best Local Similarity: 31.1%      Mismatches: 36
Query Match: 8.9%      Indels: 24
DB: 3      Gaps: 7

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US-10-507-132-2 (1-172) x US-09-449-285A-8 (1-850)

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QY 84 GlnHisPheIleGlyGlyThraArgTrp-----GluLYsValSerGluAspGluValIle 101
DB 536 CAGCACCACTTCGATTCGGCCGCTGGAATGCTCCGCCCTGGGCGAAGACCGCTTTC 595
QY 102 GlyTYrHisGlnLeuArgValProHisGlnArgTYrLYsAspTrhThMeLySgluVal 121
DB 596 GGG---CAAGAACTCCGATGAGGAGTGCAGAGGCTGCCTTCAAC-----TATGCCATC 646
QY 122 ThrMeLySglYhIALHisSer-----AlaAsnLeuHis--- 133
DB 647 ACGGCGGCGGCGTGGCGCATGCTGTCAACCGCTGCGACGCCAGGCGCATCTGACCAAT 706
QY 134 -----TTrpTYrLYsIleAspGlyValTTrpLYsPhe 144
DB 707 TGTGGCTGTGACCGGAGAGCAAGGCTACTATCAACAGCGGAGAGG---TGAAGTGG 763
QY 145 AlaGlyLeuLYsProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164

```

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DB 764 GGGGCTCTCAGCGGAGAGTCCGCTACGGC---ATCGACTTTTTCGTCGCTTTGTGAT 820
QY 165 GlyArgGlu 167
DB 821 GCCCGTGAG 829

```

## RESULT 3

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US-09-964-238-8
; Sequence 8, Application US/09964238
; Patent No. 6884779
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie
; TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
; FILE REFERENCE: 2676-4232US
; CURRENT APPLICATION NUMBER: US/09/964,238
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/449,285
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: PCT/EP98/03193
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 97201645.5
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-964-238-8

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## Alignment Scores:

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Pred. No.: 0.479      Length: 850
Score: 84.00      Matches: 32
Percent Similarity: 41.7%      Conservative: 11
Best Local Similarity: 31.1%      Mismatches: 36
Query Match: 8.9%      Indels: 24
DB: 3      Gaps: 7

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US-10-507-132-2 (1-172) x US-09-964-238-8 (1-850)

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QY 84 GlnHisPheIleGlyGlyThraArgTrp-----GluLYsValSerGluAspGluValIle 101
DB 536 CAGCACCACTTCGATTCGGCCGCTGGAATGCTCCGCCCTGGGCGAAGACCGCTTTC 595
QY 102 GlyTYrHisGlnLeuArgValProHisGlnArgTYrLYsAspTrhThMeLySgluVal 121
DB 596 GGG---CAAGAACTCCGATGAGGAGTGCAGAGGCTGCCTTCAAC-----TATGCCATC 646
QY 122 ThrMeLySglYhIALHisSer-----AlaAsnLeuHis--- 133
DB 647 ACGGCGGCGGCGTGGCGCATGCTGTCAACCGCTGCGACGCCAGGCGCATCTGACCAAT 706
QY 134 -----TTrpTYrLYsIleAspGlyValTTrpLYsPhe 144
DB 707 TGTGGCTGTGACCGGAGAGCAAGGCTACTATCAACAGCGGAGAGG---TGAAGTGG 763
QY 145 AlaGlyLeuLYsProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
DB 764 GGGGCTGTCTAGCGGAGAGTCCGCTACGGC---ATCGACTTTTCTGTCGCTTTGTGAT 820
QY 165 GlyArgGlu 167
DB 821 GCCCGTGAG 829

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## RESULT 4

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US-09-543-681A-477
; Sequence 477, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; DIAGNOSTICS AND THERAPEUTICS

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; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 477
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-477

Alignment Scores:
Pred. No.: 0.615      Length: 1017
Score: 84.00         Matches: 39
Percent Similarity: 37.3%  Conservative: 18
Best Local Similarity: 25.5%  Mismatches: 42
Query Match: 8.9%      Indels: 54
DB: 3                Gaps: 10

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QY 35 TTPASPAArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
DB 280 TGGGATAAAGCACACACCA-----CAAGTCTTGTCTG-----GAAGATGTCCTT 309
QY 55 AspLysLeuThrPgluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGln 74
DB 310 GATTAATAAGTTTAAACACAGGCCA---CACTCTTGTCTG-----GAGTCTTGTCTG 345
QY 75 MetLeuGlyAspProThrLeuArg---ThrGlnHisPheIleGlyLysThrArgTyrPglu 93
DB 346 ATGCTTGACGATCTTTGTTTAAGAGGGGCTAAACACACATTACAGGTCCTCTTGGGA 405
QY 94 LysValSerGluAspGluValIleGlyTyrHisGlnLeuArg-----GAGTCTTGTCTG 107
DB 406 GGGATA-----GAGATTATA-----GAGCGCTTAAACACACAGGCGTAAATGTT 450
QY 108 -----ValProHisGlnArgTyrLysAspThrThreLysGluValThreLys 124
DB 451 ATTTTATGATGTCACCGATGGATGGCTGTTGATGTACCTGCCATGTTATGGCTGCTAA 510
QY 125 GylHisAlaHisSerAlaAsnLeuHisTyrTyrLysLys-----IleAspGlyValTyr 142
DB 511 GGGCAAAAATGCGACGAATGTTTCAACCAAAAAGATCGGTGACTGATTATTATG 570
QY 143 -----LysPheAlaGlyLeuLysPro 149
DB 571 AATAAAGCATGTTACATTTCGGCGGACGTTTACACTCGCGGACGAGCGGATATAA 630
QY 150 AspLysArg-----TyrGlyGluPhe 156
DB 631 TTTATTTCAACGGTGGCGCAAGGCTTTTGGGGGTATTAT 669

RESULT 5
US-09-625-634A-1
; Sequence 1, Application US/09625634A
; Patent No. 6653448
; GENERAL INFORMATION:
; APPLICANT: Verneet, Corine
; APPLICANT: Rastelli, Luca
; APPLICANT: Herrmann, John
; TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: Cura-244 (15966-744) US
; CURRENT APPLICATION NUMBER: US/09/625,634A
; CURRENT FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: USN 60/194,256
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: USN 60/192,838
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 1
; LENGTH: 1070
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1047)
US-09-625-634A-1

Alignment Scores:
Pred. No.: 1.58      Length: 1070
Score: 81.00         Matches: 30
Percent Similarity: 42.7%  Conservative: 11
Best Local Similarity: 31.2%  Mismatches: 31
Query Match: 8.6%      Indels: 24
DB: 3                Gaps: 7

US-10-507-132-2 (1-172) x US-09-625-634A-1 (1-1070)
QY 91 ArgTyrP-----GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
DB 241 CGCTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 297
QY 109 ProHisGlnArgTyrLysAspThrThreLysGluValThreLysGlyHisAlaHis 128
DB 298 GGGAGCCGTGAGGCTGCTTCAAG-----TACGCATCATCCGGCGCTGCGCGCAC 351
QY 129 Ser-----AlaAsnLeuHis----- 133
DB 352 GCGGTACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 411
QY 134 -----TyrTyrLysLysIleAspGlyValTyrLysPheAlaGlyLeuLysProAspIle 151
DB 412 CAGGCTACTTACAAACCAACCGAGGCG---TGAAGTGGGGGGGCTGCTGCGCGCACGTG 468
QY 152 ArgTyrGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
DB 469 CGTTACGCG---ATGACCTTCTCCGGGCGCTTCTGAGACGCTCGGAG 513

RESULT 6
US-10-149-736-4
; Sequence 4, Application US/10149736
; Patent No. 6869777
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; APPLICANT: Harper, Scott Q.
; TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
; FILE REFERENCE: UM-06968
; CURRENT APPLICATION NUMBER: US/10/149,736
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/US01/31126
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,848
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11096
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-149-736-4

Alignment Scores:
Pred. No.: 74.9      Length: 11096
Score: 79.00         Matches: 39
Percent Similarity: 35.0%  Conservative: 23
Best Local Similarity: 22.0%  Mismatches: 71
Query Match: 8.4%      Indels: 44
DB: 3                Gaps: 5

US-10-507-132-2 (1-172) x US-10-149-736-4 (1-11096)
QY 15 AspTyrLeuGlyLeuMetThrCysValTyrGluTyrAlaAspSerTyrAspSerLysAsp 34
```

```
Db 7201 GAATCAGTGGCGATGACACAAGGATGTGGAGAAACCGAGTAATTGAAAACATCA 7260
Qy 35 TTPAPAPAGLueuArglyValIleAla----- 43
Db 7261 TGGGTCAATCTCAAAACAGCATCGCTGATAGACAGATGCTTGAGAGCTGAGCTACAG 7320
Qy 44 -----ProThrluArgIleAspTyrArgSerPheIuAspIlyeUtrpGluAlaMet 61
Db 7321 ACAGTGCACACTTCTGTAGAGACTTGAGAGACTTGTCAAGTGGCTTCAGAGAGCAGAA 7380
Qy 62 ProAlaGluGluPheValGlyMetValSerIlySgln---MetIeuGlyAspProThr 80
Db 7381 ACCACAGCAAAATGTGTGGCCGATGCTCTCAGCGGAGAAATGCTTTCAGAGACAGTGTTC 7440
Qy 81 LeuArgThrGln----- 84
Db 7441 CTGGCCCGGCGATCCGACAGCAGATGCTGACATCCAGCGCAAAATGATGCCCACAAT 7500
Qy 85 -----HisPheIleGlyIleGlyThrArgTyrGluVal-----Ser 96
Db 7501 GACATATTAAAGCATGATGGAACCGGAGAGATGTGAAGCTCTGGGGAATTCT 7560
Qy 97 GluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrIlyAspThr 116
Db 7561 GAGGAAGCAACAATGCTTCAACATCGATCGATGACATGACCAAGAGATGATGATTTTG 7620
Qy 117 ThrMetIleGluValThrMetIlySglnHisSerAlaAsnIleuIstTyrIlyS 136
Db 7621 AAGGCAAAATCTGTGACATCGACGAGCCATTGGAGGCCAGATGCTTAAGAAATGAAACCGG 7680
Qy 137 LysIleAspGlyValTyrIlyPheAlaGlyLeuIlySProAspIleArgTyr 153
Db 7681 TTGCTG-----GCATGCTGTGAAGACTGATCAAAATGG 7713
```

## RESULT 7

```
US-09-252-991A-12976/c
/ Sequence 12976, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 12976
/ LENGTH: 687
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12976
```

## Alignment Scores:

Pred. No.:	2, 73	Length:	687
Score:	77.00	Matches:	25
Percent Similarity:	44.9%	Conservative:	15
Best Local Similarity:	28.1%	Mismatches:	35
Query Match:	8.2%	Indels:	14
DB:	3	Gaps:	4

US-10-507-132-2 (1-172) x US-09-252-991A-12976 (1-687)

```
Qy 59 GluAlaMetProAlaGluGluPheValIleGlyMet---ValSerSerIlySglnMetIeuGly 77
Db 300 GAAAGATCAGCCGACGAGCGCGCTTGTGTCAGCGGCTGTGCTCAGACATATCTCGGCG 241
Qy 78 AspProThrLeuArgThrGlnHisPheIleGlyIleGlyThrArgTyr----- 92
```

```
Db 240 TACCCCGAGATCGGCTGCCCATCGAGTACAGCGGACCCGCAATGTCTGGCAGCGGCTC 181
Qy 93 ---GluIlyValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln 111
Db 180 GCCGAGTCTGTGAACACAGGCTGAGACGTTGGATCTACACATAGAGAGAGTCAACAG 121
Qy 112 ArgTyrIlyS-----AspThrThrMetIlySglnValThrMetIlySglnHis 126
Db 120 CGTCATCGCGCCGACAGAGAGGAGATGACGCGCTCTCTGAAGCGGTTCCAGACGCGCAC 61
Qy 127 -----AlaHisSerAlaAsnIleuHis 133
Db 60 GATCGATTCAATCGCAGCGCTTCTCCAC 34
```

## RESULT 8

```
US-09-252-991A-12501
/ Sequence 12501, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 12501
/ LENGTH: 2103
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12501
```

## Alignment Scores:

Pred. No.:	13, 1	Length:	2103
Score:	77.00	Matches:	25
Percent Similarity:	44.9%	Conservative:	15
Best Local Similarity:	28.1%	Mismatches:	35
Query Match:	8.2%	Indels:	14
DB:	3	Gaps:	4

US-10-507-132-2 (1-172) x US-09-252-991A-12501 (1-2103)

```
Qy 59 GluAlaMetProAlaGluGluPheValIleGlyMet---ValSerSerIlySglnMetIeuGly 77
Db 421 GAAAGATCAGCCGACGAGCGCGCTTGTGTCAGCGGCTTCTCCAGACATATCTCGGCG 480
Qy 78 AspProThrLeuArgThrGlnHisPheIleGlyIleGlyThrArgTyr----- 92
Db 481 TACCCCGAGATCGGCTGCCCATCGAGTACAGCGGACCCGCAATGTCTGGCAGCGGCTC 540
Qy 93 ---GluIlyValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln 111
Db 541 GCCGAGTCTGTGAACACAGGCTGAGACGTTGGATCTACACATAGAGAGAGTCAACAG 600
Qy 112 ArgTyrIlyS-----AspThrThrMetIlySglnValThrMetIlySglnHis 126
Db 601 CGTCATCGCGCCGACAGAGAGGAGATGACGCGCTCTCTGAAGCGGTTCCAGACGCGCAC 660
Qy 127 -----AlaHisSerAlaAsnIleuHis 133
Db 661 GATCGATTCAATCGCAGCGCTTCTCCAC 687
```

## RESULT 9

```
US-09-252-991A-13297/c
/ Sequence 13297, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```

Pred. No.:	459	Length:	24070
Score:	76.50	Matches:	56

;  
PRIOR APPLICATION NUMBER: US 60/096,409

;; PRIOR FILING DATE: 1998-08-13  
;; NUMBER OF SEQ ID NOS: 28208  
;; SEQ ID NO 1708  
;; LENGTH: 1806  
;; TYPE: DNA  
;; ORGANISM: Candida albicans  
US-09-248-796A-1708

## Alignment Scores:

Pred. No.:	14.1	Length:	1806
Score:	76.00	Matches:	39
Percent Similarity:	36.5%	Conservative:	23
Best Local Similarity:	22.9%	Mismatches:	57
Query Match:	8.1%	Indels:	51
DB:	3	Gaps:	6

US-10-507-132-2 (1-172) x US-09-248-796A-1708 (1-1806)

QY 4 GlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMetThrCysVal 23  
DB 307 CAAGAGAAATCGCTCTGGAAATTAACCATTTGAATGAAGTCACCTCATAGTA 366  
QY 24 TyrGluTyrAlaSerSerTyrAspSerLysAspTrp-----AspArgLeuArg 39  
DB 367 ATTTAAAGAGAGTTTACTGCCAAAGATCAAAATTTGACAGTTAAACAAGCGGCCACT 426  
QY 40 LysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGlu 59  
DB 427 GAATCAAAATCAAGATTTAAGAACCAATTCATCAATCCACTAGACACCTTTGTCTAT 486  
QY 60 AlaMetProAlaGlu-----GluPheValGly-----MetVal 70  
DB 487 TTTTGGCCCCAGAAAGAGTAGACAGATTTGACAGGACTTTCCCAAGAAATTTGATGAT 546  
QY 71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHis-----85  
DB 547 GAGACAGAAAGTACTTGTGTATGAGCCATTGTGATCATGCACAAAGATTTGATGATGCC 606  
QY 86 -----PheIleGlyIleThrArgTrp 92  
DB 607 AAAGATTAACGAAGTACAGCAATTGGCAACAAGATTTAAAGACATTGAAGG---AGATTA 663  
QY 93 GlnLysValSerGluAsp-----98  
DB 664 GCCAAATTCACGAGGATGATCAAAATTTGAAGAAGACAGAAATTTAGAGAGTAC 723  
QY 99 -----GluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLys 114  
DB 724 GATAGAAAGTCTGAAGAGTTGATTAATCACCGCTTTTGTATCCCGTATCAAAATTCACA 783  
QY 115 AspThr-ThrMetLysGluValThrMet 123  
DB 784 GACTTGAAGAAACCAAGAACTCACCTTA 811

## RESULT 12

US-09-614-221A-97  
; Sequence 97, Application US/09614221A  
; Patent No. 6723837  
; GENERAL INFORMATION:  
; APPLICANT: Karunanandaa, Balasulojini  
; APPLICANT: Yu, Jaehyuk  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED  
; FILE REFERENCE: 16516 075  
; CURRENT APPLICATION NUMBER: US/09/614,221A  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 626  
; SEQ ID NO 97  
; LENGTH: 1776  
; TYPE: DNA

;; ORGANISM: Saccharomyces cerevisiae  
US-09-614-221A-97

## Alignment Scores:

Pred. No.:	16	Length:	1776
Score:	75.50	Matches:	42
Percent Similarity:	32.5%	Conservative:	25
Best Local Similarity:	20.4%	Mismatches:	68
Query Match:	8.0%	Indels:	71
DB:	3	Gaps:	8

US-10-507-132-2 (1-172) x US-09-614-221A-97 (1-1776)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20  
DB 964 ATGAAGCTTCAAAAGCTGGTGGCATATCTTAAATTTTCATTTTCATTTAT-----CCT 1014  
QY 21 ThrCysValTyrGluTyrAlaSerSerTyrAspSer---LysAspTyrAspArgLeuArg 39  
DB 1015 ACCACAGCGAGTGAATGATCAATCAATGTACATTCGCCAAAGATTTGGAGAGTCTGCC 1074  
QY 40 LysValIleAlaProThr-----45  
DB 1075 AAAGGCGAGTTCCCAAGCCCTCTTTAAAGACATTGAGAAATGAAGTTGGGT 1134  
QY 46 LeuArgIleAspTyrArgSerPhe-----LeuAspLysLeuTrp 58  
DB 1135 GTGAAGCTGATTATGACACTTTTCTAAATTTTCTGCTGGAGTTGCCAAATTTAAC 1194  
QY 59 GlnAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAsp 78  
DB 1195 GAGGTTCACCAAGATTACTGTGATACATACATTCGA-----GAGAT 1239  
QY 79 ProThrLeuArgThrGlnHisPheIleGlyIleThrArgTrpGlnLysValSerLysAsp 98  
DB 1240 GGTATTCGGAACTACTTGTGTGTCGGTGTGAAGATTTGAA-----1284  
QY 99 GlnValIleGlyTyrHisGlnLeuArgValProHis-----110  
DB 1285 GAAGCTATTTAAACCATACGTGGCTCGAGAGATGCTGCTCTTGTATGAAATATT 1344  
QY 110 -----110  
DB 1345 GCGTATATGTTGAGATTTATGCGGTGATCGTCCGCTGCTGATCTATCTATCTT 1404  
QY 111 -----GlnArgTyrLysAspThrThrMetLysGlnValThrMetLysGlnHis 126  
DB 1405 TTGCTCTCGCAAGAGAGTTTGGATTCGGGACAGAGAACTTACGCGAATCTTTC 1464  
QY 127 AlaHisSerAlaAsnLeuHisIleTyrLysLysIleAspGlyValTrpLysPheAlaGly 146  
DB 1465 AAAAGGATCAAAAGCTT-----GCACAGATGCTTTGTATAGTATACAGAGA 1512  
QY 147 LeuLysProAspIleArg 152  
DB 1513 GCCCGCTCGTTACAGG 1530

## RESULT 13

US-09-557-884-1/C  
; Sequence 1, Application US/09557884  
; Patent No. 6506581  
; GENERAL INFORMATION:  
; APPLICANT: Fleischmann et al.  
; TITLE OF INVENTION: The Nucleotide sequence of  
; the Haemophilus influenzae Rd Genome, Fragments  
; thereof, and Uses Thereof  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: MD  
; COUNTRY: USA





Db 227652 AAAAGTCGGTAAGAAAGCGATTGTTTCATGATTTTACCAATAATTGGTTGCAGAT 227593  
Qy 50 -----TyrArgSerPheLeuAspLys----- 56  
Db 227592 ATTGCATCTTTATTCCTTAACAATACTTTTCCCAAAATCTATGCTAGTGACGAAGA 227533  
Qy 57 ---LeuTyrGluValMetProAlaGluGluPheValGlyMetValSerSerIysGlnMet 75  
Db 227532 TCTGTTGGAGACGACTGTTGTCAGAAAGAG-----CTCTTTCCCAAAATCAAAATT 227482  
Qy 76 LeuGlyAspProThrIleuArgThrGlnHisPheIleGlyGlyThrArgTrpGluVal 95  
Db 227481 AGTGAACCTCGTCATTAATAATTCGT-----ATTGTTATGATGATTTA 227437  
Qy 96 SerGluAspGluValIleGlyTyr-----HisGln-----Leu 106  
Db 227436 TCTCTGAATCAAAACCTTCGCAATGCATTAATCAATCAATTCATCAATCTGATTTATTA 227377  
Qy 107 ArgValProHisGlnArgTyrIysAspThrThrMetLysGluValThrMetLysGlyHis 126  
Db 227376 CGAGTGAATAATCAAGGATGAGCTGSCAAAGAAATTCAAACGCCGCCAAGAGCGCAT 227317  
Qy 127 AlaHisSerAlaAsnLeuHisTyrIysLysIleAspGlyValTrpIysPheAlaGly 146  
Db 227316 TTTCATTAATTCGTTCTGCGCTGCTGCTGATTTTAATGATCTCGACGATTTTAAAT 227257  
Qy 147 Leu-----LysProAspIleArgTyrGly-----GluPheAspPheAspArg 160  
Db 227256 TTATTTCTATTCAAAAAGCCAGATATACAAAAATGCTATTAATAAATGCGAATTTGATCT 227197  
Qy 161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172  
Db 227196 TTATTTGAAAGTGCAATGACGACGATATCCGAAAA 227161  
RESULT 15  
US-10-158-865-1/c  
Sequence 1, Application US/10158865  
Patent No. 6846651  
GENERAL INFORMATION:  
APPLICANT: Pleischmann et al.  
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag  
Patent No. 6846651  
TITLE OF INVENTION: Thereof, and Uses Thereof  
FILE REFERENCE: PB186P2C1D1  
CURRENT APPLICATION NUMBER: US/10/158,865  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 09/557,884  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/476,102  
PRIOR FILING DATE: 1995-04-21  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1830121  
TYPE: DNA  
ORGANISM: Haemophilus influenzae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (4747)..(4747)  
FEATURE:  
OTHER INFORMATION: n equals a,t,c, or g  
NAME/KEY: misc feature  
LOCATION: (9921)..(9921)  
FEATURE:  
OTHER INFORMATION: n equals a,t,c, or g  
NAME/KEY: misc feature  
LOCATION: (10150)..(10150)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (29298)..(29298)

OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (36543)..(36543)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (36551)..(36551)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (36636)..(36636)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (40808)..(40810)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (44416)..(44416)  
OTHER INFORMATION: n equals a,t,c, or g  
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NAME/KEY: misc feature  
LOCATION: (44905)..(44905)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
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LOCATION: (44975)..(44975)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (45593)..(45593)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (45732)..(45732)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (47036)..(47036)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (51334)..(51334)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (51602)..(51602)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (51786)..(51786)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (51805)..(51805)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (55369)..(55369)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (65309)..(65309)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (65313)..(65313)  
OTHER INFORMATION: n equals a,t,c, or g  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (80024)..(80024)  
OTHER INFORMATION: n equals a,t,c, or g

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? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (100091) ..(100091)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (102696) ..(102696)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (105121) ..(105121)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (107248) ..(107248)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (117136) ..(117136)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (119750) ..(119750)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (119924) ..(119924)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (120038) ..(120038)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (121344) ..(121344)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (122167) ..(122167)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (122336) ..(122336)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (131340) ..(131340)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (131360) ..(131360)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (139910) ..(139910)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (140398) ..(140398)
? OTHER INFORMATION: n equals a,t,c, or g
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? LOCATION: (142750) ..(142750)
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? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (145058) ..(145058)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (145171) ..(145171)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:

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? NAME/KEY: misc_feature
? LOCATION: (145942) ..(145942)
? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
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? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
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? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature
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? OTHER INFORMATION: n equals a,t,c, or g
? FEATURE:
? NAME/KEY: misc_feature

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Alignment Scores:
Pred. No.: 2.89e+05 Length: 1830121
Score: 75.00 Matches: 44
Percent Similarity: 35.9% Conservative: 25
Best Local Similarity: 22.9% Mismatches: 81
Query Match: 8.0% Indels: 42
DB: 3 Gaps: 8

```

US-10-507-132-2 (1-172) x US-10-158--865-1 (1-1830121)

```

QY 15 AepTyrLeuGlyLeuMetCysValTyrGluTPrAlaSPSerTyrAspSerLysAsp 34
    |||||
Db 227712 GATTATCCGCAACTTGTACTTACTTCTTATGAGTTAACTTCCGATCCGTGTTACAA 227653
    |||||
QY 35 TyrAspArgLeuArgLysValIleAlaProthLeuArgIleAsp----- 49
    |||||
Db 227652 AAAAGTCGGTAAGAAACGANTGTTGCGAGATTTTACCAATATTGTTGCGAGAT 227593
    |||||
QY 50 -----TyrArgSerPheLeuAspLys----- 56
    |||||
Db 227592 ATTGTCATCTTATTCCTAACATACTTTTTCGCCAAATCTATGCTAGGTGAGCAAGA 227533
    |||||
QY 57 ---LeuTyrGluAlaMetProAlaGluIupheValGlyMetValSerSerLysGlnMet 75
    |||||
Db 227532 TCTGTTGGGAGCGAGTGTGCGAAGAACAG-----CTCTTTTCCCAAAATCAAAT 227482
    |||||
QY 76 LeuGlyAspProthLeuArgLysGlnIleAspIleGlyLysArgTyrGluLysVal 95
    |||||
Db 227481 AGTAAACTGTCCTCATTAATAATTCGT-----ATTGTTATGATGATTTA 227437
    |||||
QY 96 SerGluAspGluValIleGlyTyr-----HisGln-----Leu 106
    |||||
Db 227436 TCTCTGAATCAAAACCTTGCATGCGATTAAATCAATTAATGACATCTGATTATTA 227377
    |||||
QY 107 ArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlnHis 126
    |||||
Db 227376 CGAGTTGAATCAACAGAGATGAGCTGCAAGAAATTCGCAACGCGCAAAAGCGCAT 227317
    |||||
QY 127 AlanHisSerAlaSerLeuHisIleTyrLysIleAspGlyValIleLysPheIleGly 146
    |||||
Db 227316 TTTCAAATTAATGCTTGTGAGCTGCTGCTGATTTTAATGATTCCTGACGATTTCAAT 227257
    |||||
QY 147 Leu-----LysProAspIleArgTyrGly-----GluPheAspPheAspArg 160
    |||||
Db 227256 TTAATTCATTAACAAAGCCAGATTAACAAATAATGCTATTAATAATCGGAAATTTGATTCGT 227197
    |||||
QY 161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
    |||||
Db 227196 TTAATTTGAAGTCGATGACGACGATATCCGAAAA 227161
    |||||

```

Search completed: December 4, 2006, 19:39:17  
Job time : 1182 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 4, 2006, 19:04:14 ; Search time 525 Seconds  
(without alignments)  
3426.362 Million cell updates/sec

Title: US-10-507-132-2  
Perfect score: 942  
Sequence: 1 MCSQVQKSDIEITFDYGLM.....WGEFDFRIFEDGRTFGDK 172

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5244920 segs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frames.p2n.model -DSV=xlp  
-Q=/abs/ABSSMB.spool/US10507132/runat\_04122006\_143849\_11068/app\_query.fastc\_1  
-DB=N.Geneseq -QMT=fastcap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes03p  
-USER=US10507132.CCN 1.1.1147 @runat\_04122006\_143849\_11068 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq 8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	942	100.0	516	10	ADCI6580 Scytalone
2	938	99.6	516	10	ADCI6592 Scytalone
3	938	99.6	600	10	ADCI6602 Scytalone

4	938	99.6	610	10	ADCI6603	Adci6603 Scytalone
5	133	19.4	467	8	ABZ52566	Abz52566 Aspergill
6	94.5	10.0	692	9	ADA28757	Ada28757 DNA encod
7	87.5	9.3	110000	14	ABBA42401_09	Continuation (10 o
8	87	9.2	2775	10	AAD57634	Aad57634 Rice dise
9	86.5	9.2	48622	14	ABE39158	Aeb39158 L. pneumo
10	86.5	9.2	88876	14	ABE39175_09	Continuation (10 o
11	86.5	9.2	110000	14	ABE39175_09	Continuation (10 o
12	86.5	9.2	110000	14	ABE42736_2	Continuation (3 of
13	85	9.0	864	2	AA14439	Aa14439 H. pylori
14	84	8.9	850	2	AA172504	Aa172504 Mouse SMA
15	84	8.9	1017	10	ADF00192	Adf00192 Bacterial
16	84	8.9	1454	13	ADK60282	Adk60282 Plant full
17	84	8.9	3154	13	ADS31849	Ads31849 Mouse win
18	84	8.9	3154	13	ADU86485	Adu86485 Mouse win
19	84	8.9	3154	15	AED95374	Aed95374 Mouse wnt
20	83	8.8	374	8	ABZ55170	Abz55170 Aspergill
21	83	8.8	2016	4	AA454512	Aa454512 Fructan e
22	83	8.8	3007	2	AAQ68842	Aaq68842 Plant bll
23	82.5	8.8	88232	11	ACN44980	Act44980 Mouse gen
24	81	8.6	1047	9	ADA27222	Ada27222 Human NOV
25	81	8.6	1070	4	ADA20986	Ada20986 Human wnt
26	81	8.6	1070	9	ADA38095	Ada38095 WNT-7B DN
27	81	8.6	1070	9	ADA27233	Ada27233 Human NOV
28	81	8.6	1350	12	ADQ79685	Adq79685 Benzocate
29	81	8.6	1350	12	ADQ79682	Adq79682 Benzocate
30	81	8.6	2160	9	ADA27231	Ada27231 Human NOV
31	81	8.6	2250	12	ADO22235	Ado22235 Human WNT
32	81	8.6	2250	13	ADU86447	Adu86447 Human wnt
33	81	8.6	2250	15	AED95372	Aed95372 Human wnt
34	81	8.6	6312	12	ADQ79681	Adq79681 Benzocate
35	80.5	8.5	2280	6	ABZ78215	Abz78215 A. niger
36	80.5	8.5	2503	10	ADC07803	Adc07803 Rice DNA
37	80	8.5	1070	11	ADM10596	Adm10596 Human WNT
38	80	8.5	2074	4	AA454511	Aa454511 Fructan e
39	79.5	8.4	4041	4	AB102973	Ab102973 Drosophil
40	79.5	8.4	20510	4	AB102972	Ab102972 Drosophil
41	79	8.4	2109	13	ADT48723	Adt48723 Bacterial
42	79	8.4	11096	6	ABK81962	Abk81962 cDNA enco
43	79	8.4	349980	6	ABO81947	Abg81947 Bifidobac
44	78.5	8.3	650	10	ADB31379	Adg31379 Human dia
45	78.5	8.3	1458	6	ADA40506	Ada40506 Infectio

## ALIGNMENTS

RESULT 1	
ADCI6590	ADCI6590 standard; DNA; 516 BP.
XX	XX
XX	ADCI6590;
XX	XX
DT	18-DEC-2003 (first entry)
XX	XX
DE	Scytalone dehydrogenase gene #SEQ ID 1.
XX	XX
KW	Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
XX	XX
XX	gene; da.
XX	XX
OS	Magnaporthe grisea.
XX	XX
FH	Key
FT	CDS
FT	1..516
FT	/tag= a
FT	/product= "scytalone dehydrogenase"
FT	/partial
FT	/note= "no stop codon"
XX	XX
PN	MO200307628-A1.
PD	18-SEP-2003.
XX	XX
PF	24-FEB-2003; 2003WO-JP001980.

```
XX 12-MAR-2002; 2002JP-0006955.
XX (TSUB ) KOMIAI CHEM IND CO LTD.
XX Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX MPI; 2003-748394/70.
XX P-PSDB; ADCl6591.
XX
XX Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
XX for SCDH inhibitors and evaluating sensitivity to them.
XX
XX Example 2; SEQ ID NO 1; 50bp; Japanese.
XX
XX The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
XX that functions in the presence of an inhibitor, comprising an optionally
XX mutated, defined amino acid sequence given in the specification. Also
XX disclosed is a method for evaluating rice blast fungus (Pyricularia
XX oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
XX inhibitors. The gene is useful for screening for new SCDH inhibitors and
XX evaluating sensitivity to them. The current sequence represents the
XX Scytalone dehydrogenase gene sequence.
XX
XX Sequence 516 BP; 119 A; 151 C; 155 G; 91 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.35e-107 Length: 516
XX Score: 942.00 Matches: 172
XX Percent Similarity: 100.0% Conservative: 0
XX Best Local Similarity: 100.0% Mismatches: 0
XX Query Match: 100.0% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-507-132-2 (1-172) x ADCl6590 (1-516)
XX
XX 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
XX 1 ATGGGCTTCCCAAGTTCAAAAGAGCGATGAGTAACTTCTCAGACTACCTGGGCTTCATG 60
XX
XX 21 ThrCysValTyrGluTrrAlaAspSerTyrAspSerLysAspTrrAspArgLeuArgLys 40
XX 61 ACTGCGCTATGATAGGCGACACACTCAGACTCCAAAGACTGGATAGCGCTGCAGAAAG 120
XX
XX 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrrGluAla 60
XX 121 GTCATTGGCCCTACTCTGGCGCATGACTACCGCTCTTCTCGACAAAGCTCTGGAGGGA 180
XX
XX 61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
XX 181 ATGCCCGCGCAGAGAGTTCCGTCGGCATGCTCGAGCAAGCAGATGCTGGGCGACCCCAAC 240
XX
XX 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrrGluLysValSerGluAspGluVal 100
XX 241 CTCGCGACGAGACATTCATCGCGGACACGCTGGGAAAGGTGTCGAGACGAGGTC 300
XX
XX 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
XX 301 ATCGGCTACCAACAGCTGGCGCTCCGCGACAGAGATTACAAGACACACATCAAGAGAG 360
XX
XX 121 ValThrMetLysGlyHisAlaHisSerAlaMetLeuHisTrrTyrLysLysIleAspGly 140
XX 361 GTCAACCATAAAGGGCCACCGCCACTCGGCAAACCTTCACCTGATACAAGAAAGATCGAGGC 420
XX
XX 141 ValTrrLysPheIleArgLysPheAspIleArgTrrGlyGluPheAspPheArg 160
XX 421 GTCGGAAGTTCGCCGCTCAAGCCGATATCCGCTGGGCGAGTTGACCTTTCACAG 480
XX
XX 161 IlePheGluAspGlyArgGluTrrPheGlyAspLys 172
XX 481 ATCTTTGAGGACGAGACGGAGACCTTTGGCGACAA 516
XX
XX RESULT 2
```

```
ADCl6592
XX ID ADCl6592 standard; DNA; 516 BP.
XX AC ADCl6592;
XX
XX 18-DEC-2003 (first entry)
XX
XX Scytalone dehydrogenase gene #SEQ ID 3.
XX
XX Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
XX gene; ds.
XX
XX Magnaporthe grisea.
XX
XX Key Location/Qualifiers
XX CDS 1..516
XX /*tag= a
XX /product= "scytalone dehydrogenase"
XX /partial
XX /note= "no stop codon"
XX
XX MO2003076628-A1.
XX
XX 18-SEP-2003.
XX
XX 24-FEB-2003; 2003WO-JP001980.
XX
XX 12-MAR-2002; 2002JP-0006955.
XX (TSUB ) KOMIAI CHEM IND CO LTD.
XX Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX MPI; 2003-748394/70.
XX P-PSDB; ADCl6593.
XX
XX Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
XX for SCDH inhibitors and evaluating sensitivity to them.
XX
XX Example 2; SEQ ID NO 3; 50bp; Japanese.
XX
XX The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
XX that functions in the presence of an inhibitor, comprising an optionally
XX mutated, defined amino acid sequence given in the specification. Also
XX disclosed is a method for evaluating rice blast fungus (Pyricularia
XX oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
XX inhibitors. The gene is useful for screening for new SCDH inhibitors and
XX evaluating sensitivity to them. The current sequence represents the
XX Scytalone dehydrogenase gene sequence.
XX
XX Sequence 516 BP; 118 A; 151 C; 156 G; 91 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 4.27e-107 Length: 516
XX Score: 938.00 Matches: 171
XX Percent Similarity: 100.0% Conservative: 1
XX Best Local Similarity: 99.4% Mismatches: 0
XX Query Match: 99.6% Indels: 0
XX DB: 10 Gaps: 0
XX
XX US-10-507-132-2 (1-172) x ADCl6592 (1-516)
XX
XX 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
XX 1 ATGGGCTTCCCAAGTTCAAAAGAGCGATGAGTAACTTCTCAGACTACCTGGGCTTCATG 60
XX
XX 21 ThrCysValTyrGluTrrAlaAspSerTyrAspSerLysAspTrrAspArgLeuArgLys 40
XX 61 ACTCGCTATGATAGGCGACACACTCAGACTCCAAAGACTGGATAGCGCTGCAGAAAG 120
XX
XX 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrrGluAla 60
XX 121 GTCATTGGCCCTACTCTGGCGCATGACTACCGCTCTTCTCGACAAAGCTCTGGAGGGA 180
XX
```

```

QY 61 MetProAlaGluGluPheValGlyMetValSerSerIleuGluIleuGlyAspProThr 80
Db 181 ATCCCGGCCGAGAGTTGTCGGCATGGTCTCAGACAGAGGAGTGGTGGAGCCACC 240
QY 81 LeuArgThrGlnHisPheIleGlyIleThrArgTrpGluValSerGluAspGluVal 100
Db 241 CTCGGACCGAGACCTTCATCGCGGACCGCTGGGAGAGAGTGTCCGACGACGAGTTC 300
QY 101 ILeGlyThrHisGlnLeuArgValProHisGlnArgTyrIleAspThrThrMetGly 120
Db 301 ATGGGCTACACACAGCTGCGCTCCGACACAGAGTACAGACACACATGAAAGGAG 360
QY 121 ValThrMetGlyHisIleHisSerAlaAsnLeuHisTrpTyrIleValIleAspGly 140
Db 361 GTCAACCATGAAGGAGCCACGCCCACTCGGCMAACCTTCACTGTACAAAGAGATCGAGGC 420
QY 141 ValTrpIlePheAlaGlyLeuIleValProAspIleArgTrpGlyGluPheAspPheAspArg 160
Db 421 GTCTGGAAGTTCGCCGCGCTCAAGCCGATATCCGCTGGGGCGAGTTCCACTTGCACAG 480
QY 161 IlePheGluAspGlyIleArgIleThrPheGlyAspLys 172
Db 481 ATCTTGAGGACGAGACGGAGACCTTTGGCGACAAA 516

RESULT 3
ADCl6602
ID ADCl6602 standard; DNA; 600 BP.
AC ADCl6602;
XX
XX 18-DEC-2003 (first entry)
DT
DE Scytalone dehydrogenase DNA #1.
KM Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
XX gene; ds.
OS Magnaporthe grisea.
XX
XX WO2003076628-A1.
XX
XX 18-SEP-2003.
XX
XX 24-FEB-2003; 2003WO-JP001980.
XX
XX 12-MAR-2002; 2002JP-00066955.
XX
XX (TSUB ) KUMIAI CHEM IND CO LTD.
XX
XX Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX WPI; 2003-748394/70.
XX
XX Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
XX PT for SCDH inhibitors and evaluating sensitivity to them.
XX
XX Example 2; Fig 3; 50pp; Japanese.
XX
XX The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
XX CC that functions in the presence of an inhibitor, comprising an optionally
XX CC mutated, defined amino acid sequence given in the specification. Also
XX CC disclosed is a method for evaluating rice blast fungus (Pyricularia
XX CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
XX CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
XX CC evaluating sensitivity to them. The current sequence represents the
XX CC Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
XX CC given in ADCl6590.
SQ Sequence 600 BP; 146 A; 176 C; 168 G; 110 T; 0 U; 0 Other;

Alignment Scores: 5.22e-107 Length: 600
Pred. No.:

```

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Score: 938.00 Matches: 171
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.4% Mismatches: 0
Query Match: 99.6% Indels: 0
DB: 10 Gaps: 0

US-10-507-132-2 (1-172) x ADCl6602 (1-600)
QY 1 MetGlySerGlnValGlnIleSerAspGluIleThrPheSerAspTyrIleuGlyLeuMet 20
Db 81 ATGGGTTGGCAAGTTCAAAAGAGCATGATGATACCTTCTCAGACTACCTGGGCTCATG 140
QY 21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
Db 141 ACTTGCGTATGATGAGTGGGACAGACGTCACGACTCCAAAGACTGGGATAGGCTCGAAAG 200
QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
Db 201 GTCAATTGGCCTACTCTGGCATTTGACTACCGCTCTTCTCGACAAAGCTTGGGAGGCA 260
QY 61 MetProAlaGluGluPheValGlyMetValSerSerIleuGluIleuGlyAspProThr 80
Db 261 ATGGCGGCGGAGAGTTCGTGGCATGGTCTGACGACAGAGTGTCTGGGAGAGTTCGAGGACGAGTC 320
QY 81 LeuArgThrGlnHisPheIleGlyIleThrArgTrpGluValSerGluAspGluVal 100
Db 321 CTCGGACCGACACACTTCATCGCGGACCGCTGGGAGAGAGTGTCCGAGGACGAGTTC 380
QY 101 ILeGlyThrHisGlnLeuArgValProHisGlnArgTyrIleAspThrThrMetGlyGlu 120
Db 381 ATCGGCTACACACAGCTGCGCTCCGACACAGAGTACMAAGACACACATGAAGAG 440
QY 121 ValThrMetGlyHisIleHisSerAlaAsnLeuHisTrpTyrIleValIleAspGly 140
Db 441 GTCAACCATGAAGGAGCCACGCCCACTCGGCMAACCTTCACTGTGACAAAGAGATCGAGGC 500
QY 141 ValTrpIlePheAlaGlyLeuIleValProAspIleArgTrpGlyGluPheAspPheAspArg 160
Db 501 GTCTGGAAGTTCGCCGCGCTCAAGCCGATATCCGCTGGGGCGAGTTCCACTTGCACAG 560

RESULT 4
ADCl6603
ID ADCl6603 standard; DNA; 610 BP.
AC ADCl6603;
XX
XX 18-DEC-2003 (first entry)
DT
DE Scytalone dehydrogenase DNA #2.
KM Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
XX gene; ds.
OS Magnaporthe grisea.
XX
XX WO2003076628-A1.
XX
XX 18-SEP-2003.
XX
XX 24-FEB-2003; 2003WO-JP001980.
XX
XX 12-MAR-2002; 2002JP-00066955.
XX
XX (TSUB ) KUMIAI CHEM IND CO LTD.
XX
XX Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX WPI; 2003-748394/70.
XX
XX

```

PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening  
PT for SCDH inhibitors and evaluating sensitivity to them.

PS Example 2; Fig 4; 50pp; Japanese.

XX The invention relates to a gene encoding scytalone dehydrogenase (SCDH),  
CC that functions in the presence of an inhibitor, comprising an optionally  
CC mutated, defined amino acid sequence given in the specification. Also  
CC disclosed is a method for evaluating rice blast fungus (Pyricularia  
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase  
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and  
CC evaluating sensitivity to them. The current sequence represents the  
CC Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is  
CC given in ADCl6592.

XX Sequence 610 BP; 148 A; 179 C; 170 G; 113 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	5,34e-107	Length:	610
Score:	938.00	Matches:	171
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.4%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-2 (1-172) x ADCl6603 (1-610)

QY 1 MetGlySerGlnValGlnIysSerAspGluIleThrPheSerAspTyrIleuGluMet 20

DB 81 ATGGGTTCCCAAGTTCAAAAGAGCGATGAGATTAACCTTTCAGACTACCTGGGCTCATG 140

QY 21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerTyrAspTrpAspArgLeuArgLys 40

DB 141 ATTGGCTTATGAGTGGGCAAGACGCTACGACTCCAAAGACTGGATGGCTGGGAAG 200

QY 41 ValIleAlaProThrIleuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

DB 201 GTCATTCGCCCTACTCTCGCGCATTCGACTACCGCTCTTCGACAAAGCTTGGGAGGCA 260

QY 61 MetProAlaGluGlnPheValGlnMetValSerSerTyrGlnMetLeuGluLysProThr 80

DB 261 ATGGCGGCGGAGAGTTCGCGCATGATCTCGAGCAAGAGGTGCTGGGCGACCCGAC 320

QY 81 LeuArgTrpGlnHisPheIleGlyGlyThrArgTrpGluValSerGluAspGluVal 100

DB 321 CTCGCGAGCAGACGACTTCATTCGCGGCGGCAAGGCTGGGAAGAGTGTCCAGAGACGAGT 380

QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrIleAspThrThrMetLysGlu 120

DB 381 ATCGGCTACACAGCTGCGCGCTCCGCGACAGAGGTACAGAGACCAATGAAGAG 440

QY 121 ValThrMetLysGlnHisAlaHisSerAlaAsnLeuHisTrpTyrTyrIleValIleAspGly 140

DB 441 GTCACCATTAAGGGCCACGCCCACTCGGCAAACTTCACCTGGATCAAGAGATCGAGG 500

QY 141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160

DB 501 GTCGGAATTCGGCGGCTCAAGCCGATATCCGCTGGGGGAGATTGCACTTTGACAG 560

QY 161 IlePheGluAspGlyValArgGluThrPheGlyAspLys 172

DB 561 ATCTTTAGAGACGAGCGGAGACCTTTGGCGAATA 596

RESULT 5

AB252566 standard; cDNA; 697 BP.

XX AB252566;

DT 28-MAR-2003 (first entry)

DE Aspergillus oryzae polynucleotide SEQ ID NO 1679.

KW Aspergillus oryzae; fermentation; fungus; industrial; EST;  
KW expressed sequence tag; gene; ss.

OS Aspergillus oryzae.

PN WO200279476-A1.

XX 10-OCT-2002.

XX 22-MAR-2002; 2002MO-IB000890.

XX 30-MAR-2001; 2001JP-00098371.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (NARE-) NAT RES INST BREWING.

XX (NORQ) NAT FOOD RES INST MIN AGRIC.

XX Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;

XX Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;

XX WPI; 2003-046817/04.

XX Claim 1; SEQ ID NO 1679; 48pp + Sequence listing; Japanese.

XX The invention relates to a polynucleotide having any of 6006 specific

XX sequences (AB250888-AB256893), which are expressed by a fungus under

XX specific culture conditions including one or more of eutrophic,

XX oligotrophic, solid, early germination, alkaline, high temperature, low

XX temperature or maltose culture or polynucleotides stringently hybridizing

XX to these sequences. The polynucleotides are useful for monitoring the

XX progress of fermentation and the growth conditions of a fungus,

XX especially of Aspergillus oryzae which is widely used in industrial

XX fermentation. Also monitoring for fungal contamination. Note: The

XX CC sequence data for this patent did not form part of the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 697 BP; 170 A; 153 C; 180 G; 189 T; 0 U; 5 Other;

US-10-507-132-2 (1-172) x AB252566 (1-697)

QY 17 LeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerTyrAsp 36

DB 184 CTCGATGTNAGAACCTCTTCACGACCTGGGCAACTGCTTAAGACACCAATCCCGGAT 243

QY 37 ArgLeuArgLysValIleAlaProThrIleuArgIleAspTyrArgSerPheLeuAspLys 56

DB 244 GGTATGCTGACTATATTTGGCGGCCGCAATTCAGATGGATTTCTGGCGGCGGACACTA 303

QY 57 LeuTrpGluAlaMetProAlaGluGlnPheValGlnMetValSerSerTyrGlnMetLeu 76

DB 304 AAGGCTACCGGCTGGAGATTTTTCGTTTATTCGAACACTACCTAGTTACAGACAGCTA 363

QY 77 GlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluValSer 96

DB 364 GGGAAACCCGATATCCAGTGAATCATTTTATTCGCTGCTCGCAATGGGCGGAACTG 423

QY 97 GluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThr 116

DB 424 GAAATAAAACGTAAAGGTTGTTTCAATATCATGGCGGTTCATCGAGGCGCCCAATAAGAC 483

QY 117 ThrMetLysGluValThrMetLysGlnHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136



```
Db 484 GGTGTCGGGTGCTGCTGCTAAGGC-----CAAGGGGTAAACACCATGATTTTAAAG 537
Qy 137 LysileaspIlyValTrrplysPheAlaGlyLeuLyproaspIleaGrtpGlyIuPhe 156
Db 538 CAGGTGAAGAGGAGTNGAAGATCGACGATTAAGTTGCTGCTTCATCGAGAGGT 597
Qy 157 AspPheaspArgIlePhe 162
Db 598 GATTTCGAGGCGCATGTTT 615

RESULT 6
ADA28757
ID ADA28757 standard; DNA; 462 BP.
AC ADA28757;
XX
XX 20-NOV-2003 (first entry)
XX
XX DNA encoding Acinetobacter baumannii protein #44.
XX
XX ds: gene; Acinetobacter baumannii; bacterial disease; antibacterial;
XX vaccine; plant biocontrol agent.
XX
XX Acinetobacter baumannii.
XX
XX US6562958-B1.
XX
XX 13-MAY-2003.
XX
XX 04-JUN-1999; . 99US-00328352.
XX
XX 09-JUN-1998; 98US-0088701P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton G, Bush D;
XX
XX WPI: 2003-576092/54.
XX
XX P-PDB; ADA32883.
XX
XX
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX vaccines, as targets for antibacterial drugs, or as biocontrol agents for
XX plants.
XX
XX Example; SEQ ID NO 44; 328bp; English.
XX
XX The invention relates to isolated Acinetobacter baumannii nucleic acids.
XX The A. baumannii nucleic acids and polypeptides are useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX vaccines, as targets for antibacterial drugs, to detect the presence of
XX A. baumannii and other Acinetobacter species in a sample, in screening
XX compounds for the ability to interfere with the A. baumannii life cycle
XX or to inhibit A. baumannii infection, and as biocontrol agents for
XX plants. The present sequence represents DNA encoding an A. baumannii
XX protein.
XX
XX Sequence 462 BP; 135 A; 76 C; 98 G; 153 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0447 Length: 462
Score: 94.50 Matches: 31
Percent Similarity: 43.7% Conservative: 28
Best Local Similarity: 23.0% Mismatches: 59
Query Match: 10.0% Indels: 17
DB: 9 Gaps: 6

US-10-507-132-2 (1-172) x ADA28757 (1-462)
Qy 15 AspTrrleuGlyLeuMetTrrCysValTrrGlyTrrPalaSpSerTrrAspSerTrrAsp 34
Db 37 GACTACCATCGTATTTTGAAGGTCAATTACGCGTTTCAATTGGTTTGTGACCAAAAAAT 96
```

```
Qy 35 TrrAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTrrArgSerPheLeu 54
Db 97 TGGGATGCGCTTTTATATAGATGTTTACCGCATCACTGAGGTGACATTTTGCAGTTTGA 156
Qy 55 AspIlyLeuTrrPalaMetProAlaGluIuPheValGlyMetValSerSerIySgln 74
Db 157 GGGAGCCCTTTATGTTGTTGTCTTCATGATATTAAGGT-----TCAGGCAACA 210
Qy 75 MetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyIyThrArgTrrGlyLys 94
Db 211 GCTTTGTCACAT-----TTGCGGCTACAGACAAATTTAAGCAATCCT---CTTATTCG 261
Qy 95 ValSerGluAspGluValIleGlyTrrHisSglnLeuArgValProHisGlnArgTrrLys 114
Db 262 ATTGAAACAAATGATCACA-----TGTTGGAATGATTAATTAATTAATTTATCGT 309
Qy 115 AspTrrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrrp 134
Db 310 -----TTTTGGAATAATGATTATTTTCATTCCTTTGGTGCCTATTAT 351

Qy 135 Tyr-----LysIlyleaspIlyValTrrplysPheAlaGlyLeu 147
Db 352 TTTACTTTGGCAAAACACAGGCGCATATGAAATAATTCGGAATT 396
```

## RESULT 7

Continuation (10 of 34) of AEB42401 from base 900001 (L. pneumophila DNA SEQ ID NO 6733.  
WP Sequence split into 34 fragments LOCUS AEB42401 Accession Aeb42401

WP	Fragment Name	Begin	End
WP	AEB42401_00	1	110000
WP	AEB42401_01	100001	210000
WP	AEB42401_02	200001	310000
WP	AEB42401_03	300001	410000
WP	AEB42401_04	400001	510000
WP	AEB42401_05	500001	610000
WP	AEB42401_06	600001	710000
WP	AEB42401_07	700001	810000
WP	AEB42401_08	800001	910000
WP	AEB42401_09	900001	1010000
WP	AEB42401_10	1000001	1110000
WP	AEB42401_11	1100001	1210000
WP	AEB42401_12	1200001	1310000
WP	AEB42401_13	1300001	1410000
WP	AEB42401_14	1400001	1510000
WP	AEB42401_15	1500001	1610000
WP	AEB42401_16	1600001	1710000
WP	AEB42401_17	1700001	1810000
WP	AEB42401_18	1800001	1910000
WP	AEB42401_19	1900001	2010000
WP	AEB42401_20	2000001	2100000
WP	AEB42401_21	2100001	2210000
WP	AEB42401_22	2200001	2310000
WP	AEB42401_23	2300001	2410000
WP	AEB42401_24	2400001	2510000
WP	AEB42401_25	2500001	2610000
WP	AEB42401_26	2600001	2710000
WP	AEB42401_27	2700001	2810000
WP	AEB42401_28	2800001	2910000
WP	AEB42401_29	2900001	3010000
WP	AEB42401_30	3000001	3110000
WP	AEB42401_31	3100001	3210000
WP	AEB42401_32	3200001	3310000
WP	AEB42401_33	3300001	3345687

Alignment Scores:  
Pred. No.: 522 Length: 110000  
Score: 87.50 Matches: 27  
Percent Similarity: 40.4% Conservative: 19  
Best Local Similarity: 23.7% Mismatches: 51  
Query Match: 9.3% Indels: 17  
DB: 14 Gaps: 2



PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;  
 PI Jarraud S;  
 XX  
 DR WPI; 2005-388305/40.

PT New genome of *Legionella pneumophila* Paris strain and derived  
 PT polypeptides, useful for detection or identification of the strain and  
 PT for treatment and prevention of infections.

PS Example 9; SEQ ID NO 3490; 660bp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)  
 CC from *Legionella pneumophila* Paris strain. (I), and their related  
 CC sequences or fragments, are useful as primers and probes for detection  
 CC and amplification, including differentiation between the Paris and  
 CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant  
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
 CC specific antibodies (Ab), also used for detection/identification of  
 CC *Legionella*, and some (II), specifically those involved in synthesis of  
 CC surface proteins, are targets for identification of inhibitors. (II), or  
 CC vectors that contain (I), are useful as vaccines and immunogenic  
 CC compositions, for treatment and prevention of infections by *L.*  
 CC *pneumophila*. The present sequence represents a *L. pneumophila* DNA.

XX Sequence 48622 BP; 15468 A; 7892 C; 9212 G; 16050 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.:	232	Length:	48622
Score:	86.50	Matches:	26
Percent Similarity:	40.4%	Conservative:	20
Best Local Similarity:	22.8%	Mismatches:	51
Query Match:	9.2%	Indels:	17
DB:	14	Gaps:	2

US-10-507-132-2 (1-172) x AEB39158 (1-48622)

OY 74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg----- 91

DB 41463 CAATATCTGGGGCATGGGCGCATGTCATAGTGAGAGTGAAGAAACGCTTAAATAATC 41404

OY 92 -----TrrGluLysValSerGluAspGluValIleGlyTyrHisGlnLeu 106

DB 41403 AGTCGTCACAGATATGGAACAAATCAATCACTTAATGATTTAGGCATACCTATATATC 41344

OY 107 ArgValProHisGlnArgTyrLys-----AspThr 116

DB 41343 CGCATACCAATCAAGGATACCAATTGGAAGAAACCTTTAATCTGCTAGATCCCAATGAA 41284

OY 117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136

DB 41283 ATTACCAAGCAATTTACACAGCAAGATTATGACCAACCGTTTAACCTGATTTATTTACA 41224

OY 137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156

DB 41223 TCGATTGACATCAACCAACCGCTTACGAAAGATCTGCTTCAAGCTCAGCCGTGCAAAAT 41164

OY 157 AspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170

DB 41163 TCGTGCATGAAATGCAAACTCAAGGAGAGGCGGCTTTGA 41122

RESULT 10

AEB35710/C

XX AEB35710 standard; DNA; 88876 BP.

XX AEB35710;

XX 08-SEP-2005 (first entry)

XX L. pneumophila DNA SEQ ID NO 42.

XX detection; infection; Antibacterial; Vaccine; ds; gene.

XX *Legionella pneumophila*.

XX WO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004WO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP) INSP PASTEUR.

XX (INRM) INRM INST NAT SANTE & RECH MEDICALE.

XX (UJLY-) UNIT LYON 1 BERNARD CLAUDE.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Buehler C, Tichit M, Etienne J, Ma L, Caralet C, Glaeser P;

XX Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;

XX Jarraud S;

XX WPI; 2005-388305/40.

PT New genome of *Legionella pneumophila* Paris strain and derived  
 PT polypeptides, useful for detection or identification of the strain and  
 PT for treatment and prevention of infections.

PS Claim 1; SEQ ID NO 42; 660bp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)  
 CC from *Legionella pneumophila* Paris strain. (I), and their related  
 CC sequences or fragments, are useful as primers and probes for detection  
 CC and amplification, including differentiation between the Paris and  
 CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant  
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
 CC specific antibodies (Ab), also used for detection/identification of  
 CC *Legionella*, and some (II), specifically those involved in synthesis of  
 CC surface proteins, are targets for identification of inhibitors. (II), or  
 CC vectors that contain (I), are useful as vaccines and immunogenic  
 CC compositions, for treatment and prevention of infections by *L.*  
 CC *pneumophila*. The present sequence represents a *L. pneumophila* DNA.

XX Sequence 88876 BP; 27350 A; 14957 C; 17861 G; 28707 T; 0 U; 1 Other;

#### Alignment Scores:

Pred. No.:	522	Length:	88876
Score:	86.50	Matches:	26
Percent Similarity:	40.4%	Conservative:	20
Best Local Similarity:	22.8%	Mismatches:	51
Query Match:	9.2%	Indels:	17
DB:	14	Gaps:	2

US-10-507-132-2 (1-172) x AEB35710 (1-88876)

OY 74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg----- 91

DB 48109 CAATATCTGGGGCATGGGCGCATGTCATAGTGAGTGAAGTGAACGCTTAAATAATC 48050

OY 92 -----TrrGluLysValSerGluAspGluValIleGlyTyrHisGlnLeu 106

DB 48049 AGTCGTCACAGATATGGAACAAATCAATCACTTAATGATTTAGGCATACCTATATATC 47990

OY 107 ArgValProHisGlnArgTyrLys-----AspThr 116

DB 47989 CGCATACCAATCAAGGATACCAATTGGAAGAAACCTTTAATCTGCTAGATCCCAATGAA 47930

OY 117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136

DB 47929 ATTACCAAGCAATTTACACAGCAAGATTATGACCAACCGTTTAACCTGATTTATTTACA 47870

OY 137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156

DB 47869 TCGATTGACATCAACCAACCGCTTACGAAAGATCTGCTTCAAGCTCAGCCGTGCAAAAT 47810

OY 157 AspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170

Db 47809 TCCTGCACTGAAATGCAACTCAAGGAGAGGCGCTTTGGA 47768  
RESULT 11  
AEB39175\_09/c  
Continuation (10 of 35) of AEB39175 from base 900001 (L. pneumophila DNA SEQ ID NO 3507.)  
WP Sequence Split into 35 fragments LOCUS AEB39175 Accession Aeb39175  
WP Fragment Name Begin End  
WP AEB39175\_00 1 110000  
WP AEB39175\_01 100001 210000  
WP AEB39175\_02 200001 310000  
WP AEB39175\_03 300001 410000  
WP AEB39175\_04 400001 510000  
WP AEB39175\_05 500001 610000  
WP AEB39175\_06 600001 710000  
WP AEB39175\_07 700001 810000  
WP AEB39175\_08 800001 910000  
WP AEB39175\_09 900001 1010000  
WP AEB39175\_10 1000001 1110000  
WP AEB39175\_11 1100001 1210000  
WP AEB39175\_12 1200001 1310000  
WP AEB39175\_13 1300001 1410000  
WP AEB39175\_14 1400001 1510000  
WP AEB39175\_15 1500001 1610000  
WP AEB39175\_16 1600001 1710000  
WP AEB39175\_17 1700001 1810000  
WP AEB39175\_18 1800001 1910000  
WP AEB39175\_19 1900001 2010000  
WP AEB39175\_20 2000001 2110000  
WP AEB39175\_21 2100001 2210000  
WP AEB39175\_22 2200001 2310000  
WP AEB39175\_23 2300001 2410000  
WP AEB39175\_24 2400001 2510000  
WP AEB39175\_25 2500001 2610000  
WP AEB39175\_26 2600001 2710000  
WP AEB39175\_27 2700001 2810000  
WP AEB39175\_28 2800001 2910000  
WP AEB39175\_29 2900001 3010000  
WP AEB39175\_30 3000001 3110000  
WP AEB39175\_31 3100001 3210000  
WP AEB39175\_32 3200001 3310000  
WP AEB39175\_33 3300001 3410000  
WP AEB39175\_34 3400001 3503610  
Alignment Scores:  
Pred. No.: 696 Length: 110000  
Score: 86.50 Matches: 26  
Percent Similarity: 40.4% Conservative: 20  
Best Local Similarity: 22.8% Mismatches: 51  
Query Match: 9.2% Indels: 17  
Gaps: 2  
US-10-507-132-2 (1-172) x AEB39175\_09 (1-110000)  
QY 74 GlnMetLeuGlyAAspProThrIleuArgThrGlnHisPheIleGlyIleThrArg----- 91  
DB 50898 CAAATACGTGGGCGCATGTGCATGTGGAGTGAATTAGGAAACCGCTTTAAAAATC 50839  
QY 92 -----TrrpGluysValserGluaspGluValIleGlyIleThrHisGlnLeu 106  
DB 50838 AGTCGCTGACGATGAGAAACAATCAATCACTTAAGATTAGGCACTATTATTC 50779  
QY 107 ArgValProHisGlnArgTyrIys-----AspThr 116  
DB 50778 CGCATACCATCAAGATTCATCAATTGGAAGACCTTTATCTCTGTAGACCTCAATGAA 50719  
QY 117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaGlnLeuHisIleStrpTyrIys 136  
DB 50718 ATTACCAAGCAATTACACAGCAAGATTAGCCAAACCGTTTAACTGCATTTATTATTA 50659  
QY 137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156  
DB 50658 TCGATTGACTCAACCAACCGCTACTGAAAGATCTGCTTCAAGCTCAGCGCGTGAATTT 50599

QY 157 AspPheAspArgIlePheGluaspGlyValArgGluThrPheGly 170  
DB 50598 TCCTGCACTGAAATGCAACTCAAGGAGAGGCGCTTTGGA 50557  
RESULT 12  
AEB42736\_2/c  
Continuation (3 of 8) of AEB42736 from base 200001 (L. pneumophila DNA SEQ ID NO 7068.)  
WP Sequence Split into 8 fragments LOCUS AEB42736 Accession Aeb42736  
WP Fragment Name Begin End  
WP AEB42736\_0 1 110000  
WP AEB42736\_1 100001 210000  
WP AEB42736\_2 200001 310000  
WP AEB42736\_3 300001 410000  
WP AEB42736\_4 400001 510000  
WP AEB42736\_5 500001 610000  
WP AEB42736\_6 600001 710000  
WP AEB42736\_7 700001 740626  
Alignment Scores:  
Pred. No.: 696 Length: 110000  
Score: 86.50 Matches: 26  
Percent Similarity: 40.4% Conservative: 20  
Best Local Similarity: 22.8% Mismatches: 51  
Query Match: 9.2% Indels: 17  
Gaps: 2  
US-10-507-132-2 (1-172) x AEB42736\_2 (1-110000)  
QY 74 GlnMetLeuGlyAAspProThrIleuArgThrGlnHisPheIleGlyIleThrArg----- 91  
DB 42889 CAAATACGTGGGCGCATGTGCATGTGGAGTGAATTAGGAAACCGCTTTAAAAATC 42830  
QY 92 -----TrrpGluysValserGluaspGluValIleGlyIleThrHisGlnLeu 106  
DB 42829 AGTCGCTGACGATGAGAAACAATCAATCACTTAAGATTAGGCACTATTATTC 42770  
QY 107 ArgValProHisGlnArgTyrIys-----AspThr 116  
DB 42769 CCATACCATCAAGATTCATCAATTGGAAGACCTTTATCTCTGTAGACCTCAATGAA 42710  
QY 117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAspLeuHisIleStrpTyrIys 136  
DB 42709 ATTACCAAGCAATTACACAGCAAGATTAGCCAAACCGTTTAACTGCATTTATTATTA 42650  
QY 137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156  
DB 42649 TCGATTGACTCAACCAACCGCTACTGAAAGATCTGCTTCAAGCTCAGCGCGTGAATTT 42590  
QY 157 AspPheAspArgIlePheGluaspGlyValArgGluThrPheGly 170  
DB 42589 TCCTGCACTGAAATGCAACTCAAGGAGAGGCGCTTTGGA 42548  
RESULT 13  
AAK14439  
ID AAK14439 standard; DNA, 864 BP.  
XX  
AC AAK14439;  
XX  
DE 31-MAR-1999 (first entry)  
XX  
XX H. pylori GHPO 811 gene.  
XX  
XX GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;  
XX  
XX peptic ulcer disease; ss.  
XX  
OS Helicobacter pylori.  
XX  
FH Key Location/Qualifiers  
FT CDS 37..834  
FT /ftag= a  
PN  
XX MO9843478-A1.

PD	08-OCT-1998.
XX	
PF	01-APR-1998; 98WC-US006371.
XX	
PR	01-APR-1997; 97US-00833457.
PR	24-JUN-1997; 97US-00881227.
PR	29-JUL-1997; 97US-00902615.
XX	
PA	(INMR ) MERIEUX ORAVAY PASTEUR MERIEUX SERUMS.
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Kleantous H, Al-Garawi A, Miller C, Tomb J, Oomen R;
XX	
DR	WPI; 1998-542293/46.
DR	P-PSDB; AAM98720.
XX	
PT	New isolated Helicobacter polynucleotides - used to develop products for
PT	the diagnosis, prevention and treatment of Helicobacter infections and
PT	gastrointestinal diseases.
XS	
XS	Claim 1; Page 1521-1522; 2054pp; English.

CC This sentence represents a polynucleotide of the invention. It was  
CC isolated from *Helicobacter pylori* and encodes a H.pylori GHO protein.  
CC The polypeptide can be used for preventing or treating *Helicobacter*  
CC infections, and gastroduodenal diseases associated with these infections,  
CC including acute, chronic, and atrophic gastritis, and peptic ulcer  
CC diseases, e.g. gastric and duodenal ulcers. They can also be used for the  
CC production of antibodies. The products can also be used for detection and  
CC diagnosis  
CC  
CC Sequence 864 BP, 283 A, 159 C, 198 G, 223 T, 0 U, 1 Other;

Alignment Scores:	
Pred. No.:	1.58
Score:	85.00
Percent Similarity:	41.1%
Best Local Similarity:	23.9%
Query Match:	9.0%
DB:	2
	866
Length:	43
Matches:	31
Conservative:	54
Mismatches:	54
Indels:	8
Gaps:	2

US-10-507-132-2 (1-172) X AAX14439 (1-864)

```

Oy      18  GIVleuemetHrcYsValTYrglu-----TPrAlaaspSerTYaspSerLeu 34
Db      326  GGCATTTTGAATTGTTT-TATCATTTCCGGGCGCTTAGCATAGCTGCAGAACCGCCGT 384
Oy      35  TrpAspArgLeuArgYsValIlealProThrLeuArgIleAspTYArgSerPheLeu 54
Db      385  AGAGTGGCGCTGAAGTGGCGCTTTTGTTGGCTTATGAGAGCGTGGATCTTTAGAGTTTTTA 444
Oy      55  AspArgLeu-----TrpGlualaMetProAlaGluGluPheValGlyMetValSerSer 72
Db      445  TACGATCCGCGCTAATTGGAGAGCGAAAGGAGCGTATGACATCGCTTGATTTGTGTTGAC 504
Oy      73  Lys-----GlnMetLeuGlyAspProThrLeu 81
Db      505  AAACACCCCTAATTGGAAGCGCTTATTATGCCGATGATGGGTGGCCACCCATTATG 564
Oy      82  ArgThrGlnHisPheIleGly-----ThrArgTrpGluYsValSerGlu----- 97
Db      565  CGGCTTACCCGCTCAAGGCGATGCAATTGCCGCCAATGGATGAAATGATATAAAATTTT 624
Oy      98  -----AspGluValIleGlyTYrHisGln----- 105
Db      625  GGTAAAGATATCCGAGAAAGTGGGTGAATGAAGACAGAGACAGCGCAAGAGTGGATGAA 688
Oy      106  -----LeuArgValProHisGlnArgTYrYsAspThrThrMetCys 119
Db      685  AAAGACACTTTCATTATTTTGCAGAAATATGGCTATGAAAGCGGCAAGCGAAGATAAAA 744
Oy      120  GluValThrMetYsGluHisAlaHisSerAlaIleuHisTPrTYrYsValIleAsp 133

```

Db	743	GAAGTGAAGAAAG-----	CATGGCTTAGAAATCCCT	780
Qy	140	GLYValTTPlysePheIaGlyIeuIyProAsp-----	IIaGyTyr	153
		:::	:::	
Db	781	TTTGTCAA-AGATTGCGCAAAATGCCCCACATCTTTAAAAAGAGCGTATATAATGG	835	

RESULT 14  
AAV72504  
AAV72504 standard; cDNA, 850 BP.

DT	20-MAR-2003 (revised)
DT	01-MAR-1999 (first entry)
XX	
DE	Mouse SMAD interacting protein SIP7 cDNA clone Th74.

KM SMAD interacting protein 1; mouse; embryogenesis; differentiation;  
KM cancer; neural disease; immune disease; therapy; diagnosis; ds.

OS Mus sp.

PN W09855512-A2

PD 10-DEC-1998.

PF 28-MAY-1998; 98WO-EP003193.

PR 02-JUN-1997; 97EP-00201645.

PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG

PI Verschueren K, Remacle J, Huylebrouck D;

DR WPI; 1999-045732/04.

PT New SMAD interacting proteins obtained by a two hybrid screening assay -  
PT useful for diagnosing developmental disorders and e.g. cancer, immune and  
PT neural disease.

PS Claim 18; Page 38; 48pp; English.

CC This cDNA clone (7b74) comprises a novel SMD interacting protein paring  
CC CDNA, designated 7b74. By using Smd1 C-domain fused to Gal4 DNA-binding  
CC domain and a mouse embryo cDNA as bait and prey, respectively, in a two-  
CC hybrid screen, a partial Smd4 and Smd interacting protein cDNAs (see  
CC AA1723202-05 and AA172512-25), were obtained, including 7b1 (see  
CC AA88318). The invention also provides recombinant expression vectors,  
CC transduced cells, a method of screening for compounds  
CC which affect the interaction between SMD and SMD interacting protein,  
CC transgenic animals useful for testing medicaments and as therapy models,  
CC and a method for post-transcriptional regulation of gene expression by  
CC members of the TGR-beta superfamily by manipulation or modulation of the  
CC interaction between Smd function and/or activity and mRNA stability.  
CC STPs and nucleic acids encoding them are useful therapeutically and in  
CC claimed kits for diagnosing diseases or disorders related to cancer,  
CC malformation, immune or neural disease, bone metabolism related diseases  
CC or disorders and diseases affecting organs such as skin, lung, kidney,  
CC pancreas, stomach, gonad, muscle or intestine. (Updated on 20-MAR-2003 to  
CC correct PA field.)

SQ Sequence 850 BP; 155 A; 293 C; 264 G; 138 T; 0 U; 0 Other;

Alignment scores:	
Pred. No.:	2.06
Length:	856
Score:	84.00
Percent Similarity:	41.7%
Best Local Similarity:	31.1%
Query Match:	8.9%
DB:	2
Length:	856
Matches:	12
Conservative:	31
Mismatches:	36
Indels:	7
Gaps:	24

US-10-507-132-2 (1-172) x AAV72504 (1-850)

```

QY      84 GlnHisPheIleGlyGlyThrArgTrp-----GluLysValSerGluAspGluValIle 101
Db      536 CAGCAACCACTTCGAGTTCGGCCGCTGGAACGTGTCGCCCTGGCGCAAGAACCGCTTC 595
QY      102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThreLysGluVal 121
Db      596 GGG-----CAAGAACTCCGAGTACGAGAGTCCGAGGCTGCTTCAAC-----TATGCCATC 646
QY      122 ThrMetLysGlyHisAlaHisSer-----AlaAsnLeuHis----- 133
Db      647 AGCGCGCGCGCGCGCGCATGCTGTACCCGCTGCTGCAAGCCAGGCGCAATCTGAGCAAT 706
QY      134 -----TrpTyrLysLysIleAspGlyValTrpLysPhe 144
Db      707 TGTGGCTGTGACCGGAGAACGAGCTACTACCAACGAGCGAAGC---TGGAAAGTGG 763
QY      145 AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
Db      764 GGGGGCTGCTCAGCGGACGTCGCTACGGC---ATCGACTTTTCTGTCGCTTGTGGAT 820
QY      165 GlyArgGlu 167
Db      821 GCCCGTAG 829

```

RESULT 15

ADP00192  
ID ADP00192 standard; DNA; 1017 BP.

AC ADP00192;

DT 12-FEB-2004 (first entry)

DE Bacterial polynucleotide #477.

KM Proteus mirabilis infection; bacterial infection; antibacterial;

KW Immunostimulant; gene; ds.

OS Proteus mirabilis.

PN US665709-B1.

XX 12-AUG-2003.

PF 05-APR-2000; 2000US-00543681.

PR 09-APR-1999; 99US-0128706P.

PA (GENO-) GENOME THERAPEUTICS CORP.

PI Breton GL;

DR WPI; 2003-895291/82.

XX P-PSDB; ADP04364.

PT New Proteus mirabilis polypeptides and polynucleotides, useful as  
PT reagents for diagnosis of bacterial disease, as components of  
PT antibacterial vaccines, as targets for antibacterial drugs, or as  
PT biocontrol agents for plants.

PS Disclosure, SEQ ID NO 477; 870bp; English.

CC The invention relates to new Proteus mirabilis polypeptides and  
CC polynucleotides. The invention also relates to antibodies against the  
CC polypeptides, methods for producing the polypeptides, a method of  
CC generating vaccines for immunising an individual against P. mirabilis, a  
CC method for evaluating a compound for the ability to bind a P. mirabilis  
CC polypeptide and a method for screening test compounds for anti-bacterial  
CC activity. The polypeptides and polynucleotides are useful as molecular  
CC targets for diagnosing, preventing and treating pathological conditions  
CC resulting from bacterial infection, as reagents for diagnosis of  
CC bacterial diseases, as components of antibacterial vaccines, as targets  
CC for antibacterial drugs or as bio-control agents for plants. This  
CC sequence represents a Proteus mirabilis polynucleotide of the invention.

XX  
SQ Sequence 1017 BP; 290 A; 186 C; 254 G; 287 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2.63	84.00	37.34	25.54	8.98	1017	39	18	42	54	10

US-10-507-132-2 (1-172) x ADP00192 (1-1017)

```

QY      35 TRPAAPAGLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
Db      280 TGGGATTAAGCAACAACGA-----GAAGATGTCCTT 309
QY      55 AspLysLeuTrpGluAlaMetProAlaGluLysPheValGlyMetValSerSerLysGln 74
Db      310 GATTAATAATGTTGAACAACGCCCA---CAGTCTTTCGTG----- 345
QY      75 MetLeuGlyAspProThrLeuArg---ThrGlnHisPheIleGlyGlyThrArgTrpGlu 93
Db      346 ATGCTTGACAGATCTTGTTTAAGAGGGGCTAAACACACATTACAGCGTACCTTGGGAA 405
QY      94 LysValSerGluAspGluValIleGlyTyrHisGlnLeuArg----- 107
Db      406 GGGATA-----GAGATTATA-----GAGCCCTTAAGCAACAAGGCGTAATGTT 450
QY      108 -----ValProHisGlnArgTyrLysAspThrThreLysGluValThreLys 124
Db      451 ATTTTATGTAAGTCCGATGATGAGGCTGTGATGTAAGTCCATGTATTGGCTGCTAAA 510
QY      125 GlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys-----IleAspGlyValTrp 142
Db      511 GGGCAAAAATGGCAGCAATGTTTACACACAAAAGATCCGGTACGTGATTATTATGG 570
QY      143 -----LysPheAlaGlyLeuLysPro 149
Db      571 AATAAAGCAGCTTACCATTTGGCGGAGCTTACACTGGCGGAGCGGAGTAACCT 630
QY      150 AspIleArg-----TrpGlyGluPhe 156
Db      631 TTTATTTCACCGTCCGCAAGGCTTTTGGGGGTATTAT 669

```

Search completed: December 4, 2006, 20:48:11  
Job time : 599 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 4, 2006, 19:08:15 ; Search time 5106 Seconds  
(without alignments)  
3231.186 Million cell updates/sec

Title: US-10-507-132-2  
Perfect score: 942  
Sequence: 1 MGSQVQKSDIEITFSDYLGIM.....WGEFDEPDRIFEDGRTFGDK 172

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapext 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6366136 segs, 31973710525 residues  
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODX=frame+.p2n.model -DEV=rlh  
-Q=/abses/ABSSWEB.spool/US10507132/runat\_04122006\_143856\_11163/app.query.fasta\_1  
-DB=GenEmbl -Qfmt=fastap -SUFix=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITs=b1ts -START=1 -END=-1 -MATRIX=b1osum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abses07  
-USER=US10507132 @CCN 1.1 5548 @runat\_04122006\_143856\_11163 -NCPu=6 -ICPU=3  
-NO MAP -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOP -DEV TIMEOUT=120  
-WREN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:.\*  
1: gb\_env:.\*  
2: gb\_pat:.\*  
3: gb\_ph:.\*  
4: gb\_pl:.\*  
5: gb\_pr:.\*  
6: gb\_ro:.\*  
7: gb\_rts:.\*  
8: gb\_sy:.\*  
9: gb\_un:.\*  
10: gb\_vl:.\*  
11: gb\_ov:.\*  
12: gb\_hlg:.\*  
13: gb\_in:.\*  
14: gb\_cm:.\*  
15: gb\_da:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	938	99.6	807	4	AB004741 Magnaporthe
2	653	69.3	770	4	AB100172 Bipolaris
3	652.5	69.3	1477	4	AF316575 Ophiostom

4	641	68.0	1215	4	AY214004	AY214004 Ceratocys
5	633	67.2	1151	4	COGS8CD1	D86079 Colletotric
6	499	53.0	427	4	AY098656	AY098656 Ophiostom
7	499	53.0	1447	4	AFU95042	U95042 Aspergillus
8	495	52.5	424	4	AY098657	AY098657 Ophiostom
9	494.5	52.5	423	4	AY098660	AY098660 Ophiostom
10	493	52.3	432	4	AY098654	AY098654 Ceratocys
11	489.5	52.0	428	4	AY098659	AY098659 Ophiostom
12	489	51.9	421	4	AY098661	AY098661 Ophiostom
13	489	51.9	433	4	AY098655	AY098655 Ceratocys
14	487	51.7	414	4	AY098663	AY098663 Ophiostom
15	487	51.7	414	4	AY098664	AY098664 Ophiostom
16	486	51.6	415	4	AY098662	AY098662 Ophiostom
17	484.5	51.4	423	4	AY098666	AY098666 Ophiostom
18	484.5	51.4	573	4	SMAS75152	AJ575152 Sordaria
19	472	50.1	433	4	AY098658	AY098658 Ophiostom
20	465.5	49.4	422	4	AY098665	AY098665 Ophiostom
21	208	22.1	110000	4	AP007161_08	Continuation (9) of
22	99.5	10.6	186614	15	AP003602	Continuation (9) of
23	94.5	10.0	462	2	AR317494	AR317494 Sequence
24	93.5	9.9	250093	12	AC114058	AC114058 Rattus no
25	92	9.8	110000	15	AP006618_50	Continuation (51) o
26	91.5	9.7	246255	12	AC158089	AC158089 Bos tauru
27	91	9.7	9158	15	AF210152	AF210152 Clostridi
28	90	9.6	75898	10	AY190604	AY190604 Halovirus
29	90	9.6	110000	15	CP000096_20	Continuation (21) o
30	90	9.6	110000	15	CR954246_09	Continuation (10) o
31	89.5	9.5	110000	4	CR382135_03	Continuation (4) of
32	88.5	9.4	110000	4	AP007150_09	Continuation (10) o
33	88.5	9.4	177466	15	AE001826	AE001826 Deinococc
34	88	9.3	9742	15	ESU57489	U57489 Eubacterium
35	88	9.3	40679	3	AY052766	AY052766 Salmonell
36	88	9.3	110000	15	CP000091_14	Continuation (15) o
37	88	9.3	230569	12	AC096163	AC096163 Rattus no
38	88	9.3	273650	12	AC096020	AC096020 Rattus no
39	87.5	9.3	110000	15	CR28337_09	Continuation (10) o
40	87.5	9.3	143840	6	AC121929	AC121929 Mus muscu
41	87.5	9.3	219269	6	AC133519	AC133519 Mus muscu
42	87	9.2	2232	4	AF095896	AF095896 Oryza sat
43	87	9.2	2664	4	AF095895	AF095895 Oryza sat
44	87	9.2	3196	4	AK066825	AK066825 Oryza sat
45	87	9.2	92928	11	AC140789	AC140789 Gallus gal

#### ALIGNMENTS

RESULT 1	AB004741	807 bp	mRNA	linear	PLN 13-NOV-1998
LOCUS	AB004741				
DEFINITION	Magnaporthe grisea mRNA for scytalone dehydratase, complete cds.				
ACCESSION	AB004741				
VERSION	AB004741.1	GI:3798733			
KEYWORDS	scytalone dehydratase; sdh1.				
SOURCE	Magnaporthe grisea				
ORGANISM	Magnaporthe grisea				
REFERENCE	1 (sites)				
AUTHORS	Motoyama, T., Imanishi, K. and Yamaguchi, I.				
TITLE	cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for pathogenicity of the rice blast fungus, Pyricularia oryzae				
JOURNAL	Biosci. Biotechnol. Biochem. 62 (3), 564-566 (1998)				
PUBMED	9571787				
REFERENCE	2 (bases 1 to 807)				
AUTHORS	Motoyama, T.				
TITLE	Direct Submision				
JOURNAL	Submitted (09-JUN-1997) Takayuki Motoyama, The Institute of Physical and Chemical Research (RIKEN), Microbial Toxicology Lab., 2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan (E-mail:tmotoyama@postman.riken.go.jp, Tel: +81-46-467-9518) Sequence updated (27-Oct-1998).				
COMMENT	Location/Qualifiers				
FEATURES					

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81..599
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## ORIGIN

## Alignment Scores:

Pred. No.:	6 61e-108	Length:	807
Score:	938.00	Matches:	171
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.4%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	4	Gaps:	0

US-10-507-132-2 (1-172) x AB004741 (1-807)

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OY      1 MetGlySerGlnValGlnLysSerAspGluLeuThrPheSerAspTyrLeuGlyLeuMet 20
DB      81 ATGGGTTTCCCAAGTTCAAAAGCGATGATTAACCTTCTCAGACTACCTGGGCTCATG 140
OY      21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerTyrAspTrpAspArgLeuAsglys 40
DB      141 ACTTGCGTCTATAGTGGCGACACCTACGACTCCAGAGACTGGGATAGGCTGCGAAAG 200
OY      41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
DB      201 GTCATTTGCCCTTACTTGGCGACTTGACTACCGCTCTTCTCGACAAGCTCTGGAGGCA 260
OY      61 MetProAlaGluGluDpheValGlyMetValSerSerTyrGlnLeuGlyAspProThr 80
DB      261 ATGCCCGCGAGAGATTGCTCGGCGATGCTCTCGAGACAGCAGTGGCGCGACCCACC 320
OY      81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
DB      321 CTCGGCACCGACACTTCACTGGCGGACGCGCTGGAGAGAGGTGTCCGAGCGAGGTC 380
OY      101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
DB      381 ATCGGGTACCACAGCTGGCGCGTCCCGCACCAAGGTACAGAGCACACCATGAAGAGAG 440
OY      121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
DB      441 GTCAACCATGAAGGCGACAGCCGCACTCGGCAAACTTCACTGTTACAAGAAAGATCGACGG 500
OY      141 ValThrLysPheHisIleGlyLeuLysProAspIleArgTrpGlyGluLysPheAspArg 160
DB      501 GTCTGAAGTCTCCCGGCTCAAGCCCGATATCCGTGGGGCGAGTTCCACTTTCACAG 560
OY      161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
DB      561 ATCTTTGAGGACCGAGCGGAGACCTTTGGGACAAA 596
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```
RESULT 2
ABI00172      770 bp      DNA      linear      PLN 01-APR-2004
LOCUS      Bipolaris oryzae BSCDgene for scytalone dehydratase, complete cds.
DEFINITION      AB100172
ACCESSION      AB100172.1  GI:32879676
KEYWORDS
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SOURCE
ORGANISM      Bipolaris oryzae
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS      Kihara,J. and Moriwaki,A.
TITLE      Cloning, functional analysis and expression of a scytalone dehydratase gene (SCD1) involved in melanin biosynthesis of the phytopathogenic fungus Bipolaris oryzae
JOURNAL      Curr. Genet. 45 (4), 197-204 (2004)
14716498
2 (bases 1 to 770)
Kihara,J. and Moriwaki,A.
Direct Submission
Submitted (16-JAN-2003) Junichi Kihara, Shimane University, Faculty of Life and Environmental Science; Nishikawatsu 1060, Matsue, Shimane 690-8504, Japan (E-mail:j.kihara@life.shimane-u.ac.jp, Tel:81-852-32-6520, Fax:81-852-32-6597)
Location/Qualifiers
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## FEATURES

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AERQQLDEBARAAAGTPTAPGQAV"
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## ORIGIN

## Alignment Scores:

Pred. No.:	4.53e-72	Length:	770
Score:	653.00 <td>Matches:</td> <td>114</td>	Matches:	114
Percent Similarity:	79.8%	Conservative:	24
Best Local Similarity:	65.9%	Mismatches:	31
Query Match:	69.3%	Indels:	4
DB:	4	Gaps:	1

US-10-507-132-2 (1-172) x AB100172 (1-770)

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OY      3 SerGlnValGlnLysSerAspGluLeuThrPheSerAspTyr-----LeuGly 18
DB      76 TCATGTGTGCAAGTAAAGTACTCTCTGCTGGGCTTAAGTGGTACAGAGGTCATGGGC 135
OY      19 LeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerTyrAspTrpAspArgLeu 38
DB      136 TGTCAATCGGCAATGCTTACAAATGGCGACACTACGACAGCAAGACTGGGAGGCTCTG 195
OY      39 ArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrp 58
DB      196 CCGAAGTGGTGGCTCCGACTGGAAGTGACTACCGGCTCTTCTTGGACAAGATATGG 255
OY      59 GluAlaMetProAlaGluGluDpheValGlyMetValSerSerTyrGlnLeuGlyAsp 78
DB      256 GAGGCGATCCAGCGGATAGTTTGTGGCCAGGCGCTTGAACCTGCGGCTCGGCAAC 315
OY      79 ProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAsp 98
DB      316 CCCCTCTCAAGACACAGCACTTCACTGGCGGACAGCTGGAGAGAGCGGCCAGGAT 375
OY      99 GluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMet 118
DB      376 GAGATTACGGATACACACAGCTGGGAGTGGCTTACACAGCATACAGGATAGTACAGG 435
OY      119 LysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIle 138
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Db      436 GCGACGCTGCAGTCAAGGCCCAAGCCCAAGCTTCAACAGCAGCTGATCAAAAAGATT 495
Qy      139 AASPGLYValTTPlyShehlaGlyLeuLySProAspIleArgTTPolYglUPheAspPhe 158
Db      496 GACGGGAGAGTGAAGATTGTCGGGCTGAACCCCGACATTAGATGATGATGATGATGATGAT 555
Qy      159 AASPAGIlePheGluASPGLYArgGluThrPheGlyASP 171
Db      556 GACAAGCTGTTTCAGAGGGCCCGCAGCAGCTGGCGGAG 594

RESULT 3
AF316575 1477 bp DNA linear PLN 22-MAY-2002
LOCUS Ophiostoma floccosum strain 387N scytalone dehydratase (OSD1) gene,
DEFINITION complete cds.
ACCESSION AF316575
VERSION AF316575.1 GI:12964737
KEYWORDS
SOURCE Ophiostoma floccosum
ORGANISM Ophiostoma floccosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE
AUTHORS Wang,H.L., Kim,S.H. and Breuil,C.
TITLE 1 (bases 1 to 1477)
A scytalone dehydratase gene from Ophiostoma floccosum restores the
melanization and pathogenicity phenotypes of a melanin-deficient
Colletotrichum lagenarium mutant
Mol. Genet. Genomics 266 (1), 126-132 (2001)
11589570
JOURNAL 2 (bases 1 to 1477)
PUBMED Wang,H. and Breuil,C.
REFERENCE Direct Submission
AUTHORS Submitted (25-OCT-2000) Wood Science, University of British
JOURNAL Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
TITLE Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 1.16e-71 Length: 1477
Score: 652.50 Matches: 113
Percent Similarity: 75.7% Conservative: 21
Best Local Similarity: 63.8% Mismatches: 22
Query Match: 69.3% Indels: 21
Db: 4 Gaps: 1

US-10-507-132-2 (1-172) x AF316575 (1-1477)
Qy 15 AASPGLYleuGlyLeuMetThrCysValTYRGLUTPalaAspSerTYRAspSerLYsAsp 34
Db 470 GACTACATAGGCGCTTCGACGTGCGCCGCTTACAGATGGGCGCAGCTATGATTCACAGGAC 529
Qy 35 TTPAspArgLeuArgLYsValIleAlaProThrLeuArgIle----- 48

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Db      530 TGGACCGCTCTCGGCAAGTGCATTGCTCCACATCTCGAATGCTAGCTTATACAAACC 589
Qy      49 -----AspTYRArgSerPhe 53
Db      590 TGCCTTCTCTATTAAACCATTAAGATCTTCTTGCTACACAGACAGGACTTACCGCTGGTTC 649
Qy      54 LeuAspLYLeuThrPoluAlaMetProAlaGluGluPheValGlyMetValSerSerLYs 73
Db      650 CTGAACAGACTGTGGAGGAGCCATGCCGCGCGAAGATTATTCGAGTATGATCTTCAGACCC 709
Qy      74 GlnMetLeuGlyASPProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTTPglu 93
Db      710 AGCGTTCTCGGCAACCCCTGCTGGGACACAACTTCTTGGCGCGCTCGCGTGGAG 769
Qy      94 LysValSerGluAspGluValIleGlyTYRHisGlnLeuArgValProHisGlnArgTYR 113
Db      770 CGCATCTCCGACACCGAGGTGCGGCTTACATCAGCTCGCGGTCCCAACAGGCTTAC 829
Qy      114 LysAspThrThrMetLYsGluValThrMetLYsGlyHisAlaHisSerAlaAsnLeuHis 133
Db      830 ACAGATACCACTCTCACACAAGTTGCCGTCAAGGGCCACGCCATTCGGCCAAACCCAC 889
Qy      134 TTPTYRLYsLYsIleAspGlyValTTPLYsPheAlaGlyLeuLYsProAspIleArgTTP 153
Db      890 TGGTACCGGAGGTGACGCGCGCTGGAAGTTTGGCCGCTCGATCCCAAGATCCGCTGG 949
Qy      154 GylGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
Db      950 TTGGAATACGATTGTGATTAAGTGTGTCAGAGCGCGGACCAACGATTGGC 1000

RESULT 4
AY214004 1215 bp DNA linear PLN 10-MAR-2004
LOCUS AY214004
DEFINITION Ceratocystis resinifera sycitalone dehydratase I (SD1) gene,
ACCESSION AY214004
VERSION AY214004.1 GI:37787189
KEYWORDS
SOURCE Ceratocystis resinifera
ORGANISM Ceratocystis resinifera
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales Incertae sedis;
Ceratocystis.
REFERENCE
AUTHORS 1 (bases 1 to 1215)
Loppau,P.A.
TITLE Canadian Populations and Melanin Biosynthesis Genes of Ceratocystis
JOURNAL resinifera
AUTHORS Unpublished
TITLE 2 (bases 1 to 1215)
Loppau,P.A.
JOURNAL Direct Submission
AUTHORS Submitted (08-JAN-2003) Wood Science, University of British
JOURNAL Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
TITLE Location/Qualifiers
FEATURES
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1.1215
/organism="Ceratocystis resinifera"
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/isolate="EJ3-21"
/specific_host="Pinus contorta"
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/country="Canada: Alberta, Edson"
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join(<233..305,379..476,545..>934)
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exon
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exon
379..476
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exon
545..934
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ORIGIN
Alignment Scores:
Pred. No.: 2,56e-70 Length: 1215
Score: 641.00 Matches: 115
Percent Similarity: 74.7% Conservative: 21
Best Local Similarity: 63.2% Mismatches: 23
Query Match: 68.0% Indels: 24
DB: 4 Gaps: 1
US-10-507-132-2 (1-172) x AY214004 (1-1215)
QY 14 SerAspTYrLeuGlyLeuMetThrCysValTYrGluTrpAlaAspSerTYrAspSerLYs 33
Db 375 GGAGATTATGTGGTCTTAACAAGCTGCCTTATACGATGGCGCTGATGCTACAGACAGCAAG 434
QY 34 AspTPAspArgLeuArgLYsValIleAlaProThrLeu----- 46
Db 435 GATTGGAGCCGCTGCTGCTGCTACCATTCGCCCAACACTAAGAGTGAGCATCTCGCTGA 494
QY 47 -----ArgIleAspTYr 50
Db 495 TATAGCAGATATATCTTATGTTCTTACTACACATATATGTTTGGCTAGATC-GACTAC 553
QY 51 ArgSerPheLeuAspLYsLeuTrpGluAlaMetProAlaGluGluPheValGlyMetVal 70
Db 554 CGCTGGTCTCTGGATGAGCTATGGGAGCAATGCCGCGGAGACTTTATTAAGATGATC 613
QY 71 SerSerLYsGluMetLeuGlyAspProThrLeuArgThrGluHisPheIleGlyGlyThr 90
Db 614 TCCGACCCCAACGTTCTCGGCAACCTCTACTAAAGACCCACACACTTCGCGCGCTTCG 673
QY 91 ArgTTPGluLYsValSerGluAspGluValIleGlyTYrHisGluLeuArgValProHis 110
Db 674 CCTGGAGACGTTTATGATGACATGAGTCGTTGGCTGGACACAGCTACGTGCCCCAC 733
QY 111 GlnArgTYrLYsAspThrThrMetLYsGluValThrMetLYsGlyHisAlaHisSerAla 130
Db 734 CAGCGCTACACTGATGCTACGAAGACCAACGCTCAAGGTCAMAAGGCCACCCACTAGCC 793
QY 131 AsnLeuHisTrpTYrLYsLYsIleAspGlyValITrPlyPheAlaGlyLeuLYsPheAsp 150
Db 794 AACCAAGCACTGGTATCAAGAAAGTGGCGGTGGAAATTGGCCGCTCTATCCGAG 853
QY 151 IleArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
Db 854 ATCCGCTGGTCAAGATGATTCAGACAAAGGTGTTGCTAGCGGCCGCTGAAGATTGGT 913
QY 171 AspLYs 172
Db 914 GATGAG 919
RESULT 5
COGSCD1 COGSCD1 1151 bp DNA linear PLN 25-DEC-2002
DEFINITION Collectotrichum lagenarium DNA for scytalone dehydratase, complete
cds.
VERSION D86079.1 GI:1395159
KEYWORDS melanin biosynthesis; scytalone dehydratase.
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SOURCE
ORGANISM Collectotrichum lagenarium
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllostachyales; Phyllostachyaceae;
mitosporic Phyllostachyaceae; Collectotrichum.
REFERENCE
AUTHORS Kubo,Y., Takano,Y., Endo,N., Yasuda,N., Tajima,S. and Furusawa,I.
TITLE Cloning and structural analysis of the melanin biosynthesis gene
JOURNAL SCD1 encoding scytalone dehydratase in Collectotrichum lagenarium
PUBMED Appl. Environ. Microbiol. 62 (12), 4340-4344 (1996)
893707
2 (bases 1 to 1151)
Kubo,Y., Takano,Y., Noriko,E., Yasuda,N., Tajima,S. and Furusawa,I.
Cloning and structural analysis of the melanin biosynthesis gene
encoding scytalone dehydratase of Collectotrichum lagenarium
Unpublished
3 (bases 1 to 1151)
REFERENCE
AUTHORS Kubo,Y.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1996) Yasuyuki Kubo, Laboratory of Plant
Pathology, Faculty of Agriculture, Kyoto Prefectural University,
Shimogamo, Kyoto, Kyoto 606, Japan (E-mail:y_kubookpu.ac.jp,
Tel:075-702-0957, Fax:075-702-0957)
FEATURES
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/isolate="104-T"
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117..121
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422..488
intron
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489..923
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polyA_site
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ORIGIN
Alignment Scores:
Pred. No.: 2,44e-69 Length: 1151
Score: 633.00 Matches: 112
Percent Similarity: 76.0% Conservative: 20
Best Local Similarity: 62.6% Mismatches: 24
Query Match: 67.2% Indels: 23
DB: 4 Gaps: 1
US-10-507-132-2 (1-172) x COGSCD1 (1-1151)
QY 15 AspTYrLeuGlyLeuMetThrCysValTYrGluTrpAlaAspSerTYrAspSerLYsAsp 34
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Db 323 GACTACCTGGTCTCAACGCCGCTCTTCGAGTGGGCGCATCTCAAGCTCCAAAGAC 382  
Qy 35 TTPASPAArgLeuArgLysValIleAlaProThrLeuArg----- 47  
Db 383 TGGGACCGTCTCCGCAAGTCATCGCCCCGAGCTCCGCGTAAGTCTCTTCCCCCAATA 442  
Qy 48 -----IleAspTyrArgSe 52  
Db 443 CACGCAACAGAAACCGTGTCCACCGGTATTAACCGAAGCAGATGACTACCGCTC 502  
Qy 52 rPhleuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerse 72  
Db 503 CTTCCTCGAAGAAATCTCGGAGGCGCATGCGCGCGAGAGTTTCATCGCCATGATCTCGA 562  
Qy 72 rLysGlnMetLeuGlyAspProThrLeuArgThrGlnIlePheIleGlyValThrArgTr 92  
Db 563 CAGTCCGCTCTCGGCAACCCGCTCTCAAGACGACACTTCATCGCGGCTCCGCTG 622  
Qy 92 pGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnAr 112  
Db 623 GGGAAAGGTCTCGGACACGAGGTTCATCGGCCACACACACTCGCGCTCGCACCAAA 682  
Qy 112 gTyrLysAspThrThMetLysGluValThMetLysGlyHisAlaHisSerAlaSer 132  
Db 683 GTAGACCGACGCGCTCCGACACCGAGGTGCGCTCAAGGCGCACGCCACAGCTAACAA 742  
Qy 132 uHsTrpTyrLysValIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleAr 152  
Db 743 GCACGTGACCGAAGGTCAACGCGGTGAGAGTTCGCGGTCTGAACCCCAAGATCCG 802  
Qy 152 gTTPGlyGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170  
Db 803 GTGTCGAGTACGACTTTCAGCCCGCTTCGCGCAACGCGCGGACTCGTCAACGCG 857

RESULT 6  
LOCUS AY098656 427 bp DNA linear PLN 16-JAN-2003  
DEFINITION Ophiostoma piceae isolate ANU scytalone dehydratase (SD) gene,  
partial cds.  
ACCESSION AY098656  
VERSION AY098656.1 GI:21238821  
KEYWORDS Ophiostoma piceae  
SOURCE Ophiostoma piceae  
ORGANISM Ophiostoma piceae  
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
1 (bases 1 to 427)  
REFERENCE  
AUTHORS Fleet,C. and Breatnall,C.  
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm  
the presence of DHN-melanin pathway in sapstain fungi  
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)  
REFERENCE  
AUTHORS Fleet,C. and Breatnall,C.  
TITLE Direct Submision  
JOURNAL Submitted (22-APR-2002) Wood Science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
FEATURES  
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## ORIGIN

## Alignment Scores:

Pred. No.:	5,24e-53	Length:	427
Score:	499.00	Matches:	91
Percent Similarity:	74.6%	Conservative:	15
Best Local Similarity:	64.1%	Mismatches:	15
Query Match:	53.0%	Indels:	22
DB:	4	Gaps:	1

US-10-507-132-2 (1-172) x AY098656 (1-427)

Qy 25 GUTTPAlAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44  
Db 1 GAGTGGCGGACAGGTACGATTCCAAGAGACTGGACCGTCTGCGCAAGTGCATCTCCC 60  
Qy 45 ThrLeu----- 46  
Db 61 ACTCTCGAGTACGCTTATACAAACCTGCTTCTATTAAACCATTAAGATCTTCTTG 120  
Qy 47 -----ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAla 63  
Db 121 CTACAGACAGATC-GACTACCGCTGCTTCTGAACAAGCTGTGGAGGCGCATCGCGCC 179  
Qy 64 GlnGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThr 83  
Db 180 GAAGAGTTTATCGGACGTGATCTTCGACCCAGCGCTTCGCGCAACCCCGCTGCGCACA 239  
Qy 84 GlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyr 103  
Db 240 CAACACTTCTTGGCGCCCTCGCGCTGGAGCGCATCTCGACACCGAGGTGTGGGCTAC 299  
Qy 104 HisGlnLeuArgValProHisGlnArgTyrLysAspThrThMetLysGluValThMet 123  
Db 300 CATCACGTGCGGTCTCCCGCACAGGTCTACAGATACCACTCTCACACAAGTTGGCGCTC 359  
Qy 124 LysGlyHisAlaHisSerAlaSerLeuHsTrpTyrLysValIleAspGlyValTrpLys 143  
Db 360 AAGGGCCAGCCCACTCGGCCAACACCAACCACTGTAACGAGGTGACGCGCTGGAAG 419  
Qy 144 PheAla 145  
Db 420 TTCGCC 425  
RESULT 7  
LOCUS AFU95042 1447 bp DNA linear PLN 12-NOV-1999  
DEFINITION Aspergillus fumigatus scytalone dehydratase (arpi) gene, complete  
cds.  
ACCESSION U95042  
VERSION U95042.1 GI:2555059  
KEYWORDS Aspergillus fumigatus  
SOURCE Aspergillus fumigatus  
ORGANISM Aspergillus fumigatus  
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
1 (bases 1 to 1447)  
REFERENCE  
AUTHORS Tsai,H.F., Washburn,R.G., Chang,Y.C. and Kwon-Chung,K.J.  
TITLE Aspergillus fumigatus arpi modulates conidial pigmentation and  
complement deposition  
JOURNAL Mol. Microbiol. 26 (1), 175-183 (1997)  
PUBMED 9383199  
REFERENCE  
AUTHORS Tsai,H.F., Wheeler,M.H., Chang,Y.C. and Kwon-Chung,K.J.  
TITLE A developmentally regulated gene cluster involved in conidial  
pigment biosynthesis in Aspergillus fumigatus  
JOURNAL J. Bacteriol. 181 (20), 6465-6477 (1999)  
PUBMED 10515939  
REFERENCE  
3 (bases 1 to 1447)

AUTHORS Tsai,H.-F., Washburn,R.G., Chang,Y.C. and Kwon-Chung,K.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-MAR-1997) LCI/MMS, NIH/NIAD, 10 Center Drive,  
 MSC1882, Bldg 10/Rm 11C304, Bethesda, MD 20892, USA

FEATURES  
 source Location/Qualifiers  
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## ORIGIN

## Alignment Scores:

Pred. No.: 2,34e-52 Length: 1447  
 Score: 499.00 Matches: 84  
 Percent Similarity: 68.2% Conservative: 32  
 Best Local Similarity: 49.4% Mismatches: 36  
 Query Match: 53.0% Indels: 18  
 DB: 4 Gaps: 1

US-10-507-132-2 (1-172) x AFU95042 (1-1447)

QY 11 IIEThPhSeRrApTyLeuGlYleuMeThCyVaLIYrGlUuTrpLaAspSerTy 30  
 Db 406 CTAAACCGGCGAGACATCTTGGCTTAAAAAAAGTCTTGTGACGGGACAGCTAT 465  
 QY 31 AAspSerTy----- 33  
 Db 466 GACGCCAAGGTAAAGTTCAACGTCCCGTCCCGGAGGGGAAAAACATATTACCAAGG 525  
 QY 34 ---AspTrpAspArgLeuArgLyVaLIleAlaProThrLeuArgIleAspTyArgSer 52  
 Db 526 TGGAGTGGGATGAGCTTGGAGACATCATGCGCCGACCTTACCGTGACCTACAGGCG 585  
 QY 53 PheLeuAspLyseLeuTrpGluaIaMetProAlaGlulGluPheValaIyMetValSerSer 72  
 Db 586 ATCGGACTGGCAAGGTGGATGACATGCGCTGCGGAAGACATACATGAGCATTTCTGAC 645  
 QY 73 LysGlMetLeuArgIleAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrp 92  
 Db 646 ATGGACTTCTTGGGTGACCCGACCGTCACAGACCCAGACATCTGCTGGGCGAGTCTGGTGG 705

QY 93 GluLyVaIseRgluAspGluValIleGlyTyRHISGlnLeuArgValProHisGlnArg 112  
 Db 706 GAAGAATCTCCGATACCGAGGTCTATTGGCACCATCTAGCTCGCGCCCATCATGAGTC 765  
 QY 113 TyRlyAspTrhThrMetLySGluValThrMetLySGlyHisAlaHisSerAlaIleu 132  
 Db 766 TACAGGACAGCACCTTGGAAACTGTCAAGCTCAAGGGGACAGGCGCATGCCAATGAG 825  
 QY 133 HisTrpTyRlyValIleAspGlyValTrpLyAspPheAlaGlyLeuLeuProAspIleArg 152  
 Db 826 CACTACTACCGGACAGGTGACCGCGGTGGAAGTTTGCCGSCCTGAACCTACCGTCCG 885  
 QY 153 TrpGlyGluPheAspPheAspArgIlePhe 162  
 Db 886 TGGATGAGTATCATTCATTCGAGGATGCTTC 915

## RESULT 8

AY098657

LOCUS

DEFINITION

AY098657.1 GI:21238823

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

mRNA

CDS

ORIGIN

Alignment Scores:

Pred. No.: 1.66e-52 Length: 424

Score: 495.00 Matches: 90

Percent Similarity: 74.5% Conservative: 15

Best Local Similarity: 63.8% Mismatches: 15

Query Match: 52.5% Indels: 22

DB: 4 Gaps: 1

US-10-507-132-2 (1-172) x AY098657 (1-424)

QY 25 GluTrpLaAspSerTyAspSerLyAspTrpAspArgLeuArgLyVaLIleAlaPro 44

Db	1	GAGTGGGGGACAGAGTACGATTCCAGAGCTGGGACCGTCTGGCAAGTGCATTCTCTCC	60
QY	45	Thirleu-----	46
Db	61	ACTCTGGCAGTACGCTTATACAACCCGCTTCTCTATTAAACCATTAAGTCTTCTTG	120
QY	47	-----ArglleasPTyArgSerPheIeuasblylsleuTTPgluaIaMetProIa	63
Db	121	CTAACAGACAAATC-GACTACCGCTGTTCTCGAACAAGCTGTGGAGGCCCATGTCCGGCC	179
QY	64	GlulgluPheValGlyMetValSerSerIysGlnMetIeuGlYAspProThirleuArgthr	83
Db	180	GAAAGGTTATTCGGCATGATCTCCACCCCAAGCGTTCTCGCAACCCCTGCTGGGACA	239
QY	84	GlnIISpHeIleGlyGlyThrArgTTPgluIysValSerGluAspGluValIleGlyIyr	103
Db	240	CAACACTTCTTCGGGCGCTCGCGCTGGAGGCGCATCTCGACACCGAGAGTCTGGGCTAC	299
QY	104	HisGlnIeuArGValProHisGlnArgTyrIysAspThrThrMetIysGluValThrMet	123
Db	300	CATCAGCTGGCGGTCCCCACCAAGTTCACAGATTACACGTCTCACACAAAGTTCCGCTC	359
QY	124	LysGlyHisAlaHisSerAlaAsnIeuHisTTPYIyIysIleAspGlyValITrIyIs	143
Db	360	AAGGCGCCACGCCCACTCGGCCAACACCACTGGTACCCCAAGGTGACGCGCTCGGAAG	419
QY	144	Phe	144
Db	420	TTC	422

LOCUS	423 bp	DNA	linear	PLN 16-JAN-2003
DEFINITION	Ophiostoma piceae isolate 187-1 scytalone dehydratase (SD) gene,			
ACCESSION	AY098660			
VERSION	AY098660.1			
KEYWORDS	GI:21238829			
SOURCE	Ophiostoma piceae			
ORGANISM	Ophiostoma piceae			
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.			
AUTHORS	1 (bases 1 to 423)			
TITLE	Pleet,C. and Breuil,C.			
JOURNAL	Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi			
REFERENCE	Mycol. Res. 106 (11), 1331-1339 (2002)			
AUTHORS	2 (bases 1 to 423)			
TITLE	Pleet,C. and Breuil,C.			
JOURNAL	Direct Submission			
REFERENCE	Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada			
FEATURES	Location/Qualifiers			
SOURCE	1..423			
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CDS				

ORIGIN	AHSANQHWYRKVDGWKTEAG <sup>a</sup>
Alignment Scores:	
Pred. No.:	1.91e-52
Score:	494.50
Percent Similarity:	74.5%
Best local Similarity:	64.5%
Query Match:	52.5%
DB:	4
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[illegible]

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ORIGIN

Alignment Scores:

Pred. No.:	3.03e-52	Length:	432
Score:	493.00	Matches:	91
Percent Similarity:	72.9%	Conservative:	14
Best Local Similarity:	63.2%	Mismatches:	16
Query Match:	52.3%	Indels:	24
DB:	4	Gaps:	1

US-10-507-132-2 (1-172) x AY098654 (1-432)

QY 25 GIUTPALAASPserlyrAspserlyrAspTPAAspArgleuArglyValIleAlaPro 44  
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1 GAGTGGGCGGACTGCTGATGCAATGCAAGACTGGGACCGTGGCTGCTACTATGCCCA 60  
45 ThrLeu----- 46  
61 ACATTAGAGTACGATCCCTGCGCAGTACAGGAGATATATATCAGTTCTTACTACAA 120  
QY 47 -----ArgIleAspTyrArgSerPheLeuAspLysLeuTyrGluAlaMet 61  
121 CATATATGTTTGTCTGATC-GACTATCCCTGCTCTGATATAGCTGTGGAGGCAAG 179  
QY 62 ProAlaGluGluPheValGlyMetValSerSerlyrGlyMetLeuGlyAspProThrLeu 81  
|||  
180 CCGCGGAGACTTCTCAAGATGATTTCCGACCCCAAGCTCTCGGCGACCTCTACTG 239  
QY 82 ArgThrGlnHisPheIleGlyArgTyrArgTyrGluValSerGluAspGluValIle 101  
|||  
240 AAGACCCACACTTCGCTGGTGGTGGCGCTGGGACGATGTATGATGACGAGTGGT 299  
QY 102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121  
|||  
300 GGCTGGCACACGATGAGTGTGCCCCACCAACGCTACACGATGCTCAAGACCACTGTC 359  
QY 122 ThrMetLysGlnHisAlaHisSerAlaAsnLeuHisTyrTyrLysValIleAspGluVal 141  
|||  
360 AAGGTAAAGGCGACCCGCCACTGGCTTACACAGCACTGGTATAGAGGTAAGTGGCGTC 419  
QY 142 TrpLysPheAla 145  
|||  
420 TGGAAATTGGC 431  
Db

RESULT 11  
AY098659 428 bp DNA linear PLN 16-JUN-2003  
AY098659 Ophiostoma minus isolate OM3 scytalone dehydratase (SD) gene,  
DEFINITION partial cds.  
ACCESSION AY098659  
VERSION AY098659.1 GI:21238827  
KEYWORDS Ophiostoma minus  
SOURCE Ophiostoma minus  
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
REFERENCE 1 (bases 1 to 428)  
AUTHORS Fleet,C. and Breuil,C.

TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm  
the presence of DHN-melanin pathway in sapstain fungi  
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)  
REFERENCE 2 (bases 1 to 428)  
AUTHORS Fleet,C. and Breuil,C.  
TITLE Direct Submission  
JOURNAL Submitted (22-APR-2002) Wood science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
FEATURES  
source location/Qualifiers  
1..428  
/organism="Ophiostoma minus"  
/mol\_type="genomic DNA"  
/isolate="OM3"  
/db\_xref="taxon:150568"  
/country="United Kingdom"  
<1..>428  
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join(<1..69,133..>428)  
/gene="SD"  
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/product="scytalone dehydratase"  
/protein\_id="AAM34805.1"  
/db\_xref="GI:21238828"  
/translation="EWADRYDSKMDRLRKCIAPLRIIDYRFLDKLWEAMPADFIFK  
MISDPNVLDGPLKTOHSGFASRMWRVSDDEVVGMQLFVPHQRVTDATSLSTVAAYKH  
AHSANQHWKXVDGWKFA"

ORIGIN

Alignment Scores:

Pred. No.:	8.25e-52	Length:	428
Score:	489.50	Matches:	88
Percent Similarity:	71.8%	Conservative:	14
Best Local Similarity:	62.0%	Mismatches:	19
Query Match:	52.0%	Indels:	21
DB:	4	Gaps:	1

US-10-507-132-2 (1-172) x AY098659 (1-428)

QY 25 GIUTPALAASPserlyrAspserlyrAspTPAAspArgleuArglyValIleAlaPro 44  
|||  
1 GAGTGGGCGGACGATGCAATGCAAGACTGGGACCGCTGGCGCAAGTGCATTCACCG 60  
45 ThrLeuArg----- 47  
61 ACTTGGCGGATGACATTAATCTCTTGGACATGCAGACGACACGACGACTGACTG 120  
QY 48 -----IleAspTyrArgSerPheLeuAspLysLeuTyrGluAlaMetProAla 63  
|||  
121 ACTGACTGACAGATGACATGACCGTCTGTTTCAACAAGCTCTGGGAGGCGCATTCGCGCA 180  
QY 64 GluGluPheValGlyMetValSerSerlyrGlnMetLeuGlyAspProThrLeuArgThr 83  
|||  
181 GACGAGTTTATGACATGATCTCGGACCCACGCGCTCTCGGACACCCCTGCTGGCGACA 240  
QY 84 GlnHisPheIleGlyTyrArgTyrPheLysValSerGluAspGluValIleGlyTyr 103  
|||  
241 CAGCACTCTTTTGGGCGCTCGCGCTGGGACCGCTCTCGACACCGAGTCAITGGCTTC 300  
QY 104 HisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMet 123  
|||  
301 CACGAGCTGCGGCTCCCCACAGGATCAACGACGCGCTCCCTGCGACGCTGGCGCGTC 360  
QY 124 LysGlnHisAlaHisSerAlaAsnLeuHisTyrTyrLysValIleAspGluValTrpLys 143  
|||  
361 AAGGCGACGACACTCGGCGCAACGACGATGTCGCAAGTGAACGCGCGTCTGGAGG 420  
QY 144 PheAla 145  
|||  
421 TTGGCC 426  
Db

```

RESULT 12
AY098661 421 bp DNA linear PLN 16-JAN-2003
LOCUS Ophiostoma piceae isolate W5 scytalone dehydratase (SD) gene,
DEFINITION partial cds.
ACCESSION AY098661
VERSION AY098661.1 GI:21238831
KEYWORDS
SOURCE
ORGANISM
Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE
AUTHORS 1 (bases 1 to 421)
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
VERSION 2 (bases 1 to 421)
KEYWORDS Fleet,C. and Breull,C.
SOURCE Fleet,C. and Breull,C.
ORGANISM Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES
source 1..421
/organism="Ophiostoma piceae"
/mol_type="genomic DNA"
/isolate="W5"
/db_xref="taxon:61273"
/country="Australia"
<1..>421
/gene="SD"
/join(<1..69,126..>421)
/product="scytalone dehydratase"
/join(<1..69,126..>421)
/gene="SD"
/codon_start=1
/product="scytalone dehydratase"
/protein_id="AA034807.1"
/db_xref="GI:21238832"
/translation="EMADRYDSQMDRLKCAPTLRIDYRSFLDKLMEAMPDEFIG
MISDPNVLGADPLKTOHFPVGASRMRVSDEIVGQHLRVPQRYTDASISIVAVGKH
AHSANQHWKRVGVWKFAG"
ORIGIN
Alignment Scores:
Pred. No.: 9.34e-52 Length: 421
Score: 489.00 Matches: 90
Percent Similarity: 74.3% Conservative: 14
Best Local Similarity: 64.3% Mismatches: 17
Query Match: 51.9% Indels: 20
Gaps: 1
US-10-507-132-2 (1-172) x AY098661 (1-421)
QY 25 GUTTPALASPSErTYrAsPSErLYsAsPTTPAsPArLgLeuArGLysValIleAlaPro 44
DB 1 GAGTGGCGGACAGrTACGArCTTAAGACTGAGACCGCTGGCGACAGTGCATTGCCCG 60
QY 45 ThrLeu----- 46
DB 61 ACCTGGCGGATATGTGGATTTCACCTGGGAGACAAGACAGACCAATTAACAAT 120
QY 47 ---ArGTLlAsPryrArGSErPhelLeuAsPlyLeuLTpGLUALaMetPfoAlaGLuGLu 65
DB 121 AACAGATC-GATTACCGGTGTCTGTAACAAGCTCTGGAGAGCCATGCGCGAGATGAG 179
QY 66 PheValGLyMetValSerSerLYsGLMeLeuGLyAsPProThrLeuArGThrGLNHis 85
DB 180 TTATATGGCATGATCTGGACCCCAACGCTCTGGCAACCCCTGCTTACGACACACAC 239
QY 86 PheIleGLyGLyThrArGTTPGLuLYsValSerGLuAsPGLuValIleGLyTYrHisGLN 105

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DB 240 TTCTTGGCGCTCAAGCTGGAGACGCTCTCCGATACAGAGATTCATGGTACACACAG 299
QY 106 leuArGValProHISGLArGrTYrLYsAsPThrThrMeLYsGLuValThrMeLYsGLY 125
DB 300 CTGGCGGTCCCGCCACGAGGTTCACACCGACGCGCTCTCTGACACGTTGCCGTCAAGGCG 359
QY 126 HIsAlAlaHISerAlaAsnLeuHISrTYrLYsLYsIleAsPGLYValTYrPlyPheAla 145
DB 360 CACGACACTCGCGCCACACGACACTGTGACCGCAAGTTGACGCGCTCTGGANATTGCC 419
RESULT 13
AY098655 433 bp DNA linear PLN 16-JAN-2003
LOCUS Ceratocystis resinifera scytalone dehydratase (SD) gene, partial
DEFINITION cds.
ACCESSION AY098655
VERSION AY098655.1 GI:21238819
KEYWORDS
SOURCE Ceratocystis resinifera
ORGANISM Ceratocystis resinifera
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
Ceratocystis.
REFERENCE
AUTHORS 1 (bases 1 to 433)
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
VERSION 2 (bases 1 to 433)
KEYWORDS Fleet,C. and Breull,C.
SOURCE Fleet,C. and Breull,C.
ORGANISM Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES
source 1..433
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/isolate="125-214"
/db_xref="taxon:95837"
/country="Canada"
<1..>433
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/join(<1..69,138..>433)
/product="scytalone dehydratase"
/join(<1..69,138..>433)
/gene="SD"
/codon_start=1
/product="scytalone dehydratase"
/protein_id="AA034801.1"
/db_xref="GI:21238820"
/translation="EMADRYDSQMDRLKRTIAPTIRIDYRSFLDKLMEAMPDEFIK
MISDPNVLGADPLKTOHFPVGASRMRVSDEIVGQHLRVPQRYTDARTTKTVKXGH
AHSANKHWKRVGVWKFAG"
ORIGIN
Alignment Scores:
Pred. No.: 9.67e-52 Length: 433
Score: 489.00 Matches: 90
Percent Similarity: 72.2% Conservative: 14
Best Local Similarity: 62.5% Mismatches: 17
Query Match: 51.9% Indels: 24
Gaps: 1
US-10-507-132-2 (1-172) x AY098655 (1-433)
QY 25 GUTTPALASPSErTYrAsPSErLYsAsPTTPAsPArLgLeuArGLysValIleAlaPro 44
DB 1 GAGTGGCGGACAGrTATACAGCAAGATTTGGACCGCTGNGTCGTACATTTGCCCA 60
QY 45 ThrLeu----- 46
DB 61 ACAGTAAAGTAGATCTCTCGCTGATATACAGATATATCTTACTTACTTAACAA 120

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OY 47 -----ArgilleaApTYrArgSerPheLeuAspIysLeuTrpGluAlaMet 61
Db 121 CATATATGTTTTCGTATGATC-GACTACCCCTCGTCTCGATAGATGAGGAAGCAATG 179
OY 62 ProAlaGluGlnPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrIleu 81
Db 180 CCGCGGAGGAGGAGCTTTTAAAGATGATCTCCGACCCCAAGCTTCTCGGACACCTTACTACTA 239
OY 82 ArgThrGlnHisPheIleGlyGlyThrArgTrpGlnIleValSerGlnAspGluValIle 101
Db 240 AAGACCCACACACTTCGTCGCGCTGCGCTGAGCGGTGATGATGATGATGATGATGATGAT 299
OY 102 GATYTHIeGlnLeuArgValProHisGlnArgTYrLysAspThrThrmetyGlnVal 121
Db 300 GGGTGGCACAGGTAGTGTGCGCCCAACGCGTACAGTCTACGAAAGACCAAGCCGTC 359
OY 122 ThrmetyGlnHisAlaHisSerAlaAsnLeuHisTrpTYrIleValIleAspGlyVal 141
Db 360 AAGGTCAAGGCGCACCCCACTGACCAACAGACTGTGATACAAAGAGGATGATGCGTC 419
OY 142 TrpLysPheAla 145
Db 420 TGGAGTTTGGC 431

RESULT 14
AY098663 414 bp DNA linear PLN 16-JAN-2003
LOCUS Ophiostoma piliferum isolate 198-2GF scytalone dehydratase (SD)
DEFINITION gene, partial cds.
ACCESSION AY098663
VERSION AY098663.1 GI:21238835
KEYWORDS
SOURCE
ORGANISM
Ophiostoma piliferum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
1 (bases 1 to 414)
Fleet,C. and Breuil,C.
Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sepetrain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 414)
Fleet,C. and Breuil,C.
Direct Submission
Submitted (22-APR-2002) Wood Science, University of British
Columbia, 4th floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES
source
1. 414
/organism="Ophiostoma piliferum"
/mol_type="genomic DNA"
/isolate="198-2GF"
/db_xref="taxon:38032"
/country="United Kingdom"
<1..>414
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/join(<1..69,119..>414)
/product="scytalone dehydratase"
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/gene="SD"
/codon_start=1
/product="scytalone dehydratase"
/protein_id="FAM34809.1"
/db_xref="GI:21238836"
/translation="EWADRYDSKDMRKLKCTAPTRIDYRSFLNLMEMAPADEPFG
MISDPSVLGNPLRTIOHFGASRWERISDTEVVGHRQLVPHQVYTDATLSOVAVKGH
AASANTHWYRKVDGVKWFAG"

ORIGIN
Alignment Scores: 1.63e-51 Length: 414
Pred. No.: 487.00 Matches: 88
Score:

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Percent Similarity: 76.1% Conservative: 17
Best Local Similarity: 63.8% Mismatches: 16
Query Match: 51.7% Indels: 17
Db: 4 Gaps: 1

US-10-507-132-2 (1-172) x AY098663 (1-414)
OY 25 GIUT-PAlaAspSerTYrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
Db 1 GAGTGGCGGAGAGGTATGATGATCTCCAGGACTGCGACCGCTTCGGAATGATCGCTCC 60
OY 45 ThrmetyG-----1 48
Db 61 ACCCTCCGCTGAAGACACCTCCCTTCACTATGCTGCCGACGCGCTGACCGACAGAT 120
OY 48 eAspTYrArgSerPheLeuAspIysLeuTrpGlnAlaMetProAlaGluGlnPheValG 68
Db 121 CGACTACCGGCTGTTCTTCAACAGCTGTGGAGGSCATGCCGCGGCGACGAGTTATCGG 180
OY 68 MetValSerSerLysGlnMetLeuGlyAspProThrIleuArgTrpGlnHisPheIleG 88
Db 181 CATGATCTCCGACCCGACGCGTCTGGCAACCGCTGCGCACCGACTTTCTTGG 240
OY 88 YGlyThrArgTrpGlnLysValSerGlnAspGluValIleGlyTYrHisGlnLeuArg 108
Db 241 CCGCTGCGCTGGGAGCGCATCTCCGACACCGAGGTGCTGCGCCACCGCAGCTCGCGT 300
OY 108 IProHisGlnArgTYrLysAspThrThrmetyGlnValIThrmetyGlnHisAlaHis 128
Db 301 CCCCACAGGTCTTACACCGATGCAACCTCTTACAGGTGCGGCTCAAGGCGCACGCCA 360
OY 128 sSerAlaAsnLeuHisTrpTYrLysIleAspGlyValIleTrpLysPheAla 145
Db 361 CTGGGCAACACCCCACTGATCCGCAAGTGCAGCGCGTGGAGTTTGGC 412

RESULT 15
AY098664 414 bp DNA linear PLN 16-JAN-2003
LOCUS Ophiostoma piliferum isolate 201-1A scytalone dehydratase (SD)
DEFINITION gene, partial cds.
ACCESSION AY098664
VERSION AY098664.1 GI:21238837
KEYWORDS
SOURCE
ORGANISM
Ophiostoma piliferum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
1 (bases 1 to 414)
Fleet,C. and Breuil,C.
Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sepetrain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 414)
Fleet,C. and Breuil,C.
Direct Submission
Submitted (22-APR-2002) Wood Science, University of British
Columbia, 4th floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES
source
1. 414
/organism="Ophiostoma piliferum"
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/db_xref="taxon:38032"
/country="Austria"
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/gene="SD"
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/join(<1..69,120..>414)
/gene="SD"
/codon_start=1
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/protein\_id="AAM34810.1"  
 /db\_xref="GI:21238838"  
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## ORIGIN

## Alignment Scores:

Pred. No.:	1 63e-51	Length:	414
Score:	487.00	Matches:	88
Percent Similarity:	76.1%	Conservative:	17
Best Local Similarity:	63.8%	Mismatches:	16
Query Match:	51.7%	Indels:	18
DB:	4	Gaps:	1

US-10-507-132-2 (1-172) x AY098664 (1-414)

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QY      25  GIuTPAlaAspSerTyAspSerTyAspTrpAspArgLeuArgLysValIleAlaPro 44
      |||
Db      1  GAGTGGGCGGATAGTACGACTCCAAAGACTGGGACCGCTGTGGCAAGTGCAATCGCTCCC 60
QY      45  Thleu-----Arg 47
      |||
Db      61  ACCCTCGGTAAACACCTCCCTTCATATGCTGCACCGACAGCTGTGACCGACAGA 120
QY      48  IleAspTyArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheVal 67
      |||
Db      121 TC-GACTACGCTGCTGCTCAACAGCTGTGGAGGCAAGCCGGCCGACGAGTTTCATC 179
QY      68  GlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIle 87
      |||
Db      180  GGCATGATCTCCGACCCCGACGCTGCGCAACCGCTGCGGCAACCGACCACTTCTTC 239
QY      88  GlyGlyThrArgTrpGlyLysValSerGluAspGluValIleGlyTyHisGlnLeuArg 107
      |||
Db      240  GGGCGCTCGGCTGGGAGCGCATCTCCGACACCGAGGTCGTGCGCCACACCAAGCTGCGC 299
QY      108 ValProHisGlnArgTyLysAspThrMetLysGluValThrMetLysGlyHisAla 127
      |||
Db      300  GTCCCCCAACAGGCTACACCGATGCAACCTCTCACAGGTGCGCGTCANAGGCCACGCGC 359
QY      128 HisSerAlaAsnLeuHisTrpTyLysLysIleAspGlyValTrpLysPheAla 145
      |||
Db      360  CACTCGGCGCAACACCGACTGTGACCGCAGGTGCACGCGCTGTGAAGTTTGCC 413

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Search completed: December 4, 2006, 20:37:01  
 Job time : 511 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: December 5, 2006, 01:03:51 ; Search time 200 Seconds  
(without alignments)  
393.206 Million cell updates/sec

Title: US-10-507-132-4

Perfect score: 172

Sequence: 1 MCSQVQKSDITFSDYLGIM.....WGFDPDRIFEDGRFTGDK 172

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	172	7	ADCI6593
2	97	56.4	172	7	ADCI6591
3	7	4.1	98	4	AAG89943
4	7	4.1	132	5	ABP02041
5	7	4.1	187	8	ADSA3113
6	7	4.1	191	10	AEE60274
7	7	4.1	198	9	ADMO4932
8	7	4.1	198	9	AEC87862
9	7	4.1	225	8	ADX91359
10	7	4.1	251	7	ABO62543
11	7	4.1	255	4	AU021761
12	7	4.1	255	4	AAM83837
13	7	4.1	255	4	ADCA6402
14	7	4.1	255	8	ADK79742
15	7	4.1	258	8	ADDO2033
16	7	4.1	258	9	AEB92523
17	7	4.1	258	10	AER35108
18	7	4.1	286	2	AAM61477
19	7	4.1	287	8	ABM93344
20	7	4.1	293	8	ADS22785
21	7	4.1	296	8	ADP45467
22	7	4.1	385	4	AAB98083
23	7	4.1	385	5	AU080276

24	7	4.1	388	4	ABB65417	ABb65417 Drosophila
25	7	4.1	429	7	ADM26078	AaM26078 Hypertrophic
26	7	4.1	450	4	AAM15851	AaM15851 Human nov
27	7	4.1	450	6	ABU54920	AbU54920 Human nov
28	7	4.1	463	7	ADB64726	AdB64726 Human pro
29	7	4.1	472	8	ADT71318	AdT71318 POUA PKS
30	7	4.1	472	4	AAB98084	AaB98084 Human pro
31	7	4.1	472	5	AAU80277	AaU80277 Human CLZ
32	7	4.1	472	5	ABP43682	AbP43682 Human pro
33	7	4.1	489	6	ABU23300	AbU23300 Protein e
34	7	4.1	509	3	ABY91965	ABY91965 PMWAV-1 h
35	7	4.1	600	4	ABG07764	ABG07764 Novel hum
36	7	4.1	606	8	ABM80136	ABM80136 Tumour-as
37	7	4.1	619	4	AAU45500	AaU45500 Propionib
38	7	4.1	619	6	ABM42019	ABM42019 Propionib
39	7	4.1	626	2	AAW41501	AaW41501 Human DP
40	7	4.1	626	3	AAU07495	AaU07495 A T-cell
41	7	4.1	626	3	AAU07494	AaU07494 A T-cell
42	7	4.1	681	9	AEA21009	AeA21009 Novel hum
43	7	4.1	716	8	ADS23909	AdS23909 Bacterial
44	7	4.1	719	4	AAU21607	AaU21607 Novel hum
45	7	4.1	719	7	ADCI6248	AdCI6248 Human neo

#### ALIGNMENTS

RESULT 1	ADCI6593	ADCI6593 standard; protein; 172 AA.
XX	XX	ADCI6593;
AC	XX	ADCI6593;
XX	XX	18-DEC-2003 (first entry)
DE	XX	Scytalone dehydrogenase #SEQ ID 4.
XX	XX	Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
KW	XX	Magnaporthe grisea.
OS	XX	WO2003076628-A1.
XX	XX	18-SEP-2003.
XX	XX	24-FEB-2003; 2003WO-IP001980.
XX	XX	12-MAR-2002; 2002JP-00066955.
PR	XX	(TSUB) KUMIAI CHEM IND CO LTD.
PA	XX	Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX	XX	WPI; 2003-748394/70.
DR	XX	N-PSDB; ADCI6592.
XX	XX	Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT	XX	for SCDH inhibitors and evaluating sensitivity to them.
PS	XX	Claim 7; SEQ ID NO 4; 50pp; Japanese.
XX	XX	The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC	XX	that functions in the presence of an inhibitor, comprising an optionally
CC	XX	mutated, defined amino acid sequence given in the specification. Also
CC	XX	disclosed is a method for evaluating rice blast fungus (Pyricularia
CC	XX	oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC	XX	inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC	XX	evaluating sensitivity to them. The current sequence represents the
CC	XX	Scytalone dehydrogenase amino acid sequence.
XX	XX	Sequence 172 AA;
SQ	XX	Query Match 100.0%; Score 172; DB 7; Length 172;

Best Local Similarity 100.0%; Pred. No. 3.3e-179;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQVOKSDSEITFSDYLGIMTCYEWADYDSKMDRLKRVAPTRIDYRSLDKLWRA 60  
DB 1 MSQVOKSDSEITFSDYLGIMTCYEWADYDSKMDRLKRVAPTRIDYRSLDKLWRA 60  
QY 61 MPAEFEVGVNVSQVQVADPTLRTOHFIIGGTWMEKSEDEVIGYHQLRVPHORYKOTYMK 120  
DB 61 MPAEFEVGVNVSQVQVADPTLRTOHFIIGGTWMEKSEDEVIGYHQLRVPHORYKOTYMK 120  
QY 121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRKGEFDPRIREFGRTFGDK 172  
DB 121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRKGEFDPRIREFGRTFGDK 172

RESULT 2  
ADCl6591  
ID ADCl6591 standard; protein; 172 AA.

AC ADCl6591;

DT 18-DEC-2003 (first entry)

DE Scytalone dehydrogenase #SEQ ID 2.

KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.

OS Magnaporthe grisea.

PN WO200307628-A1.

PD 18-SEP-2003.

PF 24-FEB-2003; 2003WO-JP001980.

PR 12-MAR-2002; 2002JP-00066955.

PA (TSUB ) KUMIAI CHEM IND CO LTD.

PI Kaku K, Matanabe S, Kawai K, Shimizu T, Nagayama K;

DR WPI; 2003-748394/70.

DR N-PSDB; ADCl6590.

PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening for SCDH inhibitors and evaluating sensitivity to them.

PS Claim 1; SEQ ID NO 2; 50pp; Japanese.

CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),  
CC that functions in the presence of an inhibitor, comprising an optionally  
CC mutated, defined amino acid sequence given in the specification. Also  
CC disclosed is a method for evaluating rice blast fungus (Pyricularia  
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase  
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and  
CC evaluating sensitivity to them. The current sequence represents the  
CC scytalone dehydrogenase amino acid sequence.

SO Sequence 172 AA;

Query Match 56.4%; Score 97; DB 7; Length 172;  
Best Local Similarity 100.0%; Pred. No. 3.1e-97;  
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 LGDPTRTRQHFICGTWMEKSEDEVIGYHQLRVPHORYKOTYMKVTHMGHAHSANLHWY 135  
DB 76 LGDPTRTRQHFICGTWMEKSEDEVIGYHQLRVPHORYKOTYMKVTHMGHAHSANLHWY 135

QY 136 KXIDGVWKFAGLKPDIRKGEFDPRIREFGRTFGDK 172  
DB 136 KXIDGVWKFAGLKPDIRKGEFDPRIREFGRTFGDK 172

RESULT 3  
AAG98943  
ID AAG98943 standard; protein; 98 AA.

AC AAG98943;

DT 26-SEP-2001 (first entry)

DE E. coli growth and proliferation related protein sequence SEQ ID NO:413.

KW Escherichia coli; growth; proliferation; microbial; antimicrobial;

KW bacterial infection; microorganism.

OS Escherichia coli.

PN WO200134810-A2.

PD 17-MAY-2001.

PF 09-NOV-2000; 2000WO-US030950.

PR 09-NOV-1999; 99US-0164415P.

PA (ELIT-) ELITRA PHARM INC.

PI Forsyth RA, Ohlsen K, Zykkind J;

DR WPI; 2001-335933/35.

DR N-PSDB; AAH84614.

PT Novel nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors.

PS Claim 19; Page 476; 522pp; English.

CC AAH84373 to AAH84499 represent Escherichia coli growth and proliferation  
CC related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli growth  
CC and proliferation related proteins given in AAG99078 and AAG98830 to  
CC AAG98999. (I) can be used as potential targets for the generation of new  
CC antimicrobial agents, and for identification of compounds which interact  
CC with the gene products of (I). In addition the expression of (I) and the  
CC purification of the proteins, the purified proteins can be used to  
CC generate reagents and screen small molecule libraries or other candidate  
CC compound libraries for compounds that can be further developed to yield  
CC novel antimicrobial compounds. In addition, nucleic acid probes  
CC complementary to (I) that are specific for particular species of  
CC microorganisms can be used to identify particular microorganism species  
CC in clinical specimens, therefore, providing a rapid and dependable method  
CC by which to identify the causative agents of a bacterial infection. Also,  
CC antibodies generated against proteins translated from mRNA transcribed  
CC from proliferation-regulated sequences can also be used to screen for  
CC specific microorganisms that produce such proteins in a species-specific  
CC manner. AAH84371 and AAH84670 represent sequencing primers used in the  
CC isolation of E. coli growth and proliferation related sequence, which are  
CC used in an example from the present invention

SO Sequence 98 AA;

Query Match 4.1%; Score 7; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LRIDYRS 52  
DB 59 LRIDYRS 65

RESULT 4

ID ABP02041 standard; protein; 132 AA.

AC ABP02041;

XX 25-JUN-2002 (first entry)  
 DT Human ORFX protein sequence SEQ ID NO:4064.  
 XX  
 DE  
 XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
 KW hyperproliferative disorder; psoriasis; benign tumor; haemorrhage;  
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;  
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
 KW hypertension; hypothyroidism; cholesterol ester storage disease;  
 KW immune deficiency; immune disorder; infectious disease;  
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
 KW myasthenia gravis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192523-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 29-MAY-2001; 2001WO-US010836.  
 XX  
 PR 30-MAY-2000; 2000US-0206132P.  
 XX  
 PR 29-AUG-2000; 2000US-0228716P.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shinkets RA, Leach MD;  
 XX  
 DR WPI; 2002-106308/14.  
 XX  
 DR N-PSDB; ABN17793.  
 XX  
 PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders.  
 XX  
 PS Disclosure; SEQ ID NO 4064; 1037bp; English.  
 XX  
 XX The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC - useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage. N.B. The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
 XX  
 SQ Sequence 132 AA;  
 Query Match 4.1%; Score 7; DB 5; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 37 RLRKVIA 43  
 DB 117 RLRKVIA 123

RESULT 5  
 ADS43113  
 ID ADS43113 standard; protein; 187 AA.  
 XX  
 AC ADS43113;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Bacterial polypeptide #21543.  
 XX  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomanan;  
 KW bacterial polypeptide.  
 XX  
 OS Bacteria.  
 XX  
 PN US200323675-A1.  
 XX  
 PD 18-DEC-2003.  
 XX  
 PF 20-FEB-2003; 2003US-00369493.  
 XX  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.  
 XX  
 PA (HINK/) HINKLE G J.  
 XX  
 PA (SLAT/) SLATER S C.  
 XX  
 PA (CHEN/) CHEN X.  
 XX  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 XX  
 DR WPI; 2004-061375/06.  
 XX  
 PT New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 XX  
 PS Claim 1; SEQ ID NO 21543; 122bp; English.  
 XX  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomanan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX  
 SQ Sequence 187 AA;  
 Query Match 4.1%; Score 7; DB 8; Length 187;

Best Local Similarity 100.0%; Pred. No. 80;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 SEDEVIG 102  
DB 154 SEDEVIG 160

# RESULT 6

AE60274  
ID AE60274 standard; protein; 191 AA.

AC AE60274;

DT 09-FEB-2006 (first entry)

DE Cat Chlamydia outer membrane protein SEQ ID NO: 69.

XX Chlamydia infection; antibacterial; conjunctivitis; ophthalmological;  
KW pneumonia; antiinflammatory; respiratory-gen.; bronchitis; diagnostic;  
KM vaccine; outer membrane protein.

OS Chlamydia sp.

PN JP200533964-A.

PD 08-DEC-2005.

PF 25-MAY-2004; E004JP-00183135.

PR 25-MAY-2004; 2004JP-00183135.

PA (UYAA-) UNITV YAMAGUCHI.

PI Shirai M, Azuma Y, Kuhara S, Hattori S, Fukushi H;

DR WPI; 2006-004059/01.

PT Novel nucleic acid derived from cat Chlamydia, useful as probe in  
PT detecting conjunctivitis, pneumonia or bronchitis.

PS Claim 6; SEQ ID NO 69; 19pp; Japanese.

XX The present sequence is one of a series of outer membrane proteins  
CC (AE60274-AE60310) derived from cat Chlamydia. The present invention  
CC relates to a 1166239 base nucleic acid sequence comprising the genome of  
CC cat Chlamydia (AE60206) or a 7552 base sequence comprising a Chlamydia  
CC plasmid (AE60207). Also claimed are cat Chlamydia proteins comprising:  
CC inclusion body membrane proteins (AE60208-AE60273); outer membrane  
CC proteins (AE60274-AE60310); type-3 secretion proteins (AE60311-  
CC AE60330); highly antigenic proteins (AE60331-AE60334); pathogenicity  
CC related proteins (AE60335-AE60392); heat shock proteins (AE60393-  
CC AE60400); and proteins which do not exist in pneumonia Chlamydia  
CC (AE60401-AE60526). Probes which target these nucleic acid or protein  
CC sequences are useful in screening methods, involving nucleic acid  
CC hybridization or base sequence determination, where the nucleic acid  
CC hybridization process is in situ hybridization or Southern hybridization  
CC process. Such screening methods are useful for detecting conjunctivitis,  
CC pneumonia and bronchitis, based on the presence or absence of a  
CC alteration in a gene (presence or absence of deletion or the point  
CC mutation). The disclosed sequences are also useful in producing vaccines  
CC for preventing infection of Chlamydia.

CC Sequence 191 AA;

Query Match 4.1%; Score 7; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ADSYDSK 33  
DB 62 ADSYDSK 68

RESULT 7  
ADM04932  
ID ADM04932 standard; protein; 198 AA.

AC ADM04932;

DT 20-MAY-2004 (first entry)

DE Human protein of the invention SEQ ID NO:3617.

XX human; gene therapy; diagnostic marker; pharmaceutical.

OS Homo sapiens.

PN EP1347046-A1.

PD 24-SEP-2003.

PF 12-APR-2002; 2002EP-00008400.

PR 22-MAR-2002; 2002JP-00137785.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Makamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Negahari K, Masuno Y;

DR WPI; 2003-723558/69.

DR N-PSDB; ADM02489.

PT New polynucleotides and polypeptides are useful in gene therapy, for  
PT developing a diagnostic marker or medicines for regulating their  
PT expression and activity, or as a target of gene therapy.

PS Claim 1; SEQ ID NO 3617; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded  
CC polypeptide. A polynucleotide of the invention may have a use in gene  
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful  
CC as a primer for synthesizing the polynucleotide or as a probe for  
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are  
CC useful in gene therapy, for developing a diagnostic marker or medicines  
CC for regulating their expression and activity, or as a target of gene  
CC therapy. The protein ADM03759-ADM06201 encoded by the polynucleotides  
CC are useful as pharmaceutical agents. The present sequence represents a  
CC protein sequence of the invention.

CC Sequence 198 AA;

Query Match 4.1%; Score 7; DB 7; Length 198;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 LGDPTLR 82  
DB 2 LGDPTLR 8

RESULT 8  
AEC87862  
ID AEC87862 standard; protein; 198 AA.

AC AEC87862;

DT 01-DEC-2005 (first entry)

DE Human cDNA clone protein NT3NE20159740, SEQ ID 3617.

XX Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-gen.;  
KM Anticancer; Gene therapy; Osteoporosis; cancer; inflammation; gastritis;  
KW stomach ulcer; gastrointestinal ulcer.

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XX OS Homo sapiens.
XX PN EPI580263-A1.
XX PD 28-SEP-2005.
XX PF 12-APR-2002; 2004EP-00027348.
XX PR 22-MAR-2002; 2002JP-00137785.
XX PR 12-APR-2002; 2002EP-00008400.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX DR WPI; 2005-667421/69.
XX DR N-PSDB; AEC85419.
XX PT New full-length cDNA sequences, useful for treating diseases, e.g.
XX PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.
XX PS Example 3; SEQ ID NO 3617; 296pp; English.
XX CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)
XX CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing
XX CC the functions of the proteins, and for developing medicines for diseases
XX CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal
XX CC ulcer. Note: The sequence data for this patent did not form part of the
XX CC printed specification but was obtained in electronic format directly from
XX CC EPO.
XX SQ Sequence 198 AA;
XX
XX Query Match 4.1%; Score 7; DB 9; Length 198;
XX Best Local Similarity 100.0%; Pred. No. 85;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 LGDPTLR 82
Db 2 LGDPTLR 8
XX
XX RESULT 9
XX ID ADX91359 standard; protein; 225 AA.
XX AC ADX91359;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polypeptide seqid 54023.
XX
XX KM plant protectant; plant growth regulant; gene therapy; plant;
XX KM recombinant DNA construct; physical array; plant breeding marker;
XX KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX KM extreme osmotic condition; pathogen tolerance; pest tolerance;
XX KM growth rate; cell cycle pathway; disease resistance;
XX KM galactomannan production; lignin production; plant growth regulator;
XX KM yield; plant growth; plant development; seed oil; protein yield;
XX KM protein content.
XX OS Unidentified.
XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.

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PR 05-NOV-2001; 2001US-00985678.
XX PA (LIU/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABAS/) TABASKA J E.
XX PA (CAO/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX DR WPI; 2004-180133/17.
XX PT New recombinant DNA construct, useful for improving plant tolerance to
XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX PT pests, for conferring increased resistance to plant disease, or for
XX PT improving yield.
XX PS Claim 1; SEQ ID NO 54023; 15pp; English.
XX CC The invention describes a recombinant DNA construct comprising a
XX CC polynucleotide consisting of a sequence encoding an amino acid sequence
XX CC available in electronic form from the US patent office at
XX CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX CC of the invention are also useful in physical arrays of molecules and as
XX CC plant breeding markers. The recombinant DNA construct is useful for
XX CC improving plant tolerance to cold, heat, drought, herbicides, extreme
XX CC osmotic conditions, pathogens or pests, for manipulating growth rate in
XX CC plant cells by modification of the cell cycle pathway, for conferring
XX CC increased resistance to plant disease, for producing galactomannan,
XX CC lignin or plant growth regulators, for increasing the rate of homologous
XX CC recombination in plants, for improving yield by modification of
XX CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX CC or by providing improved plant growth and development under at least one
XX CC stress condition or for modifying seed oil or protein yield and/or
XX CC content. This is the amino acid sequence of a plant full length insert
XX CC polypeptide that can be used in the recombinant DNA construct of the
XX CC invention.
XX SQ Sequence 225 AA;
XX
XX Query Match 4.1%; Score 7; DB 8; Length 225;
XX Best Local Similarity 100.0%; Pred. No. 96;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 QVQKSDE 10
Db 20 QVQKSDE 26
XX
XX RESULT 10
XX ID ABO62543 standard; protein; 251 AA.
XX AC ABO62543;
XX DT 29-JUL-2004 (first entry)
XX DE Klebsiella pneumoniae polypeptide seqid 9060.
XX KM Klebsiella pneumoniae polypeptide seqid 9060.
XX KM Recombinant expression vector; transcription regulatory element;
XX KM Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX OS Klebsiella pneumoniae.
XX PN US6610836-B1.
XX PD 26-AUG-2003.
XX PF 27-JAN-2000; 2000US-00489039.
XX PR 29-JAN-1999; 99US-0117747P.
XX

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PA (GENO-) GENOME THERAPEUTICS CORP.  
XX Breton GL, Osborne M;  
XX WPI, 2003-895346/82.  
DR N-PSDB; ACH96094.  
XX  
XX  
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
PT preparing a vaccine composition against Klebsiella pneumoniae.  
XX  
PS Disclosure, SEQ ID NO 9060; 932pp; English.  
XX  
XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
CC pneumoniae polypeptide. Also described are: a recombinant expression  
CC vector comprising the nucleic acid, operably linked to a transcription  
CC regulatory element; and a cell comprising the recombinant expression  
CC vector. The nucleic acid is useful for preparing a vaccine composition  
CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
XX Klebsiella pneumoniae polypeptide of the invention  
XX  
SQ Sequence 251 AA;  
  
Query Match 4.1%; Score 7; DB 7; Length 251;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 140 GYWKFG 146  
Db 212 GYWKFG 218  
  
RESULT 11  
AAU21761  
ID AAU21761 standard; protein; 255 AA.  
XX  
XX AAU21761;  
XX  
DT 06-DEC-2001 (first entry)  
XX  
XX Novel human neoplastic disease associated polypeptide #194.  
DE  
XX  
XX Human; neoplastic disease associated polypeptide; cancer;  
KW hyperproliferative disorder; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW neuroprotective; cytostatic; anti inflammatory; vasotropic.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2001515163-A1.  
PN  
XX  
PD 02-AUG-2001.  
XX  
XX  
PF 17-JAN-2001; 2001WO-US001358.  
XX  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214866P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225677P.  
PR 14-AUG-2000; 2000US-0225688P.  
PR 14-AUG-2000; 2000US-0225707P.  
PR 14-AUG-2000; 2000US-0225547P.  
PR 14-AUG-2000; 2000US-0225157P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 06-SEP-2000; 2000US-0231242P.  
PR 06-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232977P.  
PR 14-SEP-2000; 2000US-0232978P.  
PR 14-SEP-2000; 2000US-0232988P.  
PR 14-SEP-2000; 2000US-0232999P.  
PR 14-SEP-2000; 2000US-0232400P.  
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PR	11-DEC-2000	2000US-0254097P.
PR	05-JAN-2001	2001US-0259676P.
PA	(HUMA-)	HUMAN GENOME SCI INC.
XX		
XX		
PI	Rosen CA, Barash SC, Ruben SM,	
XX	WPI, 2001-465558/50.	
DR	N-PSDB; AAS34960.	
XX		
PT	Novel polypeptides and polynucleotides useful as diagnostic reagents to	
PT	diagnose diseases or disorders associated with aberrant expression or	
PT	activity of polypeptides, and for treating cancers, rheumatoid arthritis.	
XX		
XX	Claim 11; SEQ ID NO 488; 687bp; English.	
XX		
XX		
CC	The present invention relates to the isolation of novel human neoplastic	
CC	disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA	
CC	sequences encoding for these polypeptides. The sequences of the invention	
CC	are useful in the diagnosis, treatment, prevention and/or prognosis of	
CC	disorders involving neoplastic disease such as hyperproliferative	
CC	disorders (e.g. leukemias, bone cancer, bladder cancer, brain stem	
CC	glioma, adult liver cancer, childhood cerebellar astrocytoma, or	
CC	Hodgkin's lymphoma). The sequences of the invention may also be useful	
CC	for treating other disorders such as neural disorders, immune system	
CC	disorders, muscular disorders, reproductive disorders, gastrointestinal	
CC	disorders, pulmonary disorders, cardiovascular disorders and renal	
CC	disorders. The polynucleotide sequences of the invention are also useful	
CC	in gene therapy. AAV21566-AAV21851 represent the novel human neoplastic	
CC	disease associated polypeptides of the invention. Note: The sequence data	

CC	for this patent did not form part of the printed specification, but was									
CC	obtained in electronic format directly from WIPO at									
CC	ftp.wipo.int/pub/published_pct_sequences									
XX										
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DT	07-NOV-2001 (first entry)									
XX										
DE	Human immune/haematopoietic antigen SEQ ID NO:11430.									
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KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;									
XX	cytostatic; gene therapy; vaccine; metastasis.									
OS	Homo sapiens.									
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PN	WO200157182-A2.									
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PD	09-AUG-2001.									
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PF	17-JAN-2001; 2001WO-US001354.									
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PR	11-DEC-2000	2000US-0254037P
PR	05-JAN-2001	2001US-0259678P

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

**N-PSDB; AAK56618.**

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 11; SEQ ID NO 11430; 3071pp + Sequence Listing; English.

XX

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic

CC activity, and can be used in gene therapy and vaccine production. (I)

CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For

CC example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to

CC supplement the patients own production of (I). Additionally, (I)

polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the

CC protein (T) proteins and polynucleotides may be used to prevent  
CC nucleic acids into a host cell and carrying the cell to express the

CC proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially

CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703

CC to AAK87694 represent human immune/haematopoietic antigen genomic

sequences from the present invention. AAK54942 to AAK54950 and AAM82169

represent sequences used in the exemplification of the present invention

XX 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

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Query Match 4.18; Score 7; DB 4; Length 255;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

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**RECEIVED 13**

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ID	ADUC4040Z Standard; protein; 255 AA.
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ADPC46402:

[illegible]

XX 18-DEC-2003 (first entry)  
DT Human neoplastic disease-associated gene 40 protein #2.  
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DE  
XX Neoplastic disease-associated polypeptide; gene therapy;  
KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;  
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;  
KW haematologic disorder; anaemia; thrombocytopenia; allergic reaction;  
KW acutina; eczema; inflammatory disorder; ischaemia-reperfusion injury;  
KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; renal disorder;  
KW acute glomerulonephritis; end-stage renal disease;  
KW cardiovascular disorder; atherosclerosis; myocarditis;  
KW infectious disease; AIDS; cachexia; anorexia; wound healing;  
KW epithelial cell proliferation; Human.  
XX  
OS Homo sapiens.  
XX  
XX US2003082758-A1.  
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XX  
PD 01-MAY-2003.  
XX  
PF 22-MAR-2002; 2002US-0010313.  
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PR 17-JAN-2001; 2001US-00764854.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
PI
XX WPI, 2003-786918/74.
XX N-PSDB; ADC6118.
XX
XX New isolated human neoplastic disease-associated polypeptides and
PT polynucleotides, useful for diagnosing, preventing, prognosticating or
PT treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
PT disease.
XX
XX Claim 1; SEQ ID NO 488; 302pp; English.
XX
XX The invention relates to one of 238 disclosed human neoplastic disease-
CC associated polypeptides encoded by 171 disclosed cDNA sequences
CC (including their domains, epitopes, full-length proteins, allelic variants
CC or species homologues). Also included are there encoding nucleic acids, a
CC recombinant vector comprising the nucleic acid, a recombinant host cell
CC comprising the nucleic acid (expressing the protein), an isolated
CC antibody that binds specifically to the isolated polypeptide, preventing,
CC treating or ameliorating a medical condition, diagnosing a pathological
CC condition or a susceptibility to a pathological condition in a subject,
CC identifying a binding partner to the polypeptide, identifying an activator
CC in a biological assay, and the gene corresponding to the cDNA sequence.
CC The polypeptides, polynucleotides and antibodies are useful for
CC detecting, preventing, diagnosing, prognosticating, treating or
CC ameliorating medical conditions such as hyperproliferative diseases or
CC cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
CC systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
CC or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
CC anaemia or thrombocytopaenia), allergic reactions including asthma or
CC eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
CC
XX
XX Query Match 4.1%; Score 7; DB 7; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 36 DRLRKVI 42
XX |||||
XX 116 DRLRKVI 122
XX
XX RESULT 14
XX ADX79742
XX ID ADX79742 standard; protein; 255 AA.
XX
XX AC ADX79742;
XX
XX 23-MAR-2006 (revised)
XX DT 21-APR-2005 (first entry)
XX
XX plant full length insert polypeptide seqid 49108.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX

```

```

XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomanan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content.
XX
XX Zea mays.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABAS/) TABASKA J E.
XX (CAO/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI
XX WPI, 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 49108; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdat.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomanan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Revised record issued on 23-MAR-2006 : Corrected organism line
XX
XX Sequence 255 AA;
XX
XX Query Match 4.1%; Score 7; DB 8; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 2 GSOVQKS 8
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XX 115 GSOVQKS 121
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XX RESULT 15
XX ADO02033
XX ID ADO02033 standard; protein; 258 AA.
XX

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AC ADO02033;  
 XX  
 PS  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Thalecress transcription factor protein #223.  
 XX  
 KW Thalecress; transcription factor; plant; transgenic; abiotic stress;  
 KW cold tolerance; heat tolerance; drought; osmotic stress;  
 KW phosphate limitation; potassium limitation; nitrogen limitation;  
 KW hormone sensitivity; disease resistance; sugar sensing; seed germination;  
 KW flowering; inflorescence architectural change;  
 KW meristem cell differentiation; phyllotaxy; apical dominance;  
 KW trichome development; seed development; premature senescence;  
 KW delayed senescence; lethality; necrosis; plant size; leaf morphology;  
 KW seed morphology; secondary metabolism; light response; shade avoidance.  
 XX  
 OS Arabidopsis thaliana.  
 PN US2004045049-A1.  
 PD  
 XX  
 PD 04-MAR-2004.  
 XX  
 PF 10-APR-2003; 2003US-00412699.  
 XX  
 XX 13-SEP-1999; 99US-00394519.  
 PR 21-JAN-2000; 2000US-00489376.  
 PR 17-FEB-2000; 2000US-00506720.  
 PR 22-MAR-2000; 2000US-00532591.  
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 PR 22-MAR-2000; 2000US-00533030.  
 PR 22-MAR-2000; 2000US-00533392.  
 PR 22-MAR-2000; 2000US-00533648.  
 PR 06-APR-2000; 2000WO-00099448.  
 PR 16-NOV-2000; 2000US-00713994.  
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 PR 17-APR-2001; 2001US-00837444.  
 PR 30-JAN-2002; 2002US-00958131.  
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 PR 09-AUG-2002; 2002US-00225066.  
 PR 09-AUG-2002; 2002US-00225067.  
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 PR 17-DEC-2002; 2002US-0434166P.  
 PR 25-FEB-2003; 2003US-00374780.  
 XX  
 PA (ZHAN/) ZHANG J.  
 PA (FROM/) FROMM M E.  
 PA (HEAR/) HEARD J E.  
 PA (RIEC/) RIECHMANN J L.  
 PA (ADAM/) ADAM L J.  
 PA (BROU/) BROUN P E.  
 PA (PINE/) PINEDA O.  
 PA (REUB/) REUBER T L.  
 PA (KEDU/) KEDDIE J S.  
 PA (YUGG/) YU G.  
 PA (JIAN/) JIANG C.  
 PA (SAMA/) SAMAHA R S.  
 PA (PIIG/) PILGRIM M L.  
 PA (CREE/) CREELMAN R A.  
 PA (DUBE/) DUBELL A N.  
 PA (RATC/) RATCLIFFE O.  
 PA (KUMI/) KUMIMOTO R.  
 PA (SHER/) SHERMAN B K.  
 XX  
 PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE,  
 PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS,  
 PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R,  
 PI Sherman BK;  
 XX  
 DR WPI; 2004-225755/21.  
 DR N-PSDB; ADO02032.  
 XX  
 PT New transgenic plant, useful in developing phenotypes with altered or improved characteristics or traits.

XX  
 PS Claim 1; SEQ ID NO 446; 213pp; English.  
 XX  
 CC The invention relates to a transgenic plant comprises a recombinant  
 CC polynucleotide having a polynucleotide sequence or its complementary  
 CC sequence comprising a sequence encoding a polypeptide, that initiates  
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,  
 CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588  
 CC -ADO03527 or ADO0530-ADO03559. Also included are using a transgenic  
 CC plant to grow a progeny plant, an expression cassette (comprising a  
 CC constitutive, inducible or tissue-specific promoter and a recombinant  
 CC polynucleotide described above), a host cell comprising the expression  
 CC cassette, producing a modified plant having a modified trait, identifying  
 CC a factor that is modulated by or interacts with a polypeptide encoded by  
 CC the polynucleotide sequence and identifying at least one downstream  
 CC polynucleotide sequence that is subject to a regulatory effect of any of  
 CC the polypeptides encoded by the polynucleotide described above. The  
 CC transgenic plant is useful for producing a plant that has an altered  
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance  
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance  
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to  
 CC salt, tolerance to phosphate limitation, tolerance to potassium  
 CC limitation, decreased sensitivity to nitrogen limitation), altered  
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered  
 CC response to ethylene, disease resistance, altered susceptibility to  
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to  
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered  
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed  
 CC germination and seedling vigor, early flowering, late flowering, extended  
 CC period of flowering, an inflorescence architectural change, a change in  
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell  
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced  
 CC apical dominance, reduced trichome density, ectopic trichome development,  
 CC altered trichome development, altered stem morphology, increased root  
 CC growth, increased root hairs, altered seed development, altered cell  
 CC proliferation/cell differentiation, premature senescence, delayed  
 CC senescence, lethality, increased necrosis, an increase in seedling or  
 CC plant size, decreased plant size, a change in leaf morphology, increased  
 CC altered leaf development, increased leaf size and mass, glossy leaves,  
 CC leaf cell expansion, change in seed morphology, altered seed coloration,  
 CC increased seed size, decreased seed size, altered seed shape, change in  
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid  
 CC content, increased leaf insoluble sugars, decreased leaf insoluble  
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid  
 CC content, an alteration of leaf glucosinolate content, change in seed  
 CC biochemistry, an increase in seed oil content, decrease in seed oil  
 CC content, increase in seed fatty acid content, decrease in seed fatty acid  
 CC content, alteration in seed protein content, decrease in seed protein  
 CC content, alteration in seed prenyl lipid content, increase in seed  
 CC sterols, upregulation of genes involved in secondary metabolism, increase  
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in  
 CC light response or shade avoidance. The present sequence represents a  
 CC thalecress transcription factor of the invention.  
 XX  
 SQ Sequence 258 AA;  
 QY  
 DB 155 EFPDFRI 161  
 188 EFPDFRI 194

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#### SUMMARIES

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4	7	4.1	251	2	US-09-489-039A-9060
5	7	4.1	259	1	US-08-629-291A-30
6	7	4.1	259	1	US-08-658-335B-30
7	7	4.1	259	2	US-09-406-640-30
8	7	4.1	286	2	US-09-319-806-4
9	7	4.1	287	2	US-09-902-540-12543
10	7	4.1	294	2	US-09-230-637-31
11	7	4.1	361	2	US-09-270-767-42397
12	7	4.1	463	2	US-10-104-047-2880
13	7	4.1	626	2	US-09-155-770-7
14	7	4.1	806	2	US-09-949-016-8753
15	7	4.1	883	1	US-07-718-575-4
16	7	4.1	883	1	US-08-481-206-4
17	7	4.1	883	1	US-08-687-379-6
18	7	4.1	883	1	US-08-687-379-8
19	7	4.1	883	1	US-08-486-269A-4
20	7	4.1	883	2	US-08-483-327-2
21	7	4.1	883	2	US-08-666-221B-2
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24	7	4.1	883	2	US-08-439-946-2
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26	7	4.1	1323	1	US-08-026-138B-4

27	7	4.1	1336	1	US-08-231-193A-58	Sequence 58, Appl
28	7	4.1	1336	1	US-08-486-273A-58	Sequence 58, Appl
29	7	4.1	1336	2	US-08-940-086A-58	Sequence 58, Appl
30	7	4.1	1336	2	US-08-940-035A-58	Sequence 58, Appl
31	7	4.1	1336	2	US-08-935-105A-58	Sequence 58, Appl
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33	7	4.1	1336	2	US-09-386-123-58	Sequence 58, Appl
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36	7	4.1	1336	2	US-09-945-901-58	Sequence 58, Appl
37	7	4.1	1345	2	US-09-949-016-11209	Sequence 11209, A
38	6	3.5	17	2	US-09-461-325-305	Sequence 305, App
39	6	3.5	17	2	US-10-012-542-305	Sequence 305, App
40	6	3.5	17	2	US-10-115-123-305	Sequence 305, App
41	6	3.5	18	1	US-08-640-847C-36	Sequence 36, Appl
42	6	3.5	37	1	US-08-448-481-5	Sequence 5, Appl
43	6	3.5	42	1	US-08-377-687-39	Sequence 39, Appl
44	6	3.5	42	1	US-08-777-192-39	Sequence 39, Appl
45	6	3.5	42	2	US-08-971-982-39	Sequence 39, Appl

#### ALIGNMENTS

RESULT 1  
US-09-270-767-41287  
; Sequence 41287, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41287  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-41287

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Best Local Similarity 100.0%; Pred. No. 9.2;  
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Db 35 YRSFLDK 41

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; Sequence 56503, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56503  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-56503

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Best Local Similarity 100.0%; Pred. No. 9.2;  
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## RESULT 3

US-09-711-164-413  
; Sequence 413, Application US/09711164  
; Patent No. 6589738  
; GENERAL INFORMATION:  
; APPLICANT: Forsyth, R. Allyn  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET  
; FILE REFERENCE: ELITRA.008A  
; CURRENT APPLICATION NUMBER: US/09/711,164  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR APPLICATION NUMBER: US 60/164415  
; PRIOR FILING DATE: 1999-11-9  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 413  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-711-164-413

Query Match 4.1%; Score 7; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 46 LRIDYRS 52  
Db 59 LRIDYRS 65

## RESULT 4

US-09-489-039A-9060  
; Sequence 9060, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 9060  
; LENGTH: 251  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9060

Query Match 4.1%; Score 7; DB 2; Length 251;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 140 GWKFRAG 146  
Db 212 GWKFRAG 218

## RESULT 5

US-08-629-291A-30  
; Sequence 30, Application US/08629291A  
; Patent No. 5959174  
; GENERAL INFORMATION:  
; APPLICANT: Coruzzi, Gloria  
; APPLICANT: Oliveira, Igor  
; APPLICANT: Lam, Hon-Ming

APPLICANT: Hsieh, Ming-Hsiun  
; TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/629,291A  
; FILING DATE: 08-APR-1996  
; CLASSIFICATION: 800

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 5914-050  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 259 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-629-291A-30

Query Match 4.1%; Score 7; DB 1; Length 259;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 162 FEDGRET 168  
Db 48 FEDGRET 54

## RESULT 6

US-08-658-335B-30  
; Sequence 30, Application US/08658335B  
; Patent No. 5981703  
; GENERAL INFORMATION:  
; APPLICANT: Coruzzi, Gloria  
; APPLICANT: Oliveira, Igor  
; APPLICANT: Lam, Hon-Ming  
; APPLICANT: Hsieh, Ming-Hsiun  
; TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/658,335B  
; FILING DATE: 05-JUN-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:



NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 5914-052  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 259 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-658-335B-30.

Query Match 4.1%; Score 7; DB 1; Length 259;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 FEDGET 168  
Db 48 FEDGET 54

RESULT 7  
US-09-406-640-30  
Sequence 30, Application US/09406640  
Patent No. 6451546  
GENERAL INFORMATION:  
APPLICANT: Coruzzi, Gloria  
Oliveira, Igor  
Lam, Hon-Ming  
Hsieh, Ming-Heiun  
TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,640  
FILING DATE: 27-Sep-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 5914-082  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 259 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-406-640-30

Query Match 4.1%; Score 7; DB 2; Length 259;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 FEDGET 168  
Db 48 FEDGET 54

RESULT 8  
US-09-319-806-4  
Sequence 4, Application US/09319806  
Patent No. 6830891  
GENERAL INFORMATION:  
APPLICANT: Cramerl, Reto  
APPLICANT: Hemman, Stefanie  
APPLICANT: Blaser, Kurt  
TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary  
FILE REFERENCE: 10806-93  
CURRENT APPLICATION NUMBER: US/09/319,806  
CURRENT FILING DATE: 1999-08-19  
PRIOR APPLICATION NUMBER: SE9604815-2  
PRIOR FILING DATE: 1996-12-20  
PRIOR APPLICATION NUMBER: PCT/SE97/02171  
PRIOR FILING DATE: 1997-12-19  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 4  
LENGTH: 286  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
US-09-319-806-4

Query Match 4.1%; Score 7; DB 2; Length 286;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WGEFDFD 159  
Db 200 WGEFDFD 206

RESULT 9  
US-09-902-540-12543  
Sequence 12543, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 12543  
LENGTH: 287  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-12543

Query Match 4.1%; Score 7; DB 2; Length 287;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 PTLRIDY 50  
Db 232 PTLRIDY 238

RESULT 10  
US-09-230-637-31  
; Sequence 31, Application US/09230637  
; Patent No. 6264958  
; GENERAL INFORMATION:  
; APPLICANT: Hayward, Gary  
; APPLICANT: Nicholas, John  
; APPLICANT: Hardwick, J. Marie  
; APPLICANT: Reitz, Marvin  
; TITLE OF INVENTION: No. 6264958e1 Genes of Kaposi's Sarcoma  
; FILE REFERENCE: 1107.78372  
; CURRENT APPLICATION NUMBER: US/09/230,637  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: 60/022,591  
; PRIOR FILING DATE: 1996-07-25  
; PRIOR APPLICATION NUMBER: PCT US 97/12931  
; PRIOR FILING DATE: 1997-07-24  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 294  
; TYPE: PRT  
; ORGANISM: Herpes simplex  
US-09-230-637-31

Query Match 4.1%; Score 7; DB 2; Length 294;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RSFLDKL 57  
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Db 96 RSFLDKL 102

RESULT 11  
US-09-270-767-42397  
; Sequence 42397, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 42397  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-42397

Query Match 4.1%; Score 7; DB 2; Length 361;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RSFLDKL 57  
|||||  
Db 270 RSFLDKL 276

RESULT 12  
US-10-104-047-2880  
; Sequence 2880, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241e1 full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25

; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2880  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2880

Query Match 4.1%; Score 7; DB 2; Length 463;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RSFLDKL 57  
|||||  
Db 177 RSFLDKL 183

RESULT 13  
US-09-155-770-7  
; Sequence 7, Application US/09155770A  
; Patent No. 6300484  
; GENERAL INFORMATION:  
; APPLICANT: Dahl, David  
; TITLE OF INVENTION: DNA ENCODING DP-75 AND A PROCESS FOR ITS USE  
; FILE REFERENCE: 200130.418  
; CURRENT APPLICATION NUMBER: US/09/155,770A  
; CURRENT FILING DATE: 1998-09-30  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 626  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-155-770-7

Query Match 4.1%; Score 7; DB 2; Length 626;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 DRLRKYI 42  
|||||  
Db 23 DRLRKYI 29

RESULT 14  
US-09-949-016-8753  
; Sequence 8753, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8753  
; LENGTH: 806  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8753

Query Match 4.1%; Score 7; DB 2; Length 806;  
Best Local Similarity 100.0%; Pred. No. 90;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 162 FEDGRET 168  
Db 615 FEDGRET 621

RESULT 15  
US-07-718-575-4  
; Sequence 4, Application US/07718575  
; Patent No. 5202257  
; GENERAL INFORMATION:  
; APPLICANT: Heinemann Ph.D., Stephen F.  
; APPLICANT: Boulter Ph.D., James R.  
; APPLICANT: Hollmann Ph.D., Michael NMN  
; APPLICANT: Bettler Ph.D., Bernhard NMN  
; APPLICANT: Jensen Ph.D., Jan E.  
; TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Pretty, Schroeder, Bruggemann & Clark  
; STREET: 444 So. Flower St., Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: United States  
; ZIP: 90071-2921  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/718,575  
; FILING DATE: 19910813  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter Ph.D., Stephen E.  
; REGISTRATION NUMBER: 31192  
; REFERENCE/DOCKET NUMBER: P31 8962  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; TELEX: 9103330318  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 883 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-718-575-4

Query Match 4.1%; Score 7; DB 1; Length 883;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 162 FEDGRET 168  
Db 577 FEDGRET 583

Search completed: December 5, 2006, 01:14:43  
Job time : 55 secs

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OM protein - protein search, using sw model

Run on: December 5, 2006, 01:14:01 ; Search time 187 Seconds  
(without alignments)  
426.059 Million cell updates/sec

Title: US-10-507-132-4  
Perfect score: 172  
Sequence: 1 MGSQVQKSDRITFSIDYGLM.....WGEFDPRIPEDEGFEFGDK 172

Scoring table: OLIGO  
Gapop 60.0 , Gapept 60.0

Searched: 2097797 seqs, 463214858 residues

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Minimum DB seq length: 0  
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- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	4.1	75	4 US-10-425-115-186523	Sequence 186523,
2	7	4.1	98	4 US-10-287-274-413	Sequence 413, App
3	7	4.1	139	4 US-10-424-599-187642	Sequence 187642,
4	7	4.1	187	4 US-10-369-493-21543	Sequence 21543, A
5	7	4.1	198	4 US-10-108-260A-3617	Sequence 3617, Ap
6	7	4.1	219	4 US-10-425-115-35717	Sequence 35717, A
7	7	4.1	225	4 US-10-425-114-54023	Sequence 54023, A
8	7	4.1	228	4 US-10-424-599-167826	Sequence 167826,
9	7	4.1	236	4 US-10-425-115-232623	Sequence 232623,
10	7	4.1	255	4 US-10-103-313-488	Sequence 488, App
11	7	4.1	258	4 US-10-425-114-49108	Sequence 49108, A
12	7	4.1	258	4 US-10-412-659B-446	Sequence 446, App
13	7	4.1	259	4 US-10-223-047-30	Sequence 30, App1
14	7	4.1	286	5 US-10-612-358-4	Sequence 4, App1
15	7	4.1	293	4 US-10-369-493-11818	Sequence 11818, A
16	7	4.1	312	4 US-10-437-963-185545	Sequence 185545,
17	7	4.1	327	4 US-10-424-599-209185	Sequence 209185,
18	7	4.1	388	6 US-11-097-143-23043	Sequence 23043, A
19	7	4.1	429	5 US-10-506-454-684	Sequence 684, App
20	7	4.1	450	3 US-09-764-864-804	Sequence 804, App
21	7	4.1	463	4 US-10-104-047-2880	Sequence 2880, Ap
22	7	4.1	463	6 US-11-072-512-2880	Sequence 2880, Ap
23	7	4.1	470	5 US-10-810-352-68	Sequence 68, App1
24	7	4.1	486	6 US-11-079-463-7267	Sequence 7267, Ap
25	7	4.1	489	4 US-10-282-122A-51224	Sequence 51224, A
26	7	4.1	491	4 US-10-437-963-195742	Sequence 195742,
27	7	4.1	504	4 US-10-437-963-182249	Sequence 182249,

28	7	4.1	528	6 US-11-188-298-8025	Sequence 8025, Ap
29	7	4.1	533	4 US-10-437-963-108161	Sequence 108161,
30	7	4.1	600	5 US-10-450-763-38123	Sequence 38123, A
31	7	4.1	626	4 US-10-310-671-7	Sequence 7, App1
32	7	4.1	626	4 US-10-310-671-11	Sequence 11, App1
33	7	4.1	716	4 US-10-369-493-12942	Sequence 12942, A
34	7	4.1	719	4 US-10-103-313-334	Sequence 334, App
35	7	4.1	750	4 US-10-437-963-185546	Sequence 185546,
36	7	4.1	762	6 US-11-097-143-10509	Sequence 10509, A
37	7	4.1	807	4 US-10-367-094-185	Sequence 185, App
38	7	4.1	847	4 US-10-478-245-7	Sequence 7, App1
39	7	4.1	875	4 US-10-367-094-178	Sequence 178, App
40	7	4.1	877	4 US-10-367-094-183	Sequence 183, App
41	7	4.1	883	4 US-10-177-293-190	Sequence 190, App
42	7	4.1	883	5 US-10-482-029-301	Sequence 301, App
43	7	4.1	883	5 US-10-753-267-102	Sequence 102, App
44	7	4.1	883	5 US-10-936-626-141	Sequence 141, App
45	7	4.1	883	5 US-10-938-061-141	Sequence 141, App

## ALIGNMENTS

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RESULT 1
US-10-425-115-186523
; Sequence 186523, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 186523
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_10169C.1.pep
US-10-425-115-186523

Query Match      4.1%; Score 7; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      143 KPAKLR 149
Db      61 KPAKLR 67

RESULT 2
US-10-287-274-413
; Sequence 413, Application US/10287274
; Publication No. US20030181408A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlson, Karl
; APPLICANT: Zykend, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
; FILE REFERENCE: ELITTA.008DVI
; CURRENT APPLICATION NUMBER: US/10/287,274
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0

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SEQ ID NO 413  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-10-287-274-413

Query Match 4.1%; Score 7; DB 4; Length 98;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 LRIDYRS 52  
DB 59 LRIDYRS 65

RESULT 3  
US-10-424-599-187642  
Sequence 187642, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J  
APPLICANT: Kovalic, David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 187642

LENGTH: 139  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(139)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_140454C.1.pep  
US-10-424-599-187642

Query Match 4.1%; Score 7; DB 4; Length 139;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 GLKPDTR 152  
DB 124 GLKPDTR 130

RESULT 4  
US-10-369-493-21543  
Sequence 21543, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 21543

LENGTH: 187  
TYPE: PRT  
ORGANISM: Methanobacterium thermoautotrophicum

US-10-369-493-21543

Query Match 4.1%; Score 7; DB 4; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 SEDEVIG 102  
DB 154 SEDEVIG 160

RESULT 5  
US-10-108-260A-3617  
Sequence 3617, Application US/10108260A  
Publication No. US20040005560A1  
GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: NO. US20040005560A1 full length cDNA  
FILE REFERENCE: H1-A0106  
CURRENT APPLICATION NUMBER: US/10/108,260A  
CURRENT FILING DATE: 2002-03-27  
NUMBER OF SEQ ID NOS: 5458  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 3617  
LENGTH: 198  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-108-260A-3617

Query Match 4.1%; Score 7; DB 4; Length 198;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 LGDPTLR 82  
DB 2 LGDPTLR 8

RESULT 6  
US-10-425-115-335717  
Sequence 335717, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 335717  
LENGTH: 219  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_6927C.1.pep  
US-10-425-115-335717

Query Match 4.1%; Score 7; DB 4; Length 219;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSOVQKS 8  
DB 79 GSOVQKS 85

RESULT 7  
US-10-425-114-54023  
Sequence 54023, Application US/10425114

```
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54023
LENGTH: 225
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701068004_FLI pep
US-10-425-114-54023
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Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 225;
Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 4 QVOKSDE 10
DB 20 QVOKSDE 26
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```
RESULT 8
US-10-424-599-167826
Sequence 167826, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 167826
LENGTH: 228
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_122563C.1.pep
US-10-424-599-167826
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Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 228;
Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 4 QVOKSDE 10
DB 23 QVOKSDE 29
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```
RESULT 9
US-10-425-115-232623
Sequence 232623, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

```
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 232623
LENGTH: 236
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(236)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_143745C.1.pep
US-10-425-115-232623
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```
Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 236;
Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 94 KXSEDEV 100
DB 126 KXSEDEV 132
```

```
RESULT 10
US-10-103-313-488
Sequence 488, Application US/10103313
Publication No. US20030082758A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: RJ207C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 488
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (223)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc_feature
LOCATION: (232)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-488
```

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Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 255;
Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 36 DRLRKVI 42
DB 116 DRLRKVI 122
```

```
RESULT 11
US-10-425-114-49108
Sequence 49108, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
```

APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(5313) B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 49108  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: 700048791\_FLI.pep  
US-10-425-114-49108

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSQVOKS 8  
Db 115 GSQVOKS 121

RESULT 12  
US-10-412-699B-446  
Sequence 446, Application US/10412699B  
Publication No. US20040045049A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Zhang, James  
APPLICANT: Fromm, Michael E.  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Adam, Luc U.  
APPLICANT: Brown, Pierre E.  
APPLICANT: Pineda, Omaira  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddle, James S.  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Uiang, Cai-Zhong  
APPLICANT: Samaha, Raymond R.  
APPLICANT: Pilgrim, Marsha L.  
APPLICANT: Creelman, Robert A.  
APPLICANT: Dubell, Arnold N.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Kumamoto, Roderick  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
FILE REFERENCE: NBI-0048CIP  
CURRENT APPLICATION NUMBER: US/10/412,699B  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 09/394,519  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: 09/489,376  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: 09/506,720  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: 09/533,030  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,192  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,029  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/532,591  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,648  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/713,994  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 09/819,142  
PRIOR FILING DATE: 2001-03-27

Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2011  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 446  
LENGTH: 258  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G669  
US-10-412-699B-446

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 EFDPR1 161  
Db 188 EFDPR1 194

RESULT 13  
US-10-223-047-30  
Sequence 30, Application US/10223047  
Publication No. US2003002305A1  
GENERAL INFORMATION:  
APPLICANT: Coruzzi, Gloria  
Oliveira, Igor  
Lam, Hon-Ming  
Hsieh, Ming-Hsiun  
TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/223,047  
FILING DATE: 16-Aug-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/406,640  
FILING DATE: 27-Sep-1999  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 5914-082  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 259 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-10-223-047-30

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 EFDRET 168



Db 48 FEDGRET 54

Db 218 DRLKVI 224

Search completed: December 5, 2006, 01:17:56  
Job time : 188 secs

## RESULT 14

US-10-612-358-4  
; Sequence 4, Application US/10612358  
; Publication No. US2005074410A1  
; GENERAL INFORMATION:  
; APPLICANT: Cramerl, Reto  
; APPLICANT: Hemman, Stefanie  
; APPLICANT: Blaser, Kurt  
; TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary  
; FILE REFERENCE: 10806-93  
; CURRENT APPLICATION NUMBER: US/10/612,358  
; CURRENT FILING DATE: 2003-07-02  
; PRIOR APPLICATION NUMBER: SE9604815-2  
; PRIOR FILING DATE: 1996-12-20  
; PRIOR APPLICATION NUMBER: PCT/SE97/02171  
; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: US09/319806  
; PRIOR FILING DATE: 1999-08-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recombinant  
; OTHER INFORMATION: allergan rasp f4  
US-10-612-358-4

## Query Match

Best Local Similarity 4.1%; Score 7; DB 5; Length 286;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 WGEFDFD 159

Db 200 WGEFDFD 206

## RESULT 15

US-10-369-493-11818  
; Sequence 11818, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianning  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 11818  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Mesorhizobium loti  
US-10-369-493-11818

## Query Match

Best Local Similarity 4.1%; Score 7; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 DRLKVI 42

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/ CURRENT FILING DATE: 2004-09-10  
/ PRIOR APPLICATION NUMBER: JP 2002-66955  
/ PRIOR FILING DATE: 2002-03-12  
/ NUMBER OF SEQ ID NOS: 19  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 2  
/ LENGTH: 172  
/ TYPE: PRT  
/ ORGANISM: Pyricularia oryzae  
us-10-507-132-2

Query Match 56.4%; Score 97; DB 6; Length 172;  
Best Local Similarity 100.0%; Pred. No. 9e-97;  
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 LGDPTLRTHQFTGTFMKEVSEDEVYGHQLRVPHQRYKDTMKKEVTMKGHASHNLHMY 135  
Db 76 LGDPTLRTHQFTGTFMKEVSEDEVYGHQLRVPHQRYKDTMKKEVTMKGHASHNLHMY 135

Qy 136 KKIDGVWKFAGLKPDIRMGEPDFDRIFEDGRETFGDK 172  
Db 136 KKIDGVWKFAGLKPDIRMGEPDFDRIFEDGRETFGDK 172

RESULT 3  
us-10-507-132-19  
/ Sequence 19, Application US/10507132  
/ Publication No. US2006022316A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Koichiro KAKU et al.  
/ TITLE OF INVENTION: GENE CODING FOR SCYALONE DEHYDRATASE EXHIBITING RESISTANCE TO  
/ FILE REFERENCE: 1254-0258PUS1  
/ CURRENT APPLICATION NUMBER: US/10/507,132  
/ CURRENT FILING DATE: 2004-09-10  
/ PRIOR APPLICATION NUMBER: JP 2002-66955  
/ PRIOR FILING DATE: 2002-03-12  
/ NUMBER OF SEQ ID NOS: 19  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 19  
/ LENGTH: 33  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide derived from  
us-10-507-132-19

Query Match 5.2%; Score 9; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSQVOKSD 9  
Db 25 MGSQVOKSD 33

RESULT 4  
us-11-293-697-3617  
/ Sequence 3617, Application US/11293697  
/ Publication No. US20060105376A1  
/ GENERAL INFORMATION:  
/ APPLICANT: HELIX RESEARCH INSTITUTE  
/ TITLE OF INVENTION: Novel full length cDNA  
/ FILE REFERENCE: HI-A0106  
/ CURRENT APPLICATION NUMBER: US/11/293,697  
/ CURRENT FILING DATE: 2005-12-05  
/ PRIOR APPLICATION NUMBER: US/10/108,260  
/ PRIOR FILING DATE: 2002-03-28  
/ NUMBER OF SEQ ID NOS: 5458  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 3617  
/ LENGTH: 198

/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
us-11-293-697-3617

Query Match 4.1%; Score 7; DB 7; Length 198;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 LGDPTLR 82  
Db 2 LGDPTLR 8

RESULT 5  
us-11-179-064B-76  
/ Sequence 76, Application US/11179064B  
/ Publication No. US20060123508A1  
/ GENERAL INFORMATION:  
/ APPLICANT: DIXON, RICHARD A.  
/ APPLICANT: SHARMA, SHASHI B.  
/ TITLE OF INVENTION: GENETIC MANIPULATION OF CONDENSED TANNINS  
/ FILE REFERENCE: NBL042:US  
/ CURRENT APPLICATION NUMBER: US/11/179,064B  
/ CURRENT FILING DATE: 2005-07-11  
/ PRIOR APPLICATION NUMBER: 60/587,020  
/ PRIOR FILING DATE: 2004-07-09  
/ NUMBER OF SEQ ID NOS: 79  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 76  
/ LENGTH: 258  
/ TYPE: PRT  
/ ORGANISM: Arabidopsis thaliana  
us-11-179-064B-76

Query Match 4.1%; Score 7; DB 7; Length 258;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 EFDPDRI 161  
Db 188 EFDPDRI 194

RESULT 6  
us-11-056-355B-81940  
/ Sequence 81940, Application US/11056355B  
/ Publication No. US20060150283A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Brover, Vyacheslav  
/ APPLICANT: Alexandrov, Nikolai  
/ TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
/ FILE REFERENCE: 2750-1590PUS2  
/ CURRENT APPLICATION NUMBER: US/11/056,355B  
/ CURRENT FILING DATE: 2005-02-14  
/ PRIOR APPLICATION NUMBER: 60/544,190  
/ PRIOR FILING DATE: 2004-02-13  
/ NUMBER OF SEQ ID NOS: 119966  
/ SEQ ID NO 81940  
/ LENGTH: 258  
/ TYPE: prt  
/ ORGANISM: Arabidopsis thaliana  
/ FEATURE:  
/ NAME/KEY: peptide  
/ LOCATION: (1)..(258)  
/ OTHER INFORMATION: Ceres Seq. ID no. 12662413  
us-11-056-355B-81940

Query Match 4.1%; Score 7; DB 7; Length 258;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 EFDPDRI 161

Db 188 EFDPR1 194

RESULT 7  
US-10-953-349-17570  
; Sequence 17570, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17570  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-17570

Query Match 4.1%; Score 7; DB 6; Length 264;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVQKSD 10  
Db 59 QVQKSD 65

RESULT 8  
US-11-056-355B-52964  
; Sequence 52964, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 52964  
; LENGTH: 264  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(264)  
; OTHER INFORMATION: Ceres Seq. ID no. 14304596  
US-11-056-355B-52964

Query Match 4.1%; Score 7; DB 7; Length 264;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVQKSD 10  
Db 59 QVQKSD 65

RESULT 9  
US-11-056-355B-81939  
; Sequence 81939, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai

; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 81939  
; LENGTH: 279  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(279)  
; OTHER INFORMATION: Ceres Seq. ID no. 12662412  
US-11-056-355B-81939

Query Match 4.1%; Score 7; DB 7; Length 279;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 EFDPR1 161  
Db 209 EFDPR1 215

RESULT 10  
US-10-953-349-17569  
; Sequence 17569, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17569  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-17569

Query Match 4.1%; Score 7; DB 6; Length 280;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVQKSD 10  
Db 75 QVQKSD 81

RESULT 11  
US-11-174-307B-4558  
; Sequence 4558, Application US/11174307B  
; Publication No. US20060143729A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai  
; APPLICANT: BROVER, Vyacheslav  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
; FILE REFERENCE: 2750-1601PUS2  
; CURRENT APPLICATION NUMBER: US/11/174,307B  
; CURRENT FILING DATE: 2005-06-30  
; PRIOR APPLICATION NUMBER: 60/583,671  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,781  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: 60/583,651  
; PRIOR FILING DATE: 2004-06-30

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; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4558
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: WRKY; Pfam Description: WRKY DNA -binding domain
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 40846374; NR Description: putative WRKY
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 30681651; NR Description: WRKY family
; OTHER INFORMATION: transcription factor [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|24762209|gb|AA64171.1| putative WRKY family transcription
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 21436293; NR Description: putative WRKY-type DNA
; OTHER INFORMATION: binding protein [Arabidopsis thaliana] >gi|19423942|gb|AA87292.1
; OTHER INFORMATION: putative WRKY-type DNA binding protein [Arabidopsis thaliana]
; OTHER INFORMATION: >gi|4559382|gb|AAD23042.1| putative WRKY-type DNA binding protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 46394402; NR Description: TPA: WRKY transcription
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50843966; NR Description: transcription factor
; OTHER INFORMATION: WRKY31 [Oryza sativa (indica cultivar-group)]
; OTHER INFORMATION: >gi|50252562|dbj|BAD8735.1| WRKY family transcription factor-11k
; OTHER INFORMATION: [Oryza sativa (japonica cultivar-group)]
US-11-174-307B-4558

Query Match
Best Local Similarity 4.1%; Score 7; DB 7; Length 280;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVQKSDS 10
DB 75 QVQKSDS 81

RESULT 12
US-11-056-355B-52963
; Sequence 52963, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52963
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(280)
; OTHER INFORMATION: Cereas Seq. ID no. 14304595
US-11-056-355B-52963
```

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Query Match
Best Local Similarity 4.1%; Score 7; DB 7; Length 280;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVQKSDS 10
DB 75 QVQKSDS 81

RESULT 13
US-10-953-349-17568
; Sequence 17568, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17568
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-17568
```

```

Query Match
Best Local Similarity 4.1%; Score 7; DB 6; Length 292;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 QVQKSDS 10
DB 87 QVQKSDS 93
```

```

RESULT 14
US-11-056-355B-52962
; Sequence 52962, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52962
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(292)
; OTHER INFORMATION: Cereas Seq. ID no. 14304594
US-11-056-355B-52962
```

```

Query Match
Best Local Similarity 4.1%; Score 7; DB 7; Length 292;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 QVQKSDS 10
DB 87 QVQKSDS 93
```

```

RESULT 15
US-10-953-349-16815
```

; Sequence 16815, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16815  
; LENGTH: 357  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-16815

Query Match 4.1%; Score 7; DB 6; Length 357;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 OVOKSDE 10  
|||||  
Db 152 OVOKSDE 158

Search completed: December 5, 2006, 01:18:47  
Job time : 46 secs

**This Page Blank (uspto)**



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: December 5, 2006, 01:08:11 ; Search time 41 Seconds

(without alignments)  
403.641 Million cell updates/sec

Title: US-10-507-132-4

Perfect score: 172  
Sequence: 1 MGSQVQKSDERTFSDYLGLM.....WGEPDPRIFEDGRETFGDK 172

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: PIR\_80:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	98.3	172	2 JE0130	scytalone dehydrat
2	8	4.7	286	2 AE2988	amidohydrolyase [im
3	8	4.7	290	2 C98295	hypothetical prote
4	7	4.1	98	2 C65058	Ferredoxin-like pr
5	7	4.1	152	2 AB2499	hypothetical prote
6	7	4.1	187	2 A69118	conserved hypobet
7	7	4.1	196	2 S70957	hypothetical prote
8	7	4.1	261	1 F64359	conserved hypobet
9	7	4.1	294	1 SYBBS	ribonucleoside syntha
10	7	4.1	309	2 AB2944	ribonucleoside syntha
11	7	4.1	385	2 T51127	GGPP synthase [imp
12	7	4.1	485	2 T41714	hypothetical serin
13	7	4.1	528	2 T34941	probable Na+/H+ an
14	7	4.1	573	2 AB2401	hypothetical prote
15	7	4.1	818	1 E64807	outer membrane ush
16	7	4.1	883	2 I58181	glutamate receptor
17	7	4.1	883	2 S47031	glutamate receptor
18	7	4.1	883	2 S13677	glutamate receptor
19	7	4.1	921	2 I49695	glutamate receptor
20	7	4.1	939	2 I49696	glutamate receptor
21	7	4.1	1035	2 T05687	beta-galactosidase
22	7	4.1	1046	2 T34566	hypothetical prote
23	7	4.1	1298	2 A64157	N-methyl-D-asparta
24	7	4.1	1323	2 S27224	N-methyl-D-asparta
25	7	4.1	1356	2 I78557	N-methyl-D-asparta
26	7	4.1	1356	2 C45219	exopolysaccharona
27	7	4.1	1376	2 F83711	hypothetical prote
28	6	3.5	71	2 G97873	hypothetical prote
29	6	3.5	71	2 F82606	hypothetical prote

30	6	3.5	73	2 T25763	hypothetical prote
31	6	3.5	77	2 D97718	acetate kinase [Ac
32	6	3.5	80	2 AC2394	hypothetical prote
33	6	3.5	83	2 H85762	probable transpos
34	6	3.5	91	1 S00060	phospholipid trans
35	6	3.5	99	2 D95223	hypothetical prote
36	6	3.5	99	2 F98087	hypothetical prote
37	6	3.5	105	2 B75035	hypothetical prote
38	6	3.5	105	2 F71128	hypothetical prote
39	6	3.5	108	2 T17826	hypothetical prote
40	6	3.5	114	2 S18109	ribosomal protein
41	6	3.5	117	2 T09155	lipid transfer pro
42	6	3.5	118	2 E27889	Ig heavy chain V r
43	6	3.5	119	2 B27889	Ig heavy chain V r
44	6	3.5	121	2 A12244	ribosome protein a
45	6	3.5	125	2 C70162	ribosomal protein

#### ALIGNMENTS

##### RESULT 1

JE0130

scytalone dehydratase (BC 4.2.1.94) - Pyricularia oryzae

C/Species: Pyricularia oryzae

C/Date: 03-Jun-1998 #sequence\_revision 10-Jul-1998 #text\_change 31-Dec-2004

C/Accession: JE0130

R/Motocytoma, T.; Imanishi, K.; Yamaguchi, I.

Biosci. Biotechnol. Biochem. 62, 564-566, 1998

A/Title: cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for p

A/Reference number: JE0130; MUID:98233280; PMID:9571787

A/Accession: JE0130

A/Molecule type: mRNA

A/Residues: 1-172 <NOT>

A/Cross-references: UNIPARC:UPI0000179D1F; DDBJ:AB004701

C/Comment: The C-terminal protein of this enzyme is important in catalysis or/and structu

C/Superfamily: scytalone dehydratase

C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 98.3%; Score 169; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 1.2e-170;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSQVQKSDERTFSDYLGLMTQVYEMADSYDSKMDLRYIAATLADIRSFIDKIMEA	60
Db	1	MGSQVQKSDERTFSDYLGLMTQVYEMADSYDSKMDLRYIAATLADIRSFIDKIMEA	60
Qy	61	MPAEFVGMVSSKQVLDPTLRTOHFIQGRMEKVSDEVIYGHQLRVPHORVQDTTME	120
Db	61	MPAEFVGMVSSKQVLDPTLRTOHFIQGRMEKVSDEVIYGHQLRVPHORVQDTTME	120
Qy	121	VTKMGHANSANLHWYKKIDGVWKEPAGIKPDIRWGEFDFRIFEDGRETF	169
Db	121	VTKMGHANSANLHWYKKIDGVWKEPAGIKPDIRWGEFDFRIFEDGRETF	169

##### RESULT 2

AE2988  
amidohydrolyase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 31-Dec-2004

C/Accession: AE2988

R/Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F

ster, B.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AE2988

A/Status: preliminary

A/Molecule type: DNA

A;Residues: 1-286 <KUR>  
 A;Cross-references: UNIPROT:Q8UA64; UNIPARC:UPI0000164817; GB:AE008689; PIDN:PAL44323.1;  
 A;Experimental source: strain C58 (Dupont)  
 C;Genetics:  
 A;Gene: Atu3510  
 A;Map position: linear chromosome  
 C;Superfamily: nitrilase (carbon-nitrogen hydrolase)

Query Match 4.7%; Score 8; DB 2; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 EDGERTEFG 170  
 |||||  
 Db 215 EDGERTEFG 222

RESULT 3  
 C98295  
 hypothetical protein AGR\_L\_2636 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 31-Dec-2004  
 C;Accession: C98295  
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A;Reference number: A97359; PMID:21608551; PMID:11743194

A;Accession: C98295  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-290 <KUR>  
 A;Cross-references: UNIPROT:Q8UA64; UNIPARC:UPI0000002221; GB:AE007870; PIDN:AAK89885.1;  
 C;Genetics:

A;Gene: AGR\_L\_2636  
 A;Map position: linear chromosome  
 C;Superfamily: nitrilase (carbon-nitrogen hydrolase)

Query Match 4.7%; Score 8; DB 2; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 EDGERTEFG 170  
 |||||  
 Db 219 EDGERTEFG 226

RESULT 4  
 C65058  
 Ferridoxin-like protein yjco - Escherichia coli (strain K-12)  
 C;Species: Escherichia coli  
 C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 31-Dec-2004  
 C;Accession: C65058  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cl  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A;Title: The complete genome sequence of Escherichia coli K-12.  
 A;Reference number: A64720; PMID:97426617; PMID:9278503

A;Accession: C65058  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-98 <BLAT>  
 A;Cross-references: UNIPROT:Q46905; UNIPARC:UPI0000138043; GB:AE000360; GB:U00096; NID:G  
 A;Experimental source: strain K-12, substrain MG1655  
 C;Superfamily: ferredoxin-like protein, fixX type

Query Match 4.1%; Score 7; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 9.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 LRIDYRS 52  
 |||||  
 Db 59 LRIDYRS 65

RESULT 5  
 AB2499  
 hypothetical protein al17170 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1f

C;Species: Nostoc sp. PCC 7120  
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C;Accession: AB2499  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
 A;Reference number: AB1807; PMID:21595285; PMID:11759840  
 A;Accession: AB2499  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-152 <KUR>  
 A;Cross-references: UNIPROT:Q8YKX8; UNIPARC:UPI000000CF05; GB:BA000020; PIDN:BAE78254.1;  
 A;Experimental source: strain PCC 7120  
 C;Genetics:

A;Gene: al17170  
 A;Genome: plasmid

Query Match 4.1%; Score 7; DB 2; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 EDEVIIG 103  
 |||||  
 Db 58 EDEVIIG 64

RESULT 6  
 A69118  
 conserved hypothetical protein MTH1876 - Methanobacterium thermoautotrophicum (strain Del  
 C;Species: Methanobacterium thermoautotrophicum  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 12-Jul-2004  
 C;Accession: A69118  
 R;Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E  
 J.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Ujwani, N.;  
 Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi  
 A;Reference number: A69000; PMID:98037514; PMID:9371463  
 A;Accession: A69118  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-187 <MTH>  
 A;Cross-references: UNIPROT:Q27904; UNIPARC:UPI00000665EF; GB:AE000940; GB:AE000666; MID:  
 A;Experimental source: strain Delta H  
 C;Genetics:

A;Gene: MTH1876  
 A;Start codon: GTG  
 C;Superfamily: spore germination protein C2

Query Match 4.1%; Score 7; DB 2; Length 187;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SEDEVIG 102  
 |||||  
 Db 154 SEDEVIG 160

RESULT 7  
 S70957  
 hypothetical protein wbfE ctnd [imported] - Vibrio cholerae  
 C;Species: Vibrio cholerae  
 C;Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 09-Jul-2004  
 C;Accession: S70957; T44317  
 R;Bik, E.M.; Bunschoten, A.E.; Willems, R.J.L.; Chang, A.C.Y.; Mool, F.R.  
 Mol. Microbiol. 20, 799-811, 1996

A>Title: Genetic organization and functional analysis of the otn DNA essential for cell  
A/Reference number: S70952; MUID:96386047; PMID:8793876  
A/Accession: S70957  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-196 <BRL>  
A/Cross-references: UNIPROT:Q56657; UNIPARC:UPI0000081755; EMBL:X90547; NID:G1469276; PI  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995  
R/Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.  
Gene 237, 321-332, 1999  
A>Title: The genes responsible for O-antigen synthesis of Vibrio cholerae O139 are close  
A/Reference number: Z2749; MUID:99453293; PMID:10521656  
A/Accession: T44317  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-196 <YAM>  
A/Cross-references: UNIPARC:UPI0000081755; EMBL:AB012957; PIDD:BA33621.1  
A/Experimental source: strain O22  
A/Genetics:  
A/Gene: otnD  
A/Note: wbtE

Query Match 4.1%; Score 7; DB 2; Length 196;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 FSDYIGL 19  
DB 88 FSDYIGL 94

## RESULT 8

F64369  
conserved hypothetical protein M0558 - Methanococcus jannaschii  
C/Species: Methanococcus jannaschii  
C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 05-Oct-2004  
C/Accession: F64369  
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
J.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
Rosen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurest, M.A.  
Science 273, 1058-1073, 1996  
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A/Reference number: A64300; MUID:96337999; PMID:8688087  
A/Accession: F64369  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-261 <BUL>  
A/Cross-references: UNIPROT:Q57978; UNIPARC:UPI0000139A9F; GB:U67505; GB:L77117; NID:928  
C/Genetics:  
A/Map position: REV493986-493201  
C/Superfamily: HTH transcriptional regulator, archaeal type

Query Match 4.1%; Score 7; DB 1; Length 261;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 GLKPDIR 152  
DB 205 GLKPDIR 211

## RESULT 9

SYBEHS  
thymidylate synthase (EC 2.1.1.45) - saimiriine herpesvirus 1  
C/Species: saimiriine herpesvirus 1  
C/Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 05-Oct-2004  
C/Accession: A26269  
R/Hones, R.W.; Bodemer, W.; Cameron, K.R.; Niller, H.H.; Fleckenstein, B.; Randall, R.F.  
Proc. Natl. Acad. Sci. U.S.A. 83, 3604-3608, 1986  
A/Title: The A+T-rich genome of Herpesvirus saimiri contains a highly conserved gene for  
A/Reference number: A26269; MUID:86233282; PMID:3012520  
A/Accession: A26269

A/Molecule type: DNA  
A/Residues: 1-294 <HON>  
A/Cross-references: UNIPARC:UPI00001378D3; GB:M13390; NID:G331074; PIDD:AAA46175.1; PID:  
C/Superfamily: thymidylate synthase; thymidylate synthase homology  
C/Keywords: deoxyribonucleotide biosynthesis; methyltransferase  
P/11-294/Doman: thymidylate synthase homology <TDS>  
F/116/Active site: Cys #status predicted

Query Match 4.1%; Score 7; DB 1; Length 294;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 RSFLDRL 57  
DB 96 RSFLDRL 102

## RESULT 10

A82944  
ribose/galactose ABC transporter U013 [imported] - Ureaplasma urealyticum  
C/Species: Ureaplasma urealyticum  
C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 03-Aug-2001  
C/Accession: A82944  
R/Glass, J.I.; Lefkowitz, E.J.; Glase, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
submitted to Genbank, February 2000  
A/Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini  
A/Reference number: A82870  
A/Accession: A82944  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-309 <GLA>  
A/Cross-references: UNIPARC:UPI00000C1B66; GB:AE002101; GB:AF222894; NID:96898957; PIDD:  
A/Experimental source: serovar 3; biovar 1  
C/Genetics:  
A/Gene: rbsC-2; U013  
A/Genetic code: SGC3  
C/Superfamily: probable ribose ABC transporter rbsC-2

Query Match 4.1%; Score 7; DB 2; Length 309;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SDYIGLM 20  
DB 132 SDYIGLM 138

## RESULT 11

T51127  
GGP synthase [imported] - Brevibacterium linens  
C/Species: Brevibacterium linens  
C/Date: 28-Jul-2000 #sequence\_revision 28-Jul-2000 #text\_change 09-Jul-2004  
C/Accession: T51127  
R/Krubasik, P.; Sandmann, G.  
Mol. Gen. Genet. 263, 423-432, 2000  
A/Title: A carotenogenic gene cluster from Brevibacterium linens with novel lycopene cyc:  
A/Reference number: Z25303; MUID:20279196; PMID:10821176  
A/Accession: T51127  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-385 <KRU>  
A/Cross-references: UNIPROT:Q9KX76; UNIPARC:UPI00000B2FAB; EMBL:AF139916; PIDD:AA655590.  
A/Experimental source: DSM 20426; ATCC9175  
C/Genetics:  
A/Gene: crtE

Query Match 4.1%; Score 7; DB 2; Length 385;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 DRLRKVI 42  
DB 330 DRLRKVI 336

## RESULT 12

T41714

hypothetical serine-rich protein - fission yeast (*Schizosaccharomyces pombe*)C/Species: *Schizosaccharomyces pombe*

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T41714

R/Reger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, October 1999

A/Reference number: Z22012

A/Accession: T41714

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-485 &lt;RBE&gt;

A/Cross-references: UNIPROT:Q9UT50; UNIPARC:UPI000006ADBC; EMBL:AL121770; PIDD: CAB57437.

A/Experimental source: strain 972h-; coamid c821

C/Genetics:

A/Map position: 1

Query Match 4.1%; Score 7; DB 2; Length 485;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 PAEEFVG 68

DB 346 PAEEFVG 352

## RESULT 13

T34941

probable Na<sup>+</sup>/H<sup>+</sup> antiporter - *Streptomyces coelicolor*C/Species: *Streptomyces coelicolor*

C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

C/Accession: T34941

R/Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A/Reference number: Z21563

A/Accession: T34941

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-528 &lt;SAU&gt;

A/Cross-references: UNIPROT:Q9S2Y0; UNIPARC:UPI00000DB2C7; EMBL:AL109663; PIDD: CAB51980.

A/Experimental source: strain A3 (2)

C/Genetics:

A/Map position: 1

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Map position: 1

Query Match 4.1%; Score 7; DB 2; Length 528;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 VLGDPTL 81

DB 206 VLGDPTL 212

## RESULT 14

AB2401

hypothetical protein al14762 [imported] - *Nostoc* sp. (strain PCC 7120)C/Species: *Nostoc* sp. PCC 7120C/Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C/Accession: AB2401

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasanoto, S.; Watanabe, A.; Iriyuchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AB2401

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-573 <KUR>  
 A/Cross-references: UNIPROT:O8YN1; UNIPARC:UPI00000CECAF; GB:BA000019; PIDD: BAB76461.1;  
 A/Experimental source: strain PCC 7120  
 C/Genetics:

A/Map position: 1

Query Match 4.1%; Score 7; DB 2; Length 573;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FSDYGL 19

DB 538 FSDYGL 544

## RESULT 15

E64807

outer membrane usher protein ybgQ precursor - *Escherichia coli* (strain K-12)C/Species: *Escherichia coli*

C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 01-Mar-2002

C/Accession: E64807

R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coj

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of *Escherichia coli* K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: E64807

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-818 &lt;BLAT&gt;

A/Cross-references: UNIPARC:UPI00016804A; GB:AE000175; GB:U00096; NID:g1786934; PIDD:AK

A/Experimental source: strain K-12, substrain MG1655

C/Genetics:

A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

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A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

A/Map position: 1

Search completed: December 5, 2006, 01:13:45  
 Job time : 43 secs

Query Match 4.1%; Score 7; DB 1; Length 818;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 GLKPDIR 152

DB 95 GLKPDIR 101



```

CC -1- FUNCTION: Catalyzes two steps in melanin biosynthesis. From
CC scytalone they are two dehydration steps and one reduction step to
CC yield melanin.
CC -1- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +
CC H(2)O.
CC -1- PATHWAY: Fungal melanin biosynthesis; first step.
CC -1- SUBUNIT: Homotrimer. Each subunit contains an active site, located
CC in the central part of the hydrophobic core of the monomer, which
CC functions independently.
CC -----
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CC -----
DR EMBL; AB004741; BAA34046.1; -; mRNA.
DR PDB; 1IDP; X-ray; A/B/C=1-172.
DR PDB; 1STD; X-ray; @=1-172.
DR PDB; 2STD; X-ray; @=1-172.
DR PDB; 3STD; X-ray; A/B/C=10-112.
DR PDB; 4STD; X-ray; A/B/C=10-112.
DR PDB; 5STD; X-ray; A/B/C=10-112.
DR PDB; 6STD; X-ray; A/B/C=10-112.
DR PDB; 7STD; X-ray; A/B/C=10-112.
DR LinkHub; P56221; -
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_DH; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
DR 3D-structure; Lyase; Melanin biosynthesis.
KW CHAIN 1 172 Scytalone dehydratase.
FT FT 1 172 /FTId=PRO_0000097639.
FT HELIX 13 32
FT TURN 33 33
FT HELIX 35 39
FT TURN 40 41
FT STRAND 42 49
FT HELIX 51 54
FT STRAND 55 55
FT STRAND 57 62
FT HELIX 63 71
FT STRAND 72 72
FT TURN 73 76
FT TURN 79 80
FT STRAND 81 83
FT STRAND 86 96
FT TURN 97 98
FT STRAND 99 115
FT TURN 116 117
FT STRAND 121 138
FT TURN 139 140
FT TURN 141 155
SQ SEQUENCE 172 AA; 20250 MW; 2FA56296D5E0DDC CRC64;

Query Match 100.0%; Score 172; DB 1; Length 172;
Best Local Similarity 100.0%; Pred. No. 5.8e-170;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGOVQKSDIEITSDYGLMTVCYEWADSYDSKMDRLKVIAPTLRIDYRSFLDKLME 60
DB 1 MSGOVQKSDIEITSDYGLMTVCYEWADSYDSKMDRLKVIAPTLRIDYRSFLDKLME 60
QY 61 MPAAEEFGWVSSKQVLDPTLRTOHFTGGTRWEKVSDEVIYGHQLRVPHQRYKDTTKE 120
DB 61 MPAAEEFGWVSSKQVLDPTLRTOHFTGGTRWEKVSDEVIYGHQLRVPHQRYKDTTKE 120
QY 121 VTWKGAHSHANLHWYKKIDGVWKPAGLKPDIRMGEPFEDRI FEDGRTFGDK 172
DB 121 VTWKGAHSHANLHWYKKIDGVWKPAGLKPDIRMGEPFEDRI FEDGRTFGDK 172

RESULT 2
QBNJ18_9PEZI PRELIMINARY; PRT; 121 AA.
AC QBNJ18_9PEZI
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

```

```

DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DR Scytalone dehydratase (Fragment).
OS Ceratocystis dinicola.
OC Ceratocystis Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Microascales; Microascales Incertae sedis;
OC Ceratocystis.
OX NCBI_TaxId=720311;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
CC -----
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CC -----
DR EMBL; AY098655; AAM34801.1; -; Genomic_DNA.
DR HSSP; P56221; 1IDP.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_DH; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
DR NON_TER 1 121
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 14394 MW; C183FA038FCF5620 CRC64;

Query Match 13.4%; Score 23; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 IAPTLRIDYRSFLDKLMEAMP 64
DB 18 IAPTLRIDYRSFLDKLMEAMP 40

RESULT 3
QBNJ17_9PEZI PRELIMINARY; PRT; 122 AA.
AC QBNJ17_9PEZI
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Scytalone dehydratase (Fragment).
OS Ceratocystis resinifera.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Microascales; Microascales Incertae sedis;
OC Ceratocystis.
OX NCBI_TaxId=95837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
CC -----
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CC -----
DR EMBL; AY098655; AAM34801.1; -; Genomic_DNA.
DR HSSP; P56221; 1IDP.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_DH; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
DR NON_TER 1 122
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14376 MW; D807589723063C91 CRC64;

```

Query Match 13.4%; Score 23; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-15;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 IAPTLRIDYRSFLDKLMEAMPAB 64  
 DB 18 IAPTLRIDYRSFLDKLMEAMPAB 40

## RESULT 4

Q6XR11\_9PEZI PRELIMINARY; PRT; 186 AA.  
 AC Q6XR11;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 7.  
 DE Scytalone dehydratase 1.  
 GN Name=SD1;  
 OS Ceratocystis resinifera.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Microascales; Microascales incertae sedis;  
 OC Ceratocystis;  
 OC NCBI\_TaxID=55837;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Loppnau P.A.;  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

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 CC -----  
 DR EMBL: AY214004; AAO60167.1; -; Genomic\_DNA.  
 DR SMR: Q6XR11; 21-182.  
 DR GO: GO:0016836; F:hydro-lyase activity; IEA.  
 DR GO: GO:0006582; P:melanin metabolism; IEA.  
 DR InterPro: IPR004235; Scytalone\_DH.  
 DR Pfam: PF02982; Scytalone\_dh; 1.  
 DR ProDom: PD022193; Scytalone\_DH; 1.  
 DR SQUENCE 186 AA; 21516 MW; FD947DBB2534005F CRC64;

Query Match 13.4%; Score 23; DB 2; Length 186;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-15;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 IAPTLRIDYRSFLDKLMEAMPAB 64  
 DB 52 IAPTLRIDYRSFLDKLMEAMPAB 74

## RESULT 5

Q9C426\_OPHFL PRELIMINARY; PRT; 216 AA.  
 AC Q9C426;  
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 12.  
 DE Scytalone dehydratase.  
 GN Name=OSD1;  
 OS Ophiostoma floccosum.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
 OC NCBI\_TaxID=104300;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=387N;  
 RX MEDLINE=21473266; PubMed=11589570; DOI=10.1007/s004380100534;  
 RA Wang H.L., Kim S.H., Breuil C.;  
 RT "A scytalone dehydratase gene from Ophiostoma floccosum restores the  
 RT melanization and pathogenicity phenotypes of a melanin-deficient  
 RT Colletotrichum lagenarium mutant";  
 RT Mol. Genet. Genomics 266:126-132(2001).  
 RU [2]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=387N;  
 RA Wang H., Breuil C.;  
 RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

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 CC -----  
 DR EMBL: AF316575; AAK11296.1; -; Genomic\_DNA.  
 DR HSSP: P56221; 1IDP.  
 DR SMR: Q9C426; 22-182.  
 DR GO: GO:0016836; F:hydro-lyase activity; IEA.  
 DR GO: GO:0006582; P:melanin metabolism; IEA.  
 DR InterPro: IPR004235; Scytalone\_DH.  
 DR Pfam: PF02982; Scytalone\_dh; 1.  
 DR ProDom: PD022193; Scytalone\_DH; 1.  
 DR SQUENCE 216 AA; 24167 MW; D349BF74DDF3D4D CRC64;

Query Match 9.9%; Score 17; DB 2; Length 216;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 YEWADSYDSKMDRLRK 40  
 DB 36 YEWADSYDSKMDRLRK 52

## RESULT 6

SCD1\_GLOLA STANDARD; PRT; 188 AA.  
 ID SCD1\_GLOLA;  
 AC Q00455;  
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1996, sequence version 1.  
 DT 07-FEB-2006, entry version 28.  
 DE Scytalone dehydratase (EC 4.2.1.94).  
 GN Name=SCD1;  
 OS Glomerella lagenarium (Anthracoaceae fungus) (Colletotrichum lagenarium).  
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;  
 OC Colletotrichum.  
 OC NCBI\_TaxID=5462;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
 RC STRAIN=104-T;

RX MEDLINE=97111971; PubMed=8953707;  
 RA Kudo Y., Takano Y., Endo N., Yasuda N., Tajima S., Furusawa I.;  
 RT "Cloning and structural analysis of the melanin biosynthesis gene SCD1  
 RT encoding scytalone dehydratase in Colletotrichum lagenarium";  
 RT Appl. Environ. Microbiol. 62:4340-4344(1996).  
 CC -!- FUNCTION: Catalyzes two steps in melanin biosynthesis. From  
 CC scytalone they are two dehydration steps and one reduction step to  
 CC yield melanin.

CC -!- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +  
 CC H(2)O.  
 CC -!- PATHWAY: Fungal melanin biosynthesis; first step.  
 CC -!- SUBUNIT: Homotrimer. Each subunit contains an active site, located  
 CC in the central part of the hydrophobic core of the monomer, which  
 CC functions independently (by similarity).

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 CC -----  
 DR EMBL: D86079; BAA13009.1; -; Genomic\_DNA.  
 DR HSSP: P56221; 1IDP.  
 DR SMR: Q00455; 6-167.  
 DR InterPro: IPR004235; Scytalone\_DH.  
 DR Pfam: PF02982; Scytalone\_dh; 1.  
 DR ProDom: PD022193; Scytalone\_DH; 1.

KW Lyase; Melanin biosynthesis.  
 FT CHAIN 1 188 Scytalone dehydratase.  
 FT SEQUENCE 188 AA; 21687 MW; A58F3EB940321EFA CRC64;

Query Match 9.3%; Score 16; DB 1; Length 188;  
Best Local Similarity 100.0%; Pred. No. 8.6e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 EMADSYDSKDWRLRK 40  
|||  
22 EMADSYDSKDWRLRK 37

Db

RESULT 7  
Q8NTH9\_9PEZI PRELIMINARY; PRT; 121 AA.  
AC Q8NTH9;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Scytalone dehydratase (Fragment).  
OS Ophiostoma setosum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
OX NCBI\_TaxId=107467;

RN NUCLEOTIDE SEQUENCE.  
RA Fleet C., Breuill C.;  
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi.";  
RL Mycol. Res. 106:1331-1339(2002).  
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QY 42 IAPTLRIDYRSFL 54  
|||  
18 IAPTLRIDYRSFL 30

Db

RESULT 8  
Q8NTH9\_9PEZI PRELIMINARY; PRT; 121 AA.  
AC Q8NTH9;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Scytalone dehydratase (Fragment).  
OS Ophiostoma setosum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
OX NCBI\_TaxId=107467;

RN NUCLEOTIDE SEQUENCE.  
RA Fleet C., Breuill C.;  
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi.";  
RL Mycol. Res. 106:1331-1339(2002).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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CC EMBL; AY098664; AAM34810.1; -; Genomic\_DNA.  
DR HSSP; P56221; IIDP.  
DR SMR; Q8NTH9; 1-121.  
DR GO; GO:0016836; F:hydro-lyase activity; IEA.  
DR GO; GO:0006582; P:melanin metabolism; IEA.  
DR InterPro; IPR004235; Scytalone\_DH.  
DR Pfam; PF02982; Scytalone\_dh; 1.  
DR ProDom; PD022193; Scytalone\_DH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA; 14150 MW; 1941990397735E1F CRC64;

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Best Local Similarity 100.0%; Pred. No. 7.9e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 IAPTLRIDYRSFL 54  
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18 IAPTLRIDYRSFL 30

Db

RESULT 9  
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AC Q8NTH9;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Scytalone dehydratase (Fragment).  
OS Ophiostoma setosum.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
OX NCBI\_TaxId=107467;

RN NUCLEOTIDE SEQUENCE.  
RA Fleet C., Breuill C.;  
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi.";  
RL Mycol. Res. 106:1331-1339(2002).  
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CC Distributed under the Creative Commons Attribution-NonDerivs License

QY 42 IAPTLRIDYRSFL 54  
|||  
18 IAPTLRIDYRSFL 30

Db

RESULT 10  
Q8NTH9\_9PEZI PRELIMINARY; PRT; 122 AA.  
AC Q8NTH9;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Scytalone dehydratase (Fragment).  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License



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OS Ophiostoma piceae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxID=61273;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
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DR EMBL; AY098660; AAM34806.1; -, Genomic DNA.
DR HSSP; AY098661; AAM34807.1; -, Genomic DNA.
DR HSSP; P56221; 1IDP.
DR SMR; Q8N1I1; 1-122.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD02193; Scytalone_DH; 1.
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QY 42 IAPTLRIDYRSFL 54
DB 18 IAPTLRIDYRSFL 30

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AC Q8NJH8;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma setosum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxID=107467;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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DR EMBL; AY098666; AAM34812.1; -, Genomic DNA.
DR HSSP; P56221; 1IDP.
DR SMR; Q8NJH8; 1-122.
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DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD02193; Scytalone_DH; 1.
FT NON_TER 1
FT 122 1
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Query Match
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QY 42 IAPTLRIDYRSFL 54
DB 18 IAPTLRIDYRSFL 30

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AC Q8NJ11;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma piliferum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxID=38032;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
-----
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DR EMBL; AY098663; AAM34809.1; -, Genomic DNA.
DR HSSP; P56221; 1IDP.
DR SMR; Q8NJ11; 1-122.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD02193; Scytalone_DH; 1.
FT NON_TER 1
FT 122 1
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Query Match
Best Local Similarity 7.6%; Score 13; DB 2; Length 122;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 IAPTLRIDYRSFL 54
DB 18 IAPTLRIDYRSFL 30

RESULT 13
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AC Q8NJ12;
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DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma piliferum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxID=38032;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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DR EMBL; AY098662; AAM34808.1; -, Genomic DNA.
DR HSSP; P56221; 1IDP.

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DR SMR; Q8NJ12; 1-122.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
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SQ SEQUENCE 122 AA; 14221 MW; 7A99419E73E0735E CRC64;

Query Match
Best Local Similarity 100.0%; Score 13; DB 2; Length 122;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 IAPTLRIDYRSFL 54
Db 18 IAPTLRIDYRSFL 30

RESULT 14
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ID Q8NJ13_9PEZI
AC Q8NJ13;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma minus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX NCBI_TaxId=150568;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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DR EMBL; AY098659; AAM34805.1; -; Genomic_DNA.
DR HSSP; P56221; 1IDP.
DR SMR; Q8NJ13; 1-122.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14117 MW; 6FE184D0CDE657FC CRC64;

Query Match
Best Local Similarity 100.0%; Score 13; DB 2; Length 122;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 IAPTLRIDYRSFL 54
Db 18 IAPTLRIDYRSFL 30

RESULT 15
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ID Q8NJ14_9PEZI
AC Q8NJ14;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
OS Ophiostoma minus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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OX NCBI_TaxId=150568;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pleet C., Breuil C.;
RT "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT presence of DHN-melanin pathway in sapstain fungi.";
RL Mycol. Res. 106:1331-1339(2002).
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DR EMBL; AY098658; AAM34804.1; -; Genomic_DNA.
DR HSSP; P56221; 1IDP.
DR SMR; Q8NJ14; 1-122.
DR GO; GO:0016836; F:hydro-lyase activity; IEA.
DR GO; GO:0006582; P:melanin metabolism; IEA.
DR InterPro; IPR004235; Scytalone_DH.
DR Pfam; PF02982; Scytalone_dh; 1.
DR ProDom; PD022193; Scytalone_DH; 1.
FT NON_TER 1
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SQ SEQUENCE 122 AA; 14233 MW; 819384D0C70F2DDE CRC64;

Query Match
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 IAPTLRIDYRSFL 54
Db 18 IAPTLRIDYRSFL 30
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Search completed: December 5, 2006, 01:12:59  
Job time : 304 secs



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gene
CDS

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## ORIGIN

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Alignment Scores:
Pred. No.: 2,03e-178 Length: 807
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DB: Gaps: 0

US-10-507-132-4 (1-172) x AB004741 (1-807)

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QY 1 MetG1SerGlnValGlnYSerAspGlu1IleThrPheSerAspTyrLeuGlyLeuMet 20
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QY 21 ThrCyVal1IleGlu1Utrp1AaAspSerTyrAspSerTyrAspTyrAspTyrAspTyr 40
DB 141 ACTTGGCTCTATGATGTGGGACAGACTACCTCCAGAGACTGGGATAGCTCGCAAG 200
QY 41 ValIleAspProThrLeuAspTyrArgSerPheLeuAspTyrLeuTyrGlu1Aa 60
DB 201 GTCAATGGCTACTCTGCGCATTTACTACCGCTCTCTCCAGCAAGCTCTGGAGGCA 260
QY 61 MetPro1aGlu1uPheVal1GlyMetValSerSerTyrGlnValLeuGlyAspProThr 80
DB 261 ATGCCGCGCAGAGGATTGTCGCGCATGCTCTCGAGCAAGAGGCTGGGCGAACCACC 320
QY 81 LeuArgThrGlnIlePhe1IleGly1ThrArgTyrGlu1ValSerGluAspGlu1Aa 100
DB 321 CTCGCGACGACAGACTTCATCGCGGACCGCGTGGAGAGGTCTCCAGAGAGGTC 380
QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrAspThrThrMetLeuGlu 120
DB 381 ATGGGCTACCAACAGCTGCGCGTCCGCAACAGAGTACAGACACCACTAGAGAG 440
QY 121 ValThrMetLeuGlyHis1AaHisSer1AaMetLeuHisTyrTyrGly1IleAspGly 140
DB 441 GTCAACATGAGGGCCACGCCCACTCGCAACCTTCACCTGATCAAGAGATGACAGGC 500
QY 141 ValTyrPheAsp1aGlyLeu1ValProAsp1IleArgTyrGlu1GluPheAspPheAsp 160
DB 501 GTCTGGAAGTTCGCGCGCTCCAAACCGATATCGCTGGGCGAGTTCGACTTGAACAGG 560
QY 161 IlePheGluAspGlyArgGluThrPheGlyAspTyr 172
DB 561 ATCTTTAGAGACGAGCGGAGACCTTTGGCGACAAA 596

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RESULT 2
LOCUS AY098654 432 bp DNA linear PLN 16-JAN-2003
DEFINITION Ceratocystis pinicola scytalone dehydratase (SD) gene, partial cds.
ACCESSION AY098654
VERSION AY098654.1 GI:21238817
KEYWORDS

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SOURCE
ORGANISM
Ceratocystis pinicola
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
Ceratocystis.
REFERENCE
1 (bases 1 to 432)
Fleet, C. and Breuil, C.
Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 432)
Fleet, C. and Breuil, C.
Direct Submission
Submitted (22-Apr-2002) Wood Science, University of British
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
location/Qualifiers
1.432
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## ORIGIN

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Alignment Scores:
Pred. No.: 7.48e-09 Length: 432
Score: 17.00 Matches: 17
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 9.9% Indels: 0
DB: Gaps: 0

US-10-507-132-4 (1-172) x AY098654 (1-432)

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QY 48 IleAspTyrArgSerPheLeuAspTyrGlu1AaMetPro1aGlu 64
DB 138 ATGACTATCGCTCGTTCCTGGATAGCTGTGGAGGACATGCTGCCGAG 188

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RESULT 3
LOCUS AY098655 433 bp DNA linear PLN 16-JAN-2003
DEFINITION Ceratocystis resinifera scytalone dehydratase (SD) gene, partial
cds.
ACCESSION AY098655
VERSION AY098655.1 GI:21238819
KEYWORDS
SOURCE
ORGANISM
Ceratocystis resinifera
Ceratocystis resinifera
Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
Ceratocystis.
REFERENCE
1 (bases 1 to 433)
Fleet, C. and Breuil, C.
Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 433)
Fleet, C. and Breuil, C.
Direct Submission

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JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

FEATURES  
source  
1. .433  
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ORIGIN  
Alignment Scores:  
Pred. No.: 7.49e-09 Length: 433  
Score: 17.00 Matches: 17  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 9.9% Indels: 0  
DB: 4 Gaps: 0

US-10-507-132-4 (1-172) x AY098655 (1-433)

Qy 48 IleaSPYrARgSerPheLeuAspLysLeuTrpGluIaMetProIaGlu 64  
Db 138 ATCGACTACCGCTGCTTCGTGATAGCTATGGAGCAATGCTGCCGAG 188

RESULT 4  
LOCUS AY214004 1215 bp DNA linear PLN 10-MAR-2004  
DEFINITION Ceratomyx resiniifera scytalone dehydratase I (SD1) gene,  
complete cds.  
ACCESSION AY214004  
VERSION AY214004.1 GI:37787189  
KEYWORDS Ceratomyx resiniifera  
SOURCE Ceratomyx resiniifera  
ORGANISM Ceratomyx resiniifera  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Microascales; Microascales incertae sedis;  
Ceratomyx.  
1 (bases 1 to 1215)  
Loppman, P.A.  
Canadian Populations and Melanin Biosynthesis Genes of Ceratomyx  
resiniifera  
Unpublished  
2 (bases 1 to 1215)  
Loppman, P.A.  
Direct Submission  
Submitted (08-JUN-2003) Wood Science, University of British  
Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada  
location/Qualifiers  
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gene  
mRNA  
CDs

JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

FEATURES  
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1. .433  
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ORIGIN  
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Score: 17.00 Matches: 17  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 9.9% Indels: 0  
DB: 4 Gaps: 0

US-10-507-132-4 (1-172) x AY098655 (1-433)

Qy 48 IleaSPYrARgSerPheLeuAspLysLeuTrpGluIaMetProIaGlu 64  
Db 138 ATCGACTACCGCTGCTTCGTGATAGCTATGGAGCAATGCTGCCGAG 188

RESULT 4  
LOCUS AY214004 1215 bp DNA linear PLN 10-MAR-2004  
DEFINITION Ceratomyx resiniifera scytalone dehydratase I (SD1) gene,  
complete cds.  
ACCESSION AY214004  
VERSION AY214004.1 GI:37787189  
KEYWORDS Ceratomyx resiniifera  
SOURCE Ceratomyx resiniifera  
ORGANISM Ceratomyx resiniifera  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Microascales; Microascales incertae sedis;  
Ceratomyx.  
1 (bases 1 to 1215)  
Loppman, P.A.  
Canadian Populations and Melanin Biosynthesis Genes of Ceratomyx  
resiniifera  
Unpublished  
2 (bases 1 to 1215)  
Loppman, P.A.  
Direct Submission  
Submitted (08-JUN-2003) Wood Science, University of British  
Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada  
location/Qualifiers  
1. .1215  
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/mol\_type="genomic DNA"  
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/specific\_host="Pinus contorta"  
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/country="Canada: Alberta, Edson"  
<233. .>934  
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/join(<233. .305,379. .476,545. .>934)

gene  
mRNA  
CDs

JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

FEATURES  
source  
1. .433  
/organism="Ceratomyx resiniifera"  
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/protein\_id="AA034801.1"  
/db\_xref="GI:21238820"  
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ORIGIN  
Alignment Scores:  
Pred. No.: 7.49e-09 Length: 433  
Score: 17.00 Matches: 17  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 9.9% Indels: 0  
DB: 4 Gaps: 0

US-10-507-132-4 (1-172) x AY098655 (1-433)

Qy 48 IleaSPYrARgSerPheLeuAspLysLeuTrpGluIaMetProIaGlu 64  
Db 138 ATCGACTACCGCTGCTTCGTGATAGCTATGGAGCAATGCTGCCGAG 188

RESULT 4  
LOCUS AY214004 1215 bp DNA linear PLN 10-MAR-2004  
DEFINITION Ceratomyx resiniifera scytalone dehydratase I (SD1) gene,  
complete cds.  
ACCESSION AY214004  
VERSION AY214004.1 GI:37787189  
KEYWORDS Ceratomyx resiniifera  
SOURCE Ceratomyx resiniifera  
ORGANISM Ceratomyx resiniifera  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Microascales; Microascales incertae sedis;  
Ceratomyx.  
1 (bases 1 to 1215)  
Loppman, P.A.  
Canadian Populations and Melanin Biosynthesis Genes of Ceratomyx  
resiniifera  
Unpublished  
2 (bases 1 to 1215)  
Loppman, P.A.  
Direct Submission  
Submitted (08-JUN-2003) Wood Science, University of British  
Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada  
location/Qualifiers  
1. .1215  
/organism="Ceratomyx resiniifera"  
/mol\_type="genomic DNA"  
/isolate="EL3-21"  
/specific\_host="Pinus contorta"  
/db\_xref="taxon:95837"  
/country="Canada: Alberta, Edson"  
<233. .>934  
/gene="SD1"  
/join(<233. .305,379. .476,545. .>934)

gene  
mRNA  
CDs



/protein\_id="AA034807.1"  
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/translation="EMADRYDSKMDRLKCIAPTLLRIDYRSFLNKLMEAMPDEFIG  
MISDPVNLGNPLRTOHFPFGASRWRERVSDFEVIQHLRVPHQVYTDASISVAVKGH  
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ORIGIN

Alignment Scores:

Pred. No.:	0.000177	Length:	421
Score:	13.00	Matches:	13
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.6%	Indels:	0
DB:	4	Gaps:	0

US-10-507-132-4 (1-172) x AY098661 (1-421)

Qy 99 GluVal11leglyYrH1sglnleuArGyAlProH1sgln 111  
|||||  
Db 279 GAGGTCAITGGCTACCAACGAGCTGCGTCCCCACCAAG 317

RESULT 8  
LOCUS AY098660 423 bp DNA linear PLN 16-JAN-2003  
DEFINITION Ophiostoma piceae isolate 187-1 scytalone dehydratase (SD) gene,  
partial cds.  
ACCESSION AY098660  
VERSION AY098660.1 GI:21238829  
KEYWORDS  
SOURCE Ophiostoma piceae  
ORGANISM Ophiostoma piceae  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
REFERENCE 1 (bases 1 to 423)  
TITLE Fleet,C. and Breuil,C.  
Inhibitors and genetic analysis of scytalone dehydratase confirm  
the presence of DHN-melanin pathway in sapstain fungi  
Mycol. Res. 106 (11), 1331-1339 (2002)  
AUTHORS Fleet,C. and Breuil,C.  
TITLE Direct Submission  
JOURNAL Submitted (22-APR-2002) Wood Science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
LOCATION/Qualifiers

FEATURES  
source 1..423  
/organism="Ophiostoma piceae"  
/mol\_type="genomic DNA"  
/isolate="187-1"  
/db\_xref="taxon:61273"  
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/translation="EMADRYDSKMDRLKCIAPTLLRIDYRSFLNKLMEAMPDEFIG  
MISDPVNLGNPLRTOHFPFGASRWRERVSDFEVIQHLRVPHQVYTDASISVAVKGH  
AHSANQHWYRKVDGVWKFKAG"

ORIGIN

Alignment Scores:

Pred. No.:	0.000177	Length:	423
Score:	13.00	Matches:	13
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.6%	Indels:	0
DB:	4	Gaps:	0

US-10-507-132-4 (1-172) x AY098660 (1-423)

Qy 99 GluVal11leglyYrH1sglnleuArGyAlProH1sgln 111  
|||||  
Db 281 GAGGTCAITGGCTACCAACGAGCTGCGTCCCCACCAAG 319

RESULT 9  
LOCUS AY098666 423 bp DNA linear PLN 16-JAN-2003  
DEFINITION Ophiostoma setosum isolate NZFS3734 scytalone dehydratase (SD)  
gene, partial cds.  
ACCESSION AY098666  
VERSION AY098666.1 GI:21238841  
KEYWORDS  
SOURCE Ophiostoma setosum  
ORGANISM Ophiostoma setosum  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
REFERENCE 1 (bases 1 to 423)  
TITLE Fleet,C. and Breuil,C.  
Inhibitors and genetic analysis of scytalone dehydratase confirm  
the presence of DHN-melanin pathway in sapstain fungi  
Mycol. Res. 106 (11), 1331-1339 (2002)  
AUTHORS Fleet,C. and Breuil,C.  
TITLE Direct Submission  
JOURNAL Submitted (22-APR-2002) Wood Science, University of British  
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
LOCATION/Qualifiers

FEATURES  
source 1..423  
/organism="Ophiostoma setosum"  
/mol\_type="genomic DNA"  
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/country="New Zealand"  
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join(<1..69,128..>423)  
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MISDPVNLGNPLRTOHFPFGASRWRERVSDFEVIQHLRVPHQVYTDASISVAVKGH  
AHSANQHWYRKVDGVWKFKAG"

ORIGIN

Alignment Scores:

Pred. No.:	0.000177	Length:	423
Score:	13.00	Matches:	13
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.6%	Indels:	0
DB:	4	Gaps:	0

US-10-507-132-4 (1-172) x AY098666 (1-423)

Qy 99 GluVal11leglyYrH1sglnleuArGyAlProH1sgln 111  
|||||  
Db 281 GAGGTCAITGGCTACCAACGAGCTGCGTCCCCACCAAG 319

RESULT 10  
LOCUS AY098659 428 bp DNA linear PLN 16-JAN-2003  
DEFINITION Ophiostoma minus isolate OM3 scytalone dehydratase (SD) gene,  
partial cds.  
ACCESSION AY098659  
VERSION AY098659.1 GI:21238827

**KEYWORDS**  
**SOURCE** Ophiostoma minus  
**ORGANISM** Ophiostoma minus  
**REFERENCE** Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
**AUTHORS** Fleet, C. and Breuil, C.  
**TITLE** 1 (bases 1 to 428)  
**JOURNAL** Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi  
**REFERENCE** Mycol. Res. 106 (11), 1331-1339 (2002)  
**AUTHORS** Fleet, C. and Breuil, C.  
**TITLE** 2 (bases 1 to 428)  
**JOURNAL** Direct Submission  
**REFERENCE** Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
**FEATURES**  
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 /mol\_type="genomic DNA"  
 /isolate="OM3"  
 /db\_xref="taxon:150568"  
 /country="United Kingdom"  
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 /join(<1..69,133..>428)  
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 /db\_xref="GI:21238828"  
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 AHSANQHYRKVDGWKRFAG"  
**ORIGIN**  
**Alignment Scores:**  
 Pred. No.: 0.000179 Length: 428  
 Score: 13.00 Matches: 13  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 7.6% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-507-132-4 (1-172) x AY098659 (1-428)  
**QY** 99 G|UvA111eG|YThiSG|InLeuArqValProHisGln 111  
 |||||  
**Db** 286 GAGGTCA|TGGCTAC|CACGACGCTCGGCTCCCCACACG 324  
**RESULT 11**  
 AY098658 433 bp DNA linear PLN 16-JAN-2003  
**LOCUS** Ophiostoma minus isolate 58-4 scytalone dehydratase (SD) gene,  
**DEFINITION** partial cds.  
**ACCESSION** AY098658  
**VERSION** AY098658.1 GI:21238825  
**KEYWORDS**  
**SOURCE** Ophiostoma minus  
**ORGANISM** Ophiostoma minus  
**REFERENCE** Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
**AUTHORS** Fleet, C. and Breuil, C.  
**TITLE** 1 (bases 1 to 433)  
**JOURNAL** Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi  
**REFERENCE** Mycol. Res. 106 (11), 1331-1339 (2002)  
**AUTHORS** Fleet, C. and Breuil, C.  
**TITLE** 2 (bases 1 to 433)  
**JOURNAL** Direct Submission  
**REFERENCE** Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

**FEATURES**  
**source**  
 Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
 1..433  
 /organism="Ophiostoma minus"  
 /mol\_type="genomic DNA"  
 /isolate="58-4"  
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 /country="Canada"  
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 /product="scytalone dehydratase"  
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 /db\_xref="GI:21238826"  
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 AHSANQHYRKVDGWKRFAG"  
**ORIGIN**  
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 Pred. No.: 0.00018 Length: 433  
 Score: 13.00 Matches: 13  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 7.6% Indels: 0  
 DB: 4 Gaps: 0  
 US-10-507-132-4 (1-172) x AY098658 (1-433)  
**QY** 99 G|UvA111eG|YThiSG|InLeuArqValProHisGln 111  
 |||||  
**Db** 291 GAGGTCA|TGGCTAC|CACGACGCTCGGCTCCCCACACG 329  
**RESULT 12**  
 AY098665 422 bp DNA linear PLN 16-JAN-2003  
**LOCUS** Ophiostoma setosum isolate 160-38 scytalone dehydratase (SD) gene,  
**DEFINITION** partial cds.  
**ACCESSION** AY098665  
**VERSION** AY098665.1 GI:21238839  
**KEYWORDS**  
**SOURCE** Ophiostoma setosum  
**ORGANISM** Ophiostoma setosum  
**REFERENCE** Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.  
**AUTHORS** Fleet, C. and Breuil, C.  
**TITLE** 1 (bases 1 to 422)  
**JOURNAL** Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi  
**REFERENCE** Mycol. Res. 106 (11), 1331-1339 (2002)  
**AUTHORS** Fleet, C. and Breuil, C.  
**TITLE** 2 (bases 1 to 422)  
**JOURNAL** Direct Submission  
**REFERENCE** Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
**FEATURES**  
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 Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada  
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 /mol\_type="genomic DNA"  
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 /country="Canada"  
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/gene="SD"
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Alignment Scores:	
Pred. No.:	0.0022
Score:	12.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	7.0%
DB:	4
US-10-507-132-4 (1-172) x AY098665 (1-422)	
	Length: 422
	Matches: 12
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

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QY 100 ValIleGlyTyrHisGlnLeuArgValProHisGln 111
      |||||
Db 284 GTCAITGGTATACCAACAGCTGCGGTCCCAACACAG 315

```

RESULT 13				
ABI00172				
LOCUS	ABI00172	770 bp	DNA	linear
DEFINITION	Bipolaris oryzae BSCDIgene for scytalone dehydratase, complete cds.			
ACCESSION	ABI00172			
VERSION	ABI00172.1	GI:32879676		

SOURCE ORGANISM	REFERENCE
<i>Bipolaris oryzae</i>	1
<i>Bipolaris oryzae</i>	
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;	
Pleosporales; Pleosporaceae; mitosporic Coellobolus; <i>Bipolaris</i>	

**AUTHORS** Kinata, J., Moriawaki, A., Ueno, M., Tokunaga, T., Arai, S. and Honda, Y.  
**TITLE** Cloning, functional analysis and expression of a scytalone dehydratase gene (SCD1) involved in melanin biosynthesis of the phytopathogenic fungus *Biopolaris oryzae*  
**JOURNAL** *Curr. Genet.* 45 (4), 197-204 (2004)

JOURNAL. Curr. Genet. 45 (4), 197-204 (2004)  
 PUBMED 14716498  
 REFERENCE 2 (bases 1 to 770)  
 AUTHORS Kihara, J. and Moriwaki, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JAN-2003) Junichi Kihara, Shimane University, Faculty

FEATURES	Location/Qualifiers
source	1. .770

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/organism="Bipolaris oryzae"
mol_type="genomic DNA"
strain="D9/Fe-69"
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join(34..70,125..645)
CDS

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/gene="HSCD1"
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KIDRSFLDKIWEAMPADFEVYAMSDPAVLNPIPLKTOHFIGGRWETVADDELITGH
QLRVHQHYTDESATVAIVKGAHSFNTHMYKKLDGEMKFGALNPDIRWEYEDPKVFA
AEGRGQVGEAAVAAGIPEYAPGQAV"

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**ORIGIN**

Alignment Scores:	0.00337	Length:	770
Pred. No.:		Matches:	12
Score:	12.00	Conservative:	0
Percent Similarity:	100.0%		

Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	7.0%	Indels:	0
DB:	4	Gaps:	0

US-10-507-132-4 (1-172) X AB100172 (1-770)

QY 24 TyGIUTPALaapSerTYraSserLYsAspTrp 35  
DB 151 TACGAATGGGACAGACAGCTACGACAGCAAGACTGG 186

RESULT	14
AY098663	
LOCUS	414 bp DNA linear
DEFINITION	Ophiostoma piliferum isolate 198-2GF scytalone dehydratase (SD)
ACCESSION	AY098663 gene, partial cds.
VERSION	AY098663.1 GI:21238835

SOURCE	ORGANISM
	<i>Ophiostoma piliferum</i>
	<i>Ophiostoma piliferum</i>

1 (bases 1 to 414)

REFERENCE

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma

**TITLE** Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi  
**JOURNAL** Mycol. Res. 106 (11), 1331-1339 (2002)  
**DESCRIPTORS** (Abscess 1; 414)

**AUTHORS** Fleet, C. and Breuil, C.

**JOURNAL** Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada

**FEATURES** Location/Qualifiers

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source
1. .414
/organism="Ophiostoma piliferum"
/mol_type="genomic DNA"
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CDS

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/protein_id="AA034809.1"
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## ORIGIN

**Alignment Scores:**

Pred. No.:	0.0271	length:	414
Score:	11.00	Matches:	11
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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	6.4%	Indels:	0
DB:	4	Gaps:	0

US-10-507-132-4 (1-172) X AY098663 (1-414)

QY 30 TyraSPSerLysAsPTraSPargLeuArgLys 40  
DB 16 TACGACTCCAAGGACTGGAGCGTCTGGCGAAG 48

**Db**

RESULT 15	LOCUS	DEFINITION
AY098664	414 bp	DNA linear
AY098664		PLAN 16-JAN-2003
		Ophiostoma piliferum isolate 201-1A scytalone dehydratase (SD)



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 4, 2006, 16:36:09 ; Search time 583 Seconds  
(without alignments)  
3085.489 Million cell updates/sec

Title: US-10-507-132-4

Perfect score: 172

Sequence: 1.MSQVQKSDRITFSDYILGLM.....WGFDFDRIPEDGRFTFGDK 172

Scoring table:

OHGO	60.0	Xgapext 60.0
Xgapop 60.0	Xgapext 60.0	
Fgapop 60.0	Fgapext 7.0	
Delop 60.0	Delext 60.0	

Searched: 5244920 seque, 3486124231 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10484873

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB.spool/US10507132/runat\_04122006\_143523\_9593/app\_query.faeta\_1  
-DB=N.Geneseq -QFMT=fastcap -SUPFIX=colip2n.rng -MINMATCH=0.1 -LOOFCU=0  
-LOOPEXT=0 -UNITs=bits -START=1 -END=1 -MATRIX=coligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h  
-USER=US10507132.@CCN\_1.1.761.@runat\_04122006\_143523\_9593 -NCPUI=6 -ICPU=3  
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-MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

N.Geneseq\_8.\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	516	ADCI6592	Scytalone
2	172	100.0	600	ADCI6602	Scytalone
3	172	100.0	610	ADCI6603	Scytalone

4	97	56.4	516	10	ADCI6590	Adci6590 Scytalone
5	8	4.7	375	3	AAIC9354	Aaci9354 Human sec
6	8	4.7	405	6	ABIA80052	Abi80052 Human ova
7	8	4.7	512	9	ACH45193	Ach45193 Human foe
8	8	4.7	1521	4	AAH33155	Aah33155 Human col
9	8	4.7	1690	4	ABLO9311	Ablo9311 Drosophila
10	8	4.7	1690	4	ABLO9311	Ablo9311 Drosophila
11	8	4.7	4182	4	ABLO9310	Ablo9310 Human cod
12	8	4.7	12882	9	ABK42692	Abk42692 Genomic s
13	8	4.7	12882	9	ADBE0848	Adbe0848 Connectiv
14	7	4.1	21	10	ADCI6597	Adci6597 SCDH rela
15	7	4.1	23	10	ADCI6598	Adci6598 SCDH rela
16	7	4.1	27	10	ADCI6601	Adci6601 SCDH rela
17	7	4.1	41	6	ABZ49282	Abz49282 Human aic
18	7	4.1	89	2	AAT62628	Aat62628 Human gen
19	7	4.1	100	8	ACD80651	Acd80651 E. coli K
20	7	4.1	166	2	AAV13085	Aav13085 Xylanase
21	7	4.1	181	2	AAV13087	Aav13087 Xylanase
22	7	4.1	270	10	ACF71276	Acf71276 Phototrab
23	7	4.1	279	6	ABO67328	Abog67328 Listeria
24	7	4.1	294	13	ADU25639	Adu25639 CDNA enco
25	7	4.1	297	4	AAH84614	Aah84614 E. coli g
26	7	4.1	303	3	AAIC12719	Aaci12719 Human sec
27	7	4.1	308	6	ABN24458	Abn24458 Human ORF
28	7	4.1	313	6	ABN75514	Abn75514 Human ORF
29	7	4.1	326	6	ABX48280	Abx48280 Bovine ES
30	7	4.1	371	6	ABN24338	Abn24338 Human ORF
31	7	4.1	384	3	AAA43215	Aaa43215 Xenopus s
32	7	4.1	393	3	AACT74929	Aact74929 Human ORF
33	7	4.1	393	6	ABN77234	Abn77234 Human ORF
34	7	4.1	393	9	ACH29653	Ach29653 Human tes
35	7	4.1	393	12	ADP93576	Adp93576 Cotton ex
36	7	4.1	397	6	ABN17793	Abn17793 Human ORF
37	7	4.1	399	11	ACH95962	Ach95962 Klebsiell
38	7	4.1	406	5	AAE66611	Aae66611 Novel hum
39	7	4.1	411	10	ABX61362	Abx61362 Arabidops
40	7	4.1	440	4	AAK73808	Aak73808 Human imm
41	7	4.1	441	13	ADG50306	Adg50306 Novel can
42	7	4.1	445	4	AAK59769	Aak59769 Human imm
43	7	4.1	449	4	AAI83543	Aai83543 Human pol
44	7	4.1	449	9	ACH38954	Ach38954 Human foe
45	7	4.1	449	14	AED94874	Aed94874 Germ cell

# ALIGNMENTS

RESULT 1	ADCI6592	ADCI6592 standard; DNA; 516 BP.
ID	ADCI6592	
XX	ADCI6592;	
AC	ADCI6592;	
XX	18-DEC-2003	(first entry)
DT	18-DEC-2003	
XX	Scytalone dehydrogenase gene #SEQ ID 3.	
DE	Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;	
XX	Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;	
KM	gene; ds.	
KM	Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;	
XX	gene; ds.	
XX	Magnaporthe grisea.	
OS	Magnaporthe grisea.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..516
FT		/*tag= a
FT		/product= "scytalone dehydrogenase"
FT		/partial
FT		/note= "no stop codon"
XX		
XX	PN	W02003076628-A1.
XX	PD	18-SEP-2003.
XX	PF	24-FEB-2003; 2003WO-JP001980.



Db 321 CTCGCGACGACGACTTATCGCGGCGACGCGCTGGAGAGAGTGTCCGAGACGAGGTC 380  
 QY 101 IIEGLYTYRHISGLINLEUARGVALPROHISGLNARGLTYRYSASPTRTHMETLYSGLU 120  
 Db 381 ATGGGCTTCCGACGAGCTGCGGTCCGACGAGAGTACAGACCCATATAAGAG 440  
 QY 121 ValThrMetLysGlyHISAlaHisSerAlaAsnLeuHISTrpTyrLysLysLeuAspGly 140  
 Db 441 GTCACATGAAGGCGCACGCCCACTCGGCAAACTTCACTGTGTACAAAGAGATCGACGCG 500  
 QY 141 ValTrpLysPheAlaGlyLeuLysProAsp11LeaTrpGlyGluPheAspPheAspArg 160  
 Db 501 GTCGGAAGTTCGCGCGCTCCAGCCGATATCCGCTGGGCGAGTTGCACTTTGACAGG 560  
 QY 161 IIEPHEGLUASPGLYARGGLUTHRPHEGLYASPLYS 172  
 Db 561 ATCTTTAGAGACGAGCGGAGACCTTTGGCGACAAA 596

## RESULT 3

ID ADC16603 standard; DNA; 610 BP.

XX ADC16603;

DT 18-DEC-2003 (first entry)

DE Scytalone dehydrogenase DNA #2.

XX Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;

XX gene; ds.

OS Magnaporthe grisea.

PN MO2003076628-A1.

XX 18-SEP-2003.

PF 24-FEB-2003; 2003WO-JP001980.

XX 12-MAR-2002; 2002JP-00066955.

PA (TSUB ) KUMITAI CHEM IND CO LTD.

PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

DR WPI; 2003-748394/70.

PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening

XX for SCDH inhibitors and evaluating sensitivity to them.

PS Example 2; Fig 4; 50pp; Japanese.

CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),

CC that functions in the presence of an inhibitor, comprising an optionally

CC mutated, defined amino acid sequence given in the specification. Also

CC disclosed is a method for evaluating rice blast fungus (Pyricularia

CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase

CC inhibitors. The gene is useful for screening for new SCDH inhibitors and

CC evaluating sensitivity to them. The current sequence represents the

CC Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is

CC given in ADC16592.

XX Sequence 610 BP; 148 A; 179 C; 170 G; 113 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.16e-179 Length: 610  
 Score: 172.00 Matches: 172  
 Percent Similarity: 100.0% Conservatives: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 10 Gaps: 0

US-10-507-132-4 (1-172) x ADC16603 (1-610)

QY 1 MetGlySerGlnValGlnLysSerAspGlu11GThrPheSerAspTyrLeuGlyLeuMet 20  
 Db 81 ATGGGCTTCCGACGAGCTTCAAAAGAGCGATGATTAACCTTCTCAGACTTCTGGGGCTTATG 140  
 QY 21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40  
 Db 141 ACTTGGCGTATATGATGGGAGAGACGCTACGACTCCAAAGAGATCGGATAGGCTCGAAAG 200  
 QY 41 ValIleAlaProThrLeuAlaGllLeaPTrArgSerPheLeuAspLysLeuTrpGluAla 60  
 Db 201 GTCATTCGCGCTTCTCGCCCATTTGACTACCGCTCTTCTCCACAAAGCTCTGGAGGCA 260  
 QY 61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80  
 Db 261 ATGCGCGCCGAGAGAGTTCTGCGGCAATGTTCCAGACAGAGTCTCGGCGACCCACCC 320  
 QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGlyLysValSerGluAspGluVal 100  
 Db 321 CTCGCGACGCGACACTTCATCGGCGGCGCGCTGGGAGAGAGTGTCCGAGACGAGGTC 380  
 QY 101 IIEGLYTYRHISGLINLEUARGVALPROHISGLNARGLTYRYSASPTRTHMETLYSGLU 120  
 Db 381 ATCGGCTACCCACGAGCTGCGGTCCGCGACGAGAGTACAAAGACACCAATGAAAGAG 440  
 QY 121 ValThrMetLysGlyHISAlaHisSerAlaAsnLeuHISTrpTyrLysLysLeuAspGly 140  
 Db 441 GTCACATGAAGGCGCACGCCCACTCGGCAAACTTCACTGTGTACAAAGAGATCGACGCG 500  
 QY 141 ValTrpLysPheAlaGlyLeuLysProAsp11LeaTrpGlyGluPheAspPheAspArg 160  
 Db 501 GTCGGAAGTTCGCGCGCTCCAGCCGATATCCGCTGGGCGAGTTGCACTTTGACAGG 560  
 QY 161 IIEPHEGLUASPGLYARGGLUTHRPHEGLYASPLYS 172  
 Db 561 ATCTTTAGAGACGAGCGGAGACCTTTGGCGACAAA 596

## RESULT 4

ID ADC16590 standard; DNA; 516 BP.

XX ADC16590;

DT 18-DEC-2003 (first entry)

DE Scytalone dehydrogenase gene #SEQ ID 1.

XX Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;

XX gene; ds.

OS Magnaporthe grisea.

PN MO2003076628-A1.

XX 18-SEP-2003.

PF 24-FEB-2003; 2003WO-JP001980.

XX 12-MAR-2002; 2002JP-00066955.

PA (TSUB ) KUMITAI CHEM IND CO LTD.

PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

DR WPI; 2003-748394/70.

PT P-PSDB; ADC16591.

XX Key Location/Qualifiers

XX CDS 1..516

XX /\*tag= a

XX /product= "scytalone dehydrogenase"

XX /partial

XX /note= "no stop codon"

```

XX Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX Example 2, SEQ ID NO 1; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC scytalone dehydrogenase gene sequence.
XX
SQ Sequence 516 BP; 119 A; 151 C; 155 G; 91 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.21e-97 Length: 516
Score: 97.00 Matches: 97
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 56.4% Indels: 0
DB: Gaps: 0

US-10-507-132-4 (1-172) x ADC16590 (1-516)

QY 76 LeuGlyAspProthrIeuArgThrGlnHisPheIleGlyIleThrArgTrrGluVal 95
Db 226 CTGGGGGACCCGCCCTCCGACGACGACTTCATCGCGGCGACGGCTGGAGAAAGGTG 285
QY 96 SerGluAspGluValIleGlyIleGlnIleuArgValProHisGlnArgTrrLysAsp 115
Db 286 TCCGAGGACGAGGTCTACGCGCTACCAACGACTCGCGCTCCGACCAAGAGTACAAAGAC 345
QY 116 ThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnIleuHisTrrTyr 135
Db 346 ACCACATGAAAGAGGTCAACATGAAGGCGCAAGCCCACTCGGCAAACTTCACTGATAC 405
QY 136 LysLysIleAspIleValIleTrrLysPheAlaGlyIleuLysProAspIleArgTrrGlyGlu 155
Db 406 AAGCAAGATTCAGCGCGCTGGAAGTTCGCGGCTCAAGCCCAATATCCGCTGGGCGGAG 465
QY 156 PheAspPheAspArgIlePheGluAspGlyArgGluThrPheGlyAspLys 172
Db 466 TTGGACTTTACAGATCTTTGAGGACGACGAGGAGCTTTGGCCACAA 516

RESULT 5
AAC19354
ID AAC19354 standard; cDNA; 375 BP.
XX
AC AAC19354;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 23429.
XX
KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (BEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;

```

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XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1, SEQ ID NO 23429; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 375 BP; 106 A; 96 C; 67 G; 104 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 35.2 Length: 375
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: Gaps: 0

US-10-507-132-4 (1-172) x AAC19354 (1-375)

QY 70 ValSerSerLysGlnValIleuGly 77
Db 347 GTGAGCTCCAAACAGTTTAAAGA 370

RESULT 6
ABL80052
ID ABL80052 standard; cDNA; 405 BP.
XX
AC ABL80052;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:3030.
XX
KM Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US017756.
XX
PR 26-MAY-2000; 2000US-0207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
XX
DR WPI; 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.
XX

```

PS Claim 1, SEQ ID NO 3030; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of an ovarian tumour

CC polypeptide encoded by a polynucleotide (III) having a CDNA sequence (S1)

CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,

CC (III) encoding (II) having a sequence (S2), a T cell population of (II),

CC or antigen presenting cells that express (II). (I) has cytostatic

CC activity. An oligonucleotide (IV) that hybridizes to (S1) can be used for

CC detecting ovarian cancer in a patient's biological sample preferably

CC serum or ovarian tissue. The method comprises contacting a biological

CC sample from a patient with (IV), detecting the amount of polynucleotide

CC hybridizing to (IV) and comparing the amount to a predetermined cutoff

CC value and thereby detecting ovarian cancer in the patient, where the

CC amount of polynucleotide hybridizing to (IV) is detected preferably by

CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is

CC useful for stimulating and/or expanding T cells specific for an ovarian

CC tumour protein comprising contacting T cells with (III) or (II). (III) is

CC useful in design and preparation of ribozyme molecules for inhibiting

CC expression of the tumour polypeptides and proteins in tumour cells; and

CC to isolate a full length gene from a suitable library e.g., a tumour CDNA

CC library using well known techniques

XX

SQ Sequence 405 BP; 127 A; 86 C; 77 G; 115 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	37.9	Length:	405
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x ABL80052 (1-405)

QY 70 ValSerSerLysGlnValLeuGly 77  
 |||||  
 DB 111 GTGAGCTCCAAACAGTTTAAAGA 134

## RESULT 7

ACH45193  
 ID ACH45193 standard; cDNA; 512 BP.

XX ACH45193;

DT 13-OCT-2003 (first entry)

XX Human foetal brain CDNA #5918.

XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;

KW Genome mapping; biodiversity; genetic disorder.

XX Homo sapiens.

OS US2003073623-A1.

PN 17-APR-2003.

PD 30-JUL-2001; 2001US-00918995.

PF 30-JUL-2001; 2001US-00918995.

PR 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

XX (LABA/) LABAT I

XX (STAC/) STACHE-CRAIN B.

XX (DICK/) DICKSON M C.

XX (JONE/) JONES L W.

PI Dmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

PT New polynucleotide sequences obtained from various CDNA libraries, useful

PT as hybridization probes, as oligomers for PCR, for chromosome and gene

PT mapping, in the recombinant production of protein, or in generating

PT antisense DNA or RNA.

PS Claim 1, SEQ ID NO 32405; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of

CC 38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was

CC determined by the technique of SBH (sequencing by hybridisation). Also

CC included is a purified polypeptide comprising a sequence corresponding to

CC a reading frame of the novel polynucleotide. The nucleic acid sequences

CC are useful in diagnostics as expressed sequence tags (EST) for

CC identifying expressed genes or for physical mapping of the human genome,

CC in forensics, in assessing biodiversity, or in identifying mutations

CC responsible for genetic disorders and other traits. The nucleotide

CC sequences are also useful as hybridisation probes, as oligomers for PCR,

CC for chromosome and gene mapping, in the recombinant production of

CC protein, or in generating antisense DNA or RNA. The purified polypeptide

CC is useful for generating antibodies specific for it. The present sequence

CC is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?docid=20030073623

XX

SQ Sequence 512 BP; 145 A; 119 C; 103 G; 133 T; 0 U; 12 Other;

## Alignment Scores:

Pred. No.:	47.4	Length:	512
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	9	Gaps:	0

US-10-507-132-4 (1-172) x ACH45193 (1-512)

QY 70 ValSerSerLysGlnValLeuGly 77  
 |||||  
 DB 440 GTGAGCTCCAAACAGTTTAAAGA 463

## RESULT 8

AAH33155  
 ID AAH33155 standard; cDNA; 1521 BP.

XX AAH33155;

DT 03-SEP-2001 (first entry)

XX Human colon cancer antigen encoding CDNA SEQ ID NO:211.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;

KW colorectal carcinoma; ss.

XX Homo sapiens.

PN WO200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-US026524.

PR 29-SEP-1999; 99US-0157137P.

XX 03-NOV-1999; 99US-0163280P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Birse CE, Rosen CA;

XX WPI; 2001-235357/24.

XX P-PADB; AAG73724.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

PT useful for preventing, diagnosing and/or treating colorectal cancers.

XX Claim 1; Page 2354; 9803pp; English.  
PS  
XX  
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patients own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO.1027  
CC to 1052, 7921 and 7922  
XX  
SQ Sequence 1521 BP; 411 A; 355 C; 380 G; 371 T; 0 U; 4 Other;  
XX  
Alignment Scores:  
Pred. No.: 135 Length: 1521  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: Gaps: 0  
US-10-507-132-4 (1-172) x AAH3155 (1-1521)  
QY 70 ValSerGlyGlnValLeuGly 77  
DB 310 GTGAGCTCCAAACAGTTTACGA 333  
RESULT 9  
ABLO9311  
ID ABL09311 standard; cDNA; 1690 BP.  
XX  
AC ABL09311;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22415.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
XX pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
XX  
PR 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter UC, Adams M, Li FWD, Myers EW,  
XX  
XX WPI; 2001-656860/75.  
XX  
XX P-PSDB; ABB65208.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions.  
XX

PS Claim 1; SEQ ID NO 22415; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01640-ABL16175) and the encoded proteins (ABBS7737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1690 BP; 611 A; 335 C; 351 G; 393 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 149 Length: 1690  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: Gaps: 0  
US-10-507-132-4 (1-172) x ABL09311 (1-1690)  
QY 40 LysValIleAlaProThrLeuArg 47  
DB 1040 ABAAGTTATGCTCCAGCTCTGAGA 1063  
RESULT 10  
ADA53154  
ID ADA53154 standard; cDNA; 2002 BP.  
XX  
AC ADA53154;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Human coding sequence, SEQ ID 722.  
XX  
XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
XX Gene Therapy; human; secretory protein; membrane proteins; cancer;  
XX Inflammatory disease; osteoporosis; neurological disease; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX EP1293569-A2.  
XX  
XX 19-MAR-2003.  
XX  
XX 21-MAR-2002; 2002EP-0006586.  
XX  
XX 14-SEP-2001; 2001JP-00328381.  
XX  
XX 24-JAN-2002; 2002US-0350435P.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;  
XX WPI; 2003-395539/38.  
XX  
XX P-PSDB; ADA54793.  
XX  
XX New polynucleotides encoding full-length polypeptides, e.g. secretory  
XX and/or membrane proteins, useful for developing medicines for diseases in  
XX which the gene is involved, or as target molecules for gene therapy.  
XX  
XX Claim 1; SEQ ID NO 722; 205pp; English.  
XX  
XX The present invention relates to novel human secretory or membrane  
XX CC proteins (ADA54072-ADA55710) and their coding sequences (ADA5433-  
XX ADA54071). The coding sequences are useful in the gene therapy of



CC diseases caused by abnormalities of the proteins, e.g. cancer,  
CC inflammatory diseases, osteoporosis or neurological disease.

XX  
SQ Sequence 2002 BP; 526 A; 466 C; 514 G; 496 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	175	Length:	2002
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADA53154 (1-2002)

Oy 70 ValSerGlyGlnValLeuArg 77  
|||||  
Db 802 GTGAGCTCCAAACAAAGTTTGA 825

## RESULT 11

ABL09310/c  
ID ABL09310 standard; cDNA; 4182 BP.

AC ABL09310;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 22412.

XX Drosophila; developmental biology; cell signalling; insecticide;

KM pharmaceutical; gene; ss.

XX Drosophila melanogaster.

PN W0200171042-A2.

PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR P-PSDB; ABB65207.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signaling and cell-cell

XX interactions.

XX Claim 1; SEQ ID NO 22412; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA

CC sequences (AB101840-AB16175) and the encoded proteins (AB857737-

CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 4182 BP; 1284 A; 747 C; 676 G; 1475 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 356 Length: 4182

Score: 8.00 Matches: 8

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0%

Query Match: 4.7%

US-10-507-132-4 (1-172) x ABL09310 (1-4182)

Oy 40 IysValIleAlaProThrLeuArg 47  
|||||  
Db 1714 AAAGTTAGCTCCGACTGTGACA 1691

## RESULT 12

ABK42692  
ID ABK42692 standard; DNA; 12822 BP.

AC ABK42692;

DT 21-MAY-2002 (first entry)

XX Genomic sequence #591 encoding novel human connective tissue polypeptide.

KM Human; connective tissue related disorder; cancer; gene therapy;

XX cytoskeletal; gene; ds.

XX Homo sapiens.

PN W0200155343-A1.

PD 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001322.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-021647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217486P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226688P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

XX	PR	17-NOV-2000;	2000US-0249218P.
XX	PR	17-NOV-2000;	2000US-0249224P.
XX	PR	17-NOV-2000;	2000US-0249245P.
XX	PR	17-NOV-2000;	2000US-0249265P.
XX	PR	17-NOV-2000;	2000US-0249297P.
XX	PR	17-NOV-2000;	2000US-0249299P.
XX	PR	17-NOV-2000;	2000US-0249300P.
XX	PR	01-DEC-2000;	2000US-0250160P.
XX	PR	01-DEC-2000;	2000US-0250391P.
XX	PR	05-DEC-2000;	2000US-0251030P.
XX	PR	05-DEC-2000;	2000US-0251988P.
XX	PR	05-DEC-2000;	2000US-0256719P.
XX	PR	06-DEC-2000;	2000US-0251479P.
XX	PR	08-DEC-2000;	2000US-0251856P.
XX	PR	08-DEC-2000;	2000US-0251868P.
XX	PR	08-DEC-2000;	2000US-0251869P.
XX	PR	08-DEC-2000;	2000US-0251989P.
XX	PR	08-DEC-2000;	2000US-0251990P.
XX	PR	11-DEC-2000;	2000US-0254097P.
XX	PR	05-JAN-2001;	2001US-0259678P.
XX	PA	(HUMA-)	HUMAN GENOME SCI INC.
XX	PL	Rosen CA,	Barash SC, Ruben SM;
XX	DR	WPI;	2001-565190/63.
XX	PT	Nucleic acid encoding novel connective tissue associated polypeptides,	
XX	PT	used in diagnosing, preventing, creating or ameliorating a disorder such	
XX	PT	as cancer or rheumatoid arthritis.	
XX	PS	Disclosure;	SEQ ID NO 1579; 673bp; English.
XX	CC	The present invention relates to the isolation of novel human connective	
XX	CC	tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide	
XX	CC	(cDNA and genomic) sequences encoding them. The sequences of the	
XX	CC	invention are useful in the diagnosis, treatment, prevention and/or	
XX	CC	prognosis of diseases associated with connective tissue(s), including	
XX	CC	cancer. The polynucleotide sequences of the invention are also useful in	
XX	CC	gene therapy. ABA42102-ABA43116 represent genomic sequences encoding the	
XX	CC	novel human connective tissue related polypeptides. Note: The sequence	
XX	CC	data for this patent did not form part of the printed specification, but	
XX	CC	was obtained in electronic format directly from WIPO at	
XX	CC	ftp.wipo.int/pub/published_pct_sequences	
XX	SQ	Sequence 12822 BP; 3353 A; 2570 G; 2626 G; 4273 T; 0 U; 0 Other;	
	Alignment Scores:		
	Pred. No.:	1.04e+03	Length: 12822
	Score:	8.00	Matches: 8
	Percent Similarity:	100.0%	Conservative: 0
	Best Local Similarity:	100.0%	Mismatches: 0
	Query Match:	4.7%	Indels: 0
	BB:	4	Gaps: 0
	US-10-507-132-4 (1-172) x	ABA42692 (1-12822)	
OY	70	ValSerSerLysGlnValLeuGly 77	
DB	11559	GTGAGCTCCAAACAAAGTTTAGGA 11582	
	RESULT 13		
ID	ADB60848	standard; DNA; 12822 BP.	
XX	AC	ADB60848;	
XX	DT	04-DEC-2003 (first entry)	
XX	DE	Connective tissue related genomic DNA #591.	
XX	KX	cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;	

KW antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;  
KW antiinflammatory; antiallergic; antiaschemic; dermatological;  
KW nephrotic; vituicide; fungicide; antibacterial; antiparasitic;  
KW gene therapy; ds: connective tissues disorder; rheumatoid arthritis;  
KW systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;  
KW cancer metastasis; neoplasia; leukæmia; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;  
KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;  
KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;  
KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;  
KW gastrointestinal disorder; inflammatory bowel disease;  
KW organ transplant rejection; immune system disorder; Bruton's disease;  
KW X-linked lymphoproliferative syndrome;  
KW B-cell lymphoproliferative disorder; HIV; AIDS; infection;  
KW chromosome identification; chromosome mapping;  
KW connective tissue related polynucleotide; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2003054375-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 07-MAR-2002; 2002US-00092154.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 22-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 03-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0232403P.  
PR 14-SEP-2000; 2000US-0233064P.  
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PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
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PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
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PR 29-SEP-2000; 2000US-0236327P.  
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PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239335P.  
PR 13-OCT-2000; 2000US-0239337P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
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PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249246P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.

PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251888P.  
 PR 05-DEC-2000; 2000US-025179P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251899P.  
 PR 11-DEC-2000; 2000US-0251990P.  
 PR 05-JAN-2001; 2001US-0254079P.  
 PR 17-JAN-2001; 2001US-00764847.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SW, Barash SC;  
 XX  
 XX WPI; 2003-634869/60.  
 XX P-PSDB; ADB59591.  
 DR  
 DR  
 PT New connective tissue-related polypeptides and polynucleotides, useful  
 PT for treating, preventing and/or prognosing e.g. disorders of connective  
 PT tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or  
 PT neoplasias.  
 XX  
 PS Disclosure; SEQ ID NO 1579; 248bp; English.

XX The invention describes an isolated nucleic acid molecule (I), which  
 CC comprises a sequence that is at least 95 % identical to a connective  
 CC tissue-related polynucleotide encoding connective tissue antigens (CTA).  
 CC The polypeptide or polynucleotide is useful for preventing, treating, or  
 CC ameliorating medical conditions in a mammal. The connective tissue  
 CC polypeptides, polynucleotides and antibodies are particularly useful for  
 CC treating, preventing and/or prognosing disorders of connective tissues  
 CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,  
 CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or  
 CC neoplasias (e.g. leukemia), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases  
 CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass  
 CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,  
 CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

## Alignment Scores:

Pred. No.:	1.04e+03	Length:	12822
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	9	Gaps:	0

US-10-507-132-4 (1-172) x ADB60848 (1-12822)

Qy 70 ValSerSerIysGlnValIleuGly 77

Db 11559 GTGAGCTCCAAACAAGTTTACGA 11582

## RESULT 14

ADCl6597 standard; DNA; 21 BP.

XX ADCl6597;

XX 18-DEC-2003 (first entry)

XX SCDH related primer #SEQ ID 8.

XX Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor; PCR;

XX primer; ss.

XX

OS Magnaporthe grisea.

XX WO2003076628-A1.

XX 18-SEP-2003.

XX 24-FEB-2003; 2003WO-JP001980.

XX 12-MAR-2002; 2002JP-00066955.

XX (TSUB ) KUMIAI CHEM IND CO LTD.

XX Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

XX WPI; 2003-748394/70.

PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening  
 PT for SCDH inhibitors and evaluating sensitivity to them.

XX Example 3; SEQ ID NO 8; 50bp; Japanese.

XX The invention relates to a gene encoding scytalone dehydrogenase (SCDH),  
 CC that functions in the presence of an inhibitor, comprising an optionally  
 CC mutated, defined amino acid sequence given in the specification. Also  
 CC disclosed is a method for evaluating rice blast fungus (Pyricularia  
 CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase  
 CC inhibitors. The gene is useful for screening for new SCDH inhibitors and  
 CC evaluating sensitivity to them. The current sequence represents a primer  
 CC for amplifying the scytalone dehydrogenase gene sequence.

XX Sequence 21 BP, 7 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	28	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADCl6597 (1-21)

Qy 1 MetGlySerGlnValGlnIlys 7

Db 1 ATGGGTTCCCAAGTCAAAAG 21

## RESULT 15

ADCl6598/C standard; DNA; 23 BP.

XX ADCl6598;

XX 18-DEC-2003 (first entry)

XX SCDH related primer #SEQ ID 9.

XX Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor; PCR;

XX primer; ss.

XX Magnaporthe grisea.

XX WO2003076628-A1.

XX 18-SEP-2003.

XX 24-FEB-2003; 2003WO-JP001980.

XX 12-MAR-2002; 2002JP-00066955.

XX (TSUB ) KUMIAI CHEM IND CO LTD.

XX Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;

XX

DR WPI; 2003-748394/70.

XX Gene encoding for scytalone dehydrogenase (SCDH), useful for screening  
PT for SCDH inhibitors and evaluating sensitivity to them.

XX PS Example 4; SEQ ID NO 9; 50pp; Japanese.

XX CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),  
CC that functions in the presence of an inhibitor, comprising an optionally  
CC mutated, defined amino acid sequence given in the specification. Also  
CC disclosed is a method for evaluating rice blast fungus (Pyricularia  
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase  
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and  
CC evaluating sensitivity to them. The current sequence represents a primer  
CC for amplifying the scytalone dehydrogenase gene sequence.

XX SQ Sequence 23 BP; 2 A; 8 C; 6 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	30.5	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADC16598 (1-23)

QY 120 G|uValThrMetLysG|yH|s 126  
|||  
DB 21 GAGGTCAACATGAGGGCCAC 1

Search completed: December 4, 2006, 23:59:43  
Job time : 591 secs

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GenCore version 5.1.9  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 4, 2006, 17:22:59 ; Search time 194 Seconds  
(without alignments)  
2488.382 Million cell updates/sec

Title: US-10-507-132-4

Perfect score: 172

Sequence: 1 MGSQVQKSDRITFSDYIGLM.....MGFEFDRIPEDRRTFGDK 172

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 60.0 , Fgapext 7.0  
Delop 60.0 , Delext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2800955

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DBY=xjh  
-Q=/abs/ABSSMB.spool/US10507132/runat\_04122006\_143535\_9709/app.query.fasta.1  
-DB=Issued\_Patents\_NA -OPMT=fastap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss07  
-USER=US10507132 -CCN 1.1.204 -runat 04122006\_143535\_9709 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV -TIMEOUT=120  
-WARN -TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=60 -Fgapext=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database: Issued Patents NA.\*

1: /EMC\_Celerra\_SIDS3/pcodata/2/ina/1 COMB.seq.\*  
2: /EMC\_Celerra\_SIDS3/pcodata/2/ina/5 COMB.seq.\*  
3: /EMC\_Celerra\_SIDS3/pcodata/2/ina/6A COMB.seq.\*  
4: /EMC\_Celerra\_SIDS3/pcodata/2/ina/6B COMB.seq.\*  
5: /EMC\_Celerra\_SIDS3/pcodata/2/ina/7 COMB.seq.\*  
6: /EMC\_Celerra\_SIDS3/pcodata/2/ina/H COMB.seq.\*  
7: /EMC\_Celerra\_SIDS3/pcodata/2/ina/H/CTUS COMB.seq.\*  
8: /EMC\_Celerra\_SIDS3/pcodata/2/ina/PP COMB.seq.\*  
9: /EMC\_Celerra\_SIDS3/pcodata/2/ina/RE COMB.seq.\*  
10: /EMC\_Celerra\_SIDS3/pcodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	4.7	375	3	US-09-513-999C-23429
2	8	4.7	2002	4	US-10-094-749-722
3	8	4.7	88268	3	US-09-949-016-14178
4	8	4.7	152132	3	US-09-949-016-13845
5	8	4.7	152145	3	US-09-949-016-12371
6	7	4.1	166	3	US-09-189-0608-23
7	7	4.1	181	3	US-09-189-0608-25
8	7	4.1	297	3	US-09-711-164-242

9	7	4.1	303	3	US-09-513-999C-16794	Sequence 16794, A
10	7	4.1	377	3	US-09-270-767-9687	Sequence 9687, Ap
11	7	4.1	337	3	US-09-370-767-24969	Sequence 24969, A
12	7	4.1	399	3	US-09-489-039A-1757	Sequence 1757, Ap
13	7	4.1	463	3	US-09-513-999C-3332	Sequence 3332, Ap
14	7	4.1	479	3	US-09-621-976-15423	Sequence 15423, A
15	7	4.1	488	3	US-09-513-999C-1132	Sequence 1132, Ap
16	7	4.1	601	3	US-09-949-016-26290	Sequence 26290, A
17	7	4.1	601	3	US-09-949-016-38776	Sequence 38776, A
18	7	4.1	601	3	US-09-949-016-38777	Sequence 38777, A
19	7	4.1	601	3	US-09-949-016-103519	Sequence 103519, A
20	7	4.1	601	3	US-09-949-016-118088	Sequence 118088, A
21	7	4.1	601	3	US-09-949-016-118089	Sequence 118089, A
22	7	4.1	601	3	US-09-949-016-143766	Sequence 143766, A
23	7	4.1	601	3	US-09-949-016-143767	Sequence 143767, A
24	7	4.1	601	3	US-09-949-016-163784	Sequence 163784, A
25	7	4.1	601	3	US-09-949-016-163785	Sequence 163785, A
26	7	4.1	601	3	US-09-280-116-93	Sequence 169814, A
27	7	4.1	756	3	US-09-489-039A-1889	Sequence 1889, Ap
28	7	4.1	861	3	US-09-319-806-3	Sequence 5281, Ap
29	7	4.1	864	3	US-09-902-540-5281	Sequence 5281, Ap
30	7	4.1	1083	3	US-09-270-767-10805	Sequence 10805, A
31	7	4.1	1197	3	US-09-543-681A-3467	Sequence 3467, Ap
32	7	4.1	1590	3	US-09-902-540-4236	Sequence 4236, Ap
33	7	4.1	2089	3	US-09-155-770-6	Sequence 6, App1
34	7	4.1	2236	4	US-09-422-999E-3	Sequence 3, App1
35	7	4.1	2236	4	US-09-949-016-1937	Sequence 1937, Ap
36	7	4.1	2349	3	US-09-805-455-1	Sequence 1, App1
37	7	4.1	2381	4	US-10-089-057A-3	Sequence 3, App1
38	7	4.1	2525	3	US-10-104-047-910	Sequence 910, App
39	7	4.1	2604	3	US-09-107-532A-739	Sequence 739, App
40	7	4.1	2649	3	US-08-400-067-2	Sequence 2, App1
41	7	4.1	2741	3	US-09-949-016-2882	Sequence 2882, Ap
42	7	4.1	2955	2	US-08-687-379-5	Sequence 5, App1
43	7	4.1	2955	2	US-08-687-379-7	Sequence 7, App1
44	7	4.1	3061	3	US-09-949-016-4055	Sequence 4055, Ap
45	7	4.1	3407	3	US-08-483-327-1	Sequence 1, App1

## ALIGNMENTS

RESULT 1  
US-09-513-999C-23429  
; Sequence 23429, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Ducleart, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513, 999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 23429  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 13  
; OTHER INFORMATION: y=c or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 14  
; OTHER INFORMATION: m=a or c  
; US-09-513-999C-23429  
Alignment Scores:

Pred. No.: 10.2 Length: 375  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-513-999C-23429 (1-375)

OY 70 ValSerSerlysglnValleugly 77  
DB 347 GTGAGCTCCAAACAAGTTTAGGA 370

## RESULT 2

US-10-094-749-722  
Sequence 722, Application US/10094749  
Patent No. 6979557  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOHICO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOMYUKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASUHO, YASUHIKO  
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
FILE REFERENCE: 084335/0160  
CURRENT APPLICATION NUMBER: US/10/094,749  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/350,435  
PRIOR FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: JP 2001-328381  
PRIOR FILING DATE: 2001-09-14  
NUMBER OF SEQ ID NOS: 3381  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 722  
LENGTH: 2002  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-094-749-722

## Alignment Scores:

Pred. No.: 50.1 Length: 2002  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 4 Gaps: 0

US-10-507-132-4 (1-172) x US-10-094-749-722 (1-2002)

OY 70 ValSerSerlysglnValleugly 77  
DB 802 GTGAGCTCCAAACAAGTTTAGGA 825

## RESULT 3

US-09-949-016-14178  
Sequence 14178, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14178  
LENGTH: 88268  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(88268)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14178

## Alignment Scores:

Pred. No.: 1.81e+03 Length: 88268  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-949-016-14178 (1-88268)

OY 46 LeuArgGlyAspTyrArgSerPhe 53  
DB 49601 CTTAGATTGATTACGATCTTTC 49624

## RESULT 4

US-09-949-016-13845  
Sequence 13845, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13845  
LENGTH: 152132  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-13845

## Alignment Scores:

Pred. No.: 3.04e+03 Length: 152132  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-949-016-13845 (1-152132)

OY 95 ValSerGluAspGluValleugly 102  
DB 102 GTGAGCTCCAAACAAGTTTAGGA 102



Db 118339 GTATCAGAGATGATCATCGCG 118362

RESULT 5

US-09-949-016-12371  
Sequence 12371, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C0001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12371

LENGTH: 152145

TYPE: DNA

ORGANISM: Human

US-09-949-016-12371

Alignment Scores:

Pred. No.: 3.04e+03

Score: 8.00 Length: 152145

Percent Similarity: 100.0% Matches: 8

Best Local Similarity: 100.0% Conservative: 0

Query Match: 4.7% Mismatches: 0

DB: 3 Indels: 0

Gaps: 0

US-10-507-132-4 (1-172) x US-09-949-016-12371 (1-152145)

Oy 95 Valsesglunapgiuvallegly 102

Db 118339 GTATCAGAGATGATCATCGCG 118362

RESULT 6

US-09-189-0608-23/C

Sequence 23, Application US/091890608

Patent No. 6270968

GENERAL INFORMATION:

APPLICANT: Dalboge, Henrik

APPLICANT: Sandal, Thomas

APPLICANT: Kaupinen, Markus

APPLICANT: Borge, Didrichsen

TITLE OF INVENTION: Method Of Providing No. 6270968e1 DNA Sequences

FILE REFERENCE: 4772.204-US

CURRENT APPLICATION NUMBER: US/09/189,0608

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: PCT/DK97/00216

PRIOR FILING DATE: 1997-05-12

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 23

LENGTH: 166

TYPE: DNA

ORGANISM: Hybrid

US-09-189-0608-23

Alignment Scores:

Pred. No.: 59

Score: 7.00 Length: 166

Percent Similarity: 100.0% Matches: 7

Best Local Similarity: 100.0% Conservative: 0

Query Match: 4.1% Mismatches: 0

DB: 3 Indels: 0

Gaps: 0

US-10-507-132-4 (1-172) x US-09-189-0608-23 (1-166)

Oy 106 LeuargValProhigargin 112

Db 34 CTGAGAGTGCACACGCGT 14

RESULT 7

US-09-189-0608-25/C

Sequence 25, Application US/091890608

Patent No. 6270968

GENERAL INFORMATION:

APPLICANT: Dalboge, Henrik

APPLICANT: Sandal, Thomas

APPLICANT: Kaupinen, Markus

APPLICANT: Borge, Didrichsen

TITLE OF INVENTION: Method Of Providing No. 6270968e1 DNA Sequences

FILE REFERENCE: 4772.204-US

CURRENT APPLICATION NUMBER: US/09/189,0608

PRIOR FILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: PCT/DK97/00216

PRIOR FILING DATE: 1997-05-12

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25

LENGTH: 181

TYPE: DNA

ORGANISM: Hybrid

US-09-189-0608-25

Alignment Scores:

Pred. No.: 64

Score: 7.00 Length: 181

Percent Similarity: 100.0% Matches: 7

Best Local Similarity: 100.0% Conservative: 0

Query Match: 4.1% Mismatches: 0

DB: 3 Indels: 0

Gaps: 0

US-10-507-132-4 (1-172) x US-09-189-0608-25 (1-181)

Oy 106 LeuargValProhigargin 112

Db 34 CTGAGAGTGCACACGCGT 14

RESULT 8

US-09-711-164-242

Sequence 242, Application US/09711164

Patent No. 6589738

GENERAL INFORMATION:

APPLICANT: Forsyth, R. Allyn

APPLICANT: Ohlsen, Karl

APPLICANT: Zykkind, Judith

TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF

FILE REFERENCE: ELITRA.008A

CURRENT APPLICATION NUMBER: US/09/711,164

PRIOR FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: US 60/164415

PRIOR FILING DATE: 1999-11-9

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 242

LENGTH: 297

TYPE: DNA

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(297)

US-09-711-164-242

Alignment Scores:

Pred. No.: 102

Score: 7.00 Length: 297

Percent Similarity: 100.0% Matches: 7

Best Local Similarity: 100.0% Conservative: 0

Query Match: 4.1% Mismatches: 0

DB: 3 Indels: 0

Gaps: 0

US-10-507-132-4 (1-172) x US-09-711-164-242 (1-297)

DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-711-164-242 (1-297)

QY 46 LeuArgIleAspTyrArgSer 52  
 DB 175 TTAGCTATTGACATTCGACAGT 195

# RESULT 9

US-09-513-999C-16794  
 ; Sequence 16794, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR FILING DATE: 1999-02-26  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 16794  
 ; LENGTH: 303  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-513-999C-16794

## Alignment Scores:

Pred. No.: 104 Length: 303  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 4.1% Indels: 0  
 DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-513-999C-16794 (1-303)

QY 82 ArgThrGlnHisPheIleGly 88  
 DB 11 AGGACACAGCATTTATTGGC 31

# RESULT 10

US-09-270-767-9687/C  
 ; Sequence 9687, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 9687  
 ; LENGTH: 377  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila melanogaster  
 ; US-09-270-767-9687

## Alignment Scores:

Pred. No.: 128 Length: 377  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 4.1% Indels: 0  
 DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-270-767-9687 (1-377)

QY 50 TyrArgSerPheLeuAspLys 56  
 DB 140 TATCGTTCCTTCCTCGACAAA 120

# RESULT 11

US-09-270-767-24969/C  
 ; Sequence 24969, Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 24969  
 ; LENGTH: 377  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila melanogaster  
 ; US-09-270-767-24969

## Alignment Scores:

Pred. No.: 128 Length: 377  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 4.1% Indels: 0  
 DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-270-767-24969 (1-377)

QY 50 TyrArgSerPheLeuAspLys 56  
 DB 140 TATCGTTCCTTCCTCGACAAA 120

# RESULT 12

US-09-489-039A-1757  
 ; Sequence 1757, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 1757  
 ; LENGTH: 399  
 ; TYPE: DNA  
 ; ORGANISM: Klebsiella pneumoniae  
 ; US-09-489-039A-1757

## Alignment Scores:

Pred. No.: 135 Length: 399  
 Score: 7.00 Matches: 7  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 4.1% Indels: 0  
 DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-489-039A-1757 (1-399)

QY 140 GlyValTyrPhePheAlaGly 146  
 DB 3 GCGCTGTGGAAGTTCCCGCGC 23

# RESULT 13

US-09-513-999C-3332/C  
 ; Sequence 3332, Application US/09513999C

Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.Y.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513.999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 3332  
LENGTH: 463  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 230..463  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 150  
OTHER INFORMATION: b=c or g or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 450..  
OTHER INFORMATION: r=a or g  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 74  
OTHER INFORMATION: Xaa=asp or gly  
US-09-513-999C-3332

Alignment Scores:  
Pred. No.: 156 Length: 463  
Score: 7.00 Matches: 7  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.1% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-513-999C-3332 (1-463)

QY 69 MetValSerGlyVal 75  
DB 343 ATGGTGTCTCCAAACAAGTA 323

RESULT 14  
US-09-621-976-15423  
Sequence 15423, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621.976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 15423  
LENGTH: 479  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-621-976-15423

Alignment Scores:  
Pred. No.: 161 Length: 479  
Score: 7.00 Matches: 7  
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.1% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-621-976-15423 (1-479)

QY 36 AspArgLeuArgGlyValIle 42  
DB 252 GACCGCTCCGCAAGTCAATC 272

RESULT 15  
US-09-513-999C-1132/c  
Sequence 1132, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.Y.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513.999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 1132  
LENGTH: 488  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 331..486  
US-09-513-999C-1132

Alignment Scores:  
Pred. No.: 164 Length: 488  
Score: 7.00 Matches: 7  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.1% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-513-999C-1132 (1-488)

QY 94 LysValSerGluAspGluVal 100  
DB 401 AAGGTGCGAGAGATGAATT 381

Search completed: December 4, 2006, 18:39:27  
Job time : 221 secs

**This Page Blank (uspto)**

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## OM protein - nucleic search, using frame\_p2n model

Run on: December 4, 2006, 17:25:38 ; Search time 892 Seconds  
(without alignments)  
3554.047 Million cell updates/sec

Title: US-10-507-132-4

Perfect score: 172

Sequence: 1 MGSQVQKSDPITPFDYGLM.....MGFEFDPRIPEDEGRTFGDK 172

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 60.0 , Fgapext 7.0  
Delop 60.0 , Delext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word\_size: 1

Total number of hits satisfying chosen parameters: 37767826

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

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Published Applications NA.Main:\*  
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14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10J\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10K\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10L\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	8	4.7	512	3	US-09-918-995-32405	Sequence 32405, A
3	8	4.7	600	10	US-10-972-079-49239	Sequence 49239, A
4	8	4.7	1521	6	US-10-106-698-221	Sequence 221, App
5	8	4.7	1690	13	US-11-097-143-11207	Sequence 11207, A
6	8	4.7	1877	12	US-10-301-480-36243	Sequence 36243, A
7	8	4.7	1877	12	US-10-301-480-36244	Sequence 36244, A
8	8	4.7	1877	12	US-10-301-480-36245	Sequence 36245, A
9	8	4.7	1877	12	US-10-301-480-36246	Sequence 36246, A
10	8	4.7	1877	12	US-10-301-480-36247	Sequence 36247, A
11	8	4.7	1877	12	US-10-301-480-36248	Sequence 36248, A
12	8	4.7	1877	12	US-10-301-480-36249	Sequence 36249, A
13	8	4.7	1877	12	US-10-301-480-36250	Sequence 36250, A
14	8	4.7	1877	12	US-10-301-480-36251	Sequence 36251, A
15	8	4.7	1877	12	US-10-301-480-36252	Sequence 36252, A
16	8	4.7	1877	12	US-10-301-480-36253	Sequence 36253, A
17	8	4.7	1877	12	US-10-301-480-36254	Sequence 36254, A
18	8	4.7	1877	12	US-10-301-480-36255	Sequence 36255, A
19	8	4.7	1877	12	US-10-301-480-36256	Sequence 36256, A
20	8	4.7	1877	12	US-10-301-480-36257	Sequence 36257, A
21	8	4.7	1877	12	US-10-301-480-36258	Sequence 36258, A
22	8	4.7	1877	12	US-10-301-480-36259	Sequence 36259, A
23	8	4.7	1877	12	US-10-301-480-36260	Sequence 36260, A
24	8	4.7	1877	12	US-10-301-480-36261	Sequence 36261, A
25	8	4.7	1877	12	US-10-301-480-36262	Sequence 36262, A
26	8	4.7	1877	12	US-10-301-480-36263	Sequence 36263, A
27	8	4.7	1877	12	US-10-301-480-36264	Sequence 36264, A
28	8	4.7	1877	12	US-10-301-480-36265	Sequence 36265, A
29	8	4.7	1877	12	US-10-301-480-36266	Sequence 36266, A
30	8	4.7	1877	12	US-10-301-480-36267	Sequence 36267, A
31	8	4.7	1877	12	US-10-301-480-36268	Sequence 36268, A
32	8	4.7	1877	12	US-10-301-480-36269	Sequence 36269, A
33	8	4.7	1877	12	US-10-301-480-36270	Sequence 36270, A
34	8	4.7	1877	12	US-10-301-480-36271	Sequence 36271, A
35	8	4.7	1877	12	US-10-301-480-36272	Sequence 36272, A
36	8	4.7	1877	12	US-10-301-480-36273	Sequence 36273, A
37	8	4.7	1877	12	US-10-301-480-36274	Sequence 36274, A
38	8	4.7	1877	12	US-10-301-480-36275	Sequence 36275, A
39	8	4.7	1877	12	US-10-301-480-36276	Sequence 36276, A
40	8	4.7	1877	12	US-10-301-480-36277	Sequence 36277, A
41	8	4.7	1877	12	US-10-301-480-36278	Sequence 36278, A
42	8	4.7	1877	12	US-10-301-480-36279	Sequence 36279, A
43	8	4.7	1877	12	US-10-301-480-36280	Sequence 36280, A
44	8	4.7	1877	12	US-10-301-480-36281	Sequence 36281, A
45	8	4.7	1877	12	US-10-301-480-36282	Sequence 36282, A

## ALIGNMENTS

RESULT 1  
US-09-867-701-3030  
Sequence 3030, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Agiate, Paul A.  
APPLICANT: Jones, Robert  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.497  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 3030  
LENGTH: 405  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-867-701-3030

Alignment Scores:  
Pred. No.: 115  
Score: 8.00  
Percent Similarity: 100.0%

Length: 405  
Matches: 8  
Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-867-701-3030 (1-405)

Qy 70 ValSerSerlysglnValleugly 77  
Db 111 GTGAGCTCCAAACAGTTTAGGA 134

## RESULT 2

US-09-918-995-32405  
; Sequence 32405, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32405  
; LENGTH: 512  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(512)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-32405

## Alignment Scores:

Pred. No.:	142	Length:	512
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x US-09-918-995-32405 (1-512)

Qy 70 ValSerSerlysglnValleugly 77  
Db 440 GTGAGCTCCAAACAGTTTAGGA 463

## RESULT 3

US-10-972-079-49239/C  
; Sequence 49239, Application US/10972079  
; Publication No. US20050153317A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: ROSENFELD, David  
; APPLICANT: KERR, Richard  
; APPLICANT: BATES, Stephen  
; APPLICANT: HOLM, Tom  
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER  
; FILE REFERENCE: MM1110-2  
; CURRENT APPLICATION NUMBER: US/10/972,079  
; CURRENT FILING DATE: 2004-10-22  
; PRIOR APPLICATION NUMBER: US 60/514,333  
; PRIOR FILING DATE: 2003-10-24  
; NUMBER OF SEQ ID NOS: 96631  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 49239  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Chicken 1986894295080\_1

US-10-972-079-49239

## Alignment Scores:

Pred. No.:	164	Length:	600
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x US-10-972-079-49239 (1-600)

Qy 38 LeuArglyValIleAlaProthr 45  
Db 560 CTTAGAAAGTCATTCTCCACCA 537

## RESULT 4

US-10-106-698-221/C  
; Sequence 221, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 221  
; LENGTH: 1521  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-106-698-221

## Alignment Scores:

Pred. No.:	382	Length:	1521
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x US-10-106-698-221 (1-1521)

Qy 70 ValSerSerlysglnValleugly 77  
Db 1212 GTGAGCTCCAAACAGTTTAGGA 1189

## RESULT 5

US-11-097-143-11207  
; Sequence 11207, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CI000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11207.  
; LENGTH: 1690  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-11207

Alignment Scores:  
Pred. No.: 420 Length: 1690  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 13 Gaps: 0

US-10-507-132-4 (1-172) x US-11-097-143-11207 (1-1690)

QY 40 LeuArgIleAspTyrArgSerPhe 47  
DB 1040 AAAGTATAGCTCGACTGTGAGA 1063

RESULT 6  
US-10-301-480-36243  
; Sequence 36243, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36243  
; LENGTH: 1877  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-36243

Alignment Scores:  
Pred. No.: 462 Length: 1877  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 12 Gaps: 0

US-10-507-132-4 (1-172) x US-10-301-480-36243 (1-1877)

QY 46 LeuArgIleAspTyrArgSerPhe 53  
DB 542 CTTAGATTGATTACAGATCTTTC 565

RESULT 7  
US-10-301-480-36244  
; Sequence 36244, Application US/10301480  
; Publication No. US20060057564A1

; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36244  
; LENGTH: 1877  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-36244

Alignment Scores:  
Pred. No.: 462 Length: 1877  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 12 Gaps: 0

US-10-507-132-4 (1-172) x US-10-301-480-36244 (1-1877)

QY 46 LeuArgIleAspTyrArgSerPhe 53  
DB 542 CTTAGATTGATTACAGATCTTTC 565

RESULT 8  
US-10-301-480-649652  
; Sequence 649652, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 649652  
; LENGTH: 1877  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-649652

Alignment Scores:  
Pred. No.: 462 Length: 1877  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 12 Gaps: 0

US-10-507-132-4 (1-172) x US-10-301-480-649652 (1-1877)

QY 46 LeuArgIleAspTyrArgSerPhe 53  
DB 542 CTTAGATTGATTACAGATCTTTC 565

RESULT 9  
US-10-301-480-649653  
; Sequence 649653, Application US/10301480

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; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 649653
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-649653
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Pred. No.: 462      Length: 1877
Score: 8.00      Matches: 8
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 4.7%      Indels: 0
DB: 12      Gaps: 0
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US-10-507-132-4 (1-172) x US-10-301-480-649653 (1-1877)

Qy 46 LeuAigIleAsPTyRrGserphe 53

Db 542 CTTAGATTGATTACAGATCTTTC 565

RESULT 10

; Sequence 722, Application US/10094749

; Publication No. US20030219741A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUTKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO

; APPLICANT: SEKI, NAHICO

; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTOKUJI

; APPLICANT: NAGAHARI, KENJI

; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

; FILE REFERENCE: 084335/0160

; CURRENT APPLICATION NUMBER: US/10/094,749

; PRIOR FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 60/350,435

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: JP 2001-328381

; PRIOR FILING DATE: 2001-09-14

; NUMBER OF SEQ ID NOS: 3381

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 722

; LENGTH: 2002

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-094-749-722

Alignment Scores:

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Pred. No.: 490      Length: 2002
Score: 8.00      Matches: 8
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match: 4.7%      Indels: 0
DB: 7      Gaps: 0
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US-10-507-132-4 (1-172) x US-10-094-749-722 (1-2002)

Qy 70 ValSerSerTyGGINvalleugly 77

Db 802 GTGAGCTCCAAACAGTTTAGGA 825

RESULT 11

; US-11-097-143-11206/C

; Sequence 11206, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; FILE REFERENCE: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; CURRENT APPLICATION NUMBER: US/11/097,143

; PRIOR FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11206

; LENGTH: 4182

; TYPE: DNA

; ORGANISM: DROSOPHILA

; US-11-097-143-11206

; GENERAL INFORMATION:

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; FILE REFERENCE: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; CURRENT APPLICATION NUMBER: US/11/097,143

; PRIOR FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: 60/350,435

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: JP 2001-328381

; PRIOR FILING DATE: 2001-09-14

; NUMBER OF SEQ ID NOS: 3381

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 722

; LENGTH: 2002

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-094-749-722



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; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1579
; LENGTH: 12822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1579

Alignment Scores:
Pred. No.: 2.55e+03 Length: 12822
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-764-847-1579 (1-12822)

QY 70 ValSerSerLySGInValleuGly 77
Db 11559 GTAGCTCCAAACAAGTTTAGGA 11582

RESULT 13
US-10-092-154-1579
; Sequence 1579, Application US/10092154
; Publication No. US2003054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1579
; LENGTH: 12822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1579

Alignment Scores:
Pred. No.: 2.55e+03 Length: 12822
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: 6 Gaps: 0

US-10-507-132-4 (1-172) x US-10-092-154-1579 (1-12822)

QY 70 ValSerSerLySGInValleuGly 77
Db 11559 GTAGCTCCAAACAAGTTTAGGA 11582

RESULT 14
US-10-027-632-53712/c
; Sequence 53712, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
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; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53712
; LENGTH: 715517
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(715517)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-53712

Alignment Scores:
Pred. No.: 1.03e+05 Length: 715517
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: 6 Gaps: 0

US-10-507-132-4 (1-172) x US-10-027-632-53712 (1-715517)

QY 37 ArgLeuArgLyValIleAlaPro 44
Db 315054 AGACTCAGAAAGTATAGCACTT 315031

RESULT 15
US-10-027-632-53712/c
; Sequence 53712, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53712
; LENGTH: 715517
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(715517)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-53712
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## Alignment Scores:

Pred. No.:	1.03e+05	Length:	715517
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	7	Gaps:	0

US-10-507-132-4 (1-172) x US-10-027-632-53712 (1-715517)

QY 37 ArgLeuArgIysValIleAlaPro 44

Db 315054 AGACTCAGAAAGTGATGACACCT 315031

Search completed: December 4, 2006, 17:43:24  
Job time : 1056 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 4, 2006, 17:43:39 ; Search time 170 Seconds  
(without alignments)  
3112.203 Million cell updates/sec

Title: US-10-507-132-4

Perfect score: 172

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Word size: 1

Total number of hits satisfying chosen parameters: 5860957

Minimum DB seq length: 0

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-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=ab8806h  
-USER=US10507132 -CCGN 1 1 215 -@runat\_04122006\_143543\_9822 -NCPU=6 -ICPU=3  
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-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

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Published Applications NA New:  
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3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	172	100.0	516	6	US-10-507-132-3
2	172	100.0	600	6	US-10-507-132-13
3	172	100.0	610	6	US-10-507-132-16
4	169	98.3	538	6	US-10-507-132-15
5	169	98.3	545	6	US-10-507-132-14
6	125	72.7	729	6	US-10-507-132-18

7	125	72.7	732	6	US-10-507-132-17	Sequence 17, Appl
8	97	56.4	516	6	US-10-507-132-1	Sequence 1, Appl
9	8	4.7	497	6	US-11-266-748A-184560	Sequence 184560, A
10	8	4.7	926	8	US-11-266-748A-71004	Sequence 71004, A
11	8	4.7	926	8	US-11-266-748A-123815	Sequence 123815, A
12	8	4.7	1586	9	US-11-218-305-4533	Sequence 4533, Ap
13	8	4.7	4332	9	US-11-266-748A-32509	Sequence 32509, A
14	8	4.7	4332	9	US-11-218-305-16760	Sequence 16760, A
15	7	4.1	21	6	US-10-507-132-8	Sequence 8, Appl
16	7	4.1	23	6	US-10-507-132-9	Sequence 9, Appl
17	7	4.1	27	6	US-10-507-132-12	Sequence 12, Appl
18	7	4.1	201	6	US-10-284-444-4992	Sequence 4992, Ap
19	7	4.1	201	6	US-10-284-444-4993	Sequence 4993, Ap
20	7	4.1	201	6	US-10-284-444-11652	Sequence 11652, A
21	7	4.1	201	6	US-10-284-444-11653	Sequence 11653, A
22	7	4.1	201	6	US-10-284-444-11654	Sequence 11654, A
23	7	4.1	201	6	US-10-284-444-11655	Sequence 11655, A
24	7	4.1	235	8	US-11-266-748A-169345	Sequence 169345, A
25	7	4.1	372	8	US-11-266-748A-377254	Sequence 377254, A
26	7	4.1	372	8	US-11-266-748A-460633	Sequence 460633, A
27	7	4.1	393	10	US-11-314-834-2587	Sequence 2587, Ap
28	7	4.1	420	8	US-11-266-748A-303484	Sequence 303484, Ap
29	7	4.1	441	6	US-10-513-369-1608	Sequence 1608, Ap
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31	7	4.1	450	8	US-11-266-748A-147540	Sequence 147540, A
32	7	4.1	466	8	US-11-266-748A-303304	Sequence 303304, A
33	7	4.1	550	10	US-11-292-078-13846	Sequence 13846, A
34	7	4.1	629	8	US-11-266-748A-53897	Sequence 53897, A
35	7	4.1	629	8	US-11-266-748A-235129	Sequence 235129, A
36	7	4.1	629	8	US-11-266-748A-235129	Sequence 235129, A
37	7	4.1	638	8	US-11-266-748A-412196	Sequence 412196, A
38	7	4.1	650	10	US-11-292-078-112	Sequence 112, App
39	7	4.1	650	10	US-11-292-078-118	Sequence 118, App
40	7	4.1	710	8	US-11-266-748A-253499	Sequence 253499, A
41	7	4.1	710	8	US-11-266-748A-314016	Sequence 314016, A
42	7	4.1	762	8	US-11-217-529-2570	Sequence 2570, Ap
43	7	4.1	764	8	US-11-266-748A-273078	Sequence 273078, A
44	7	4.1	764	8	US-11-266-748A-333595	Sequence 333595, A
45	7	4.1	777	8	US-11-179-064B-75	Sequence 75, Appl

#### ALIGNMENTS

RESULT 1  
US-10-507-132-3  
; Sequence 3, Application US/10507132  
; Publication No. US20060223136A1  
; GENERAL INFORMATION:  
; APPLICANT: Koichiro KAKU et al.  
; TITLE OF INVENTION: GENE CODING FOR SCYLLATONE DEHYDRATASE EXHIBITING RESISTANCE TO  
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT  
; FILE REFERENCE: 1254-0258PUS1  
; CURRENT APPLICATION NUMBER: US/10/507,132  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: JP 2002-66955  
; PRIOR FILING DATE: 2002-03-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 516  
; TYPE: DNA  
; ORGANISM: Pyricularia oryzae  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(516)  
; US-10-507-132-3

Alignment Scores:  
Pred. No.: 5,56e-180  
Score: 172.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 100.0%  
Length: 516  
Matches: 172  
Conservative: 0  
Mismatch: 0  
Indels: 0

DB: 6 Gaps: 0

US-10-507-132-4 (1-172) x US-10-507-132-3 (1-516)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20

DB 1 ATGGGTTCCCAAGTTCAAAAGACGATGATTAACCTTCTCAGACTACCTGGGCTCATAG 60

QY 21 ThrCysValTyrGlnUtrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40

DB 61 ACTTGCGTCTATGAGTGGCCAGACACTACAGACTCCAAAGACTGGGATAGGCTGCCAAAG 120

QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

DB 121 GTCATGGCCCTACTCTGGGCACTGACCTACCTCTCTCGACAAAGCTTGGGAGGCA 180

QY 61 MetProAlaGlnGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80

DB 181 ATGCCCGCCGAGAGTTCCTCGGCACTGCTCGAGCAAGAGTGTGGGCGCACCCACCC 240

QY 81 LeuArgTrpGlnHisPheIleGlyGlyThrArgTrpGlnLysValSerGlnAspGluVal 100

DB 241 CTCGCAAGCAGAGACTTCATCGGCGCAGCGCTGGAGAGAGTGTCCAGAGCAGAGTTC 300

QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120

DB 301 ATGGCTTACCAACAGCTGGCGCTGCCGACCAAGAGTACAAAGGACCAACCATGAAGAG 360

QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140

DB 361 GTCACCATGAAAGGCGCAGCCCACTCGGCMAACCTTCACCTGATCAAGAAAGATCGAGCG 420

QY 141 ValThrLysPheAlaGlyLeuLysProAspIleArgTrpGlyGlnPheAspPheAspArg 160

DB 421 GTCGGAAGTTCGCCGCTCAAGCCGATATCCGCTGGGCGAGTTCCGCTTGACAGG 480

QY 161 IlePheGlnAspGlyArgGlnThrPheGlyAspLys 172

DB 481 ATCTTTGAGGACGGAAGGAGACCTTTGGCGACAA 516

RESULT 2

US-10-507-132-13

Sequence 13, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:

APPLICANT: Koichiro KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO

FILE REFERENCE: 1254-0258PUS1

CURRENT APPLICATION NUMBER: US/10/507,132

CURRENT FILING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: JP 2002-66955

PRIOR FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

LENGTH: 600

TYPE: DNA

ORGANISM: Pyricularia oryzae

US-10-507-132-13

Alignment Scores:

Pred. No.: 6,4e-180 Length: 600

Score: 172.00 Matches: 172

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

Gaps: 0

US-10-507-132-4 (1-172) x US-10-507-132-13 (1-600)

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DB 81 ATGGGTTCCCAAGTTCAAAAGACGATGATTAACCTTCTCAGACTACCTGGGCTCATAG 140

QY 21 ThrCysValTyrGlnUtrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40

DB 141 ACTTGCGTCTATGAGTGGCCAGACACTACAGACTCCAAAGACTGGGATAGGCTGCCAAAG 200

QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

DB 201 GTCATGGCCCTACTCTGGGCACTGACCTACCTCTCTCGACAAAGCTTGGGAGGCA 260

QY 61 MetProAlaGlnGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80

DB 261 ATGCCCGCCGAGAGTTCCTCGGCACTGCTCGAGCAAGAGTGTGGGCGCACCCACCC 320

QY 81 LeuArgTrpGlnHisPheIleGlyGlyThrArgTrpGlnLysValSerGlnAspGluVal 100

DB 321 CTCGCAAGCAGAGACTTCATCGGCGCAGCGCTGGAGAGAGTTCGAGAGCAGAGTTC 380

QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120

DB 381 ATGGCTTACCAACAGCTGGCGCTGCCGACCAAGAGTACAAAGGACCAACCATGAAGAG 440

QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140

DB 441 GTCACCATGAAAGGCGCAGCCCACTCGGCMAACCTTCACCTGATCAAGAAAGATCGAGCG 500

QY 141 ValThrLysPheAlaGlyLeuLysProAspIleArgTrpGlyGlnPheAspPheAspArg 160

DB 501 GTCGGAAGTTCGCCGCTCAAGCCGATATCCGCTGGGCGAGTTCCGCTTGACAGG 560

QY 161 IlePheGlnAspGlyArgGlnThrPheGlyAspLys 172

DB 561 ATCTTTGAGGACGGAAGGAGACCTTTGGCGACAA 596

RESULT 3

US-10-507-132-16

Sequence 16, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:

APPLICANT: Koichiro KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO

FILE REFERENCE: 1254-0258PUS1

CURRENT APPLICATION NUMBER: US/10/507,132

CURRENT FILING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: JP 2002-66955

PRIOR FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 16

LENGTH: 610

TYPE: DNA

ORGANISM: Pyricularia oryzae

US-10-507-132-16

Alignment Scores:

Pred. No.: 6,5e-180 Length: 610

Score: 172.00 Matches: 172

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

Gaps: 0

US-10-507-132-4 (1-172) x US-10-507-132-16 (1-610)

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QY 21 ThrCysValTyrGlnUtrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40

DB 141 ACTTGCGTCTATGAGTGGCCAGACACTACAGACTCCAAAGACTGGGATAGGCTGCCAAAG 200

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Db 201 GTGATTCGCGCTACTGCGCATTTGACTACCGCTCTTCCGCAAGCTCTGGAGGCA 260  
QY 61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80  
Db 261 ATGCGGCGCCAGAGATTCGTGCGGATGCTCTCGAGCAAGGAGTGTGGGCGAGCCACC 320  
QY 81 LeuArgThrGlnHisPheIleGlyLysThrArgTrpGluLysValSerGluAspGluVal 100  
Db 321 CTCGCGACGAGCACTTCATCGGCGGACCGGCTGGAGAGAGTGTCTCGAGAGAGAGTTC 380  
QY 101 IleGlyTrpHisGlnLeuArgValProHisGlnArgTyArgSerPheLeuMetLysGln 120  
Db 381 ATGCGGTACCAACGAGTGTGCGGCTCCGCAACAGAGTACAGACACCATGAGAGAG 440  
QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyArgLysValLeuAspGly 140  
Db 441 GTACACCATGAAAGGCGCACCGCCACTCGGCAAACTTCACTGTACAAAGAAATCGACGGC 500  
QY 141 ValTrpLysPheAlaGluLeuLysProAspIleArgTrpGluLysPheAspPheAspArg 160  
Db 501 GTCTGAGAGTTCGCCGCGCTCAAGCCGCAATTCGCGTGGGCGAGTTGACTTTGACAGG 560  
QY 161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172  
Db 561 ATCTTGAGGACGAGCGGAGACCTTTGGCGACAAA 596

## RESULT 4

US-10-507-132-15  
; Sequence 15, Application US/10507132  
; Publication No. US2006022136A1  
; GENERAL INFORMATION:  
; APPLICANT: Koichiro KAKU et al.  
; TITLE OF INVENTION: GENE CODING FOR SCYTHALONE DEHYDRATASE EXHIBITTING RESISTANCE TO  
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT  
; FILE REFERENCE: 1254-0258PUS1  
; CURRENT APPLICATION NUMBER: US/10/507,132  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: JP 2002-66955  
; PRIOR FILING DATE: 2002-03-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 538  
; TYPE: DNA  
; ORGANISM: Pyricularia oryzae  
US-10-507-132-15

## Alignment Scores:

Pred. No.:	1,17e-176	Length:	538
Score:	169.00	Matches:	169
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	98.3%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x US-10-507-132-15 (1-538)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyArgLysLeuMet 20  
Db 31 ATGGGTTCCGAAAGTTCAAAGAGCGATGATTAACCTTCTCAGACTACGCGGCTCATG 90  
QY 21 ThrCysValTyArgLysPheValSerSerTyArgSerLysAspTrpAspArgLeuArgLys 40  
Db 91 ACTTGCTCTATAGTGGGAGACAGCTACGACTCCAGAGCTGGAGTAAAGCTCGCAAG 150  
QY 41 Val11leAlaProThrLeuArg11eAspTyArgSerPheLeuAspLysLeuTrpGluAla 60  
Db 151 GTGATTCGCGCTACTGCGCATTTGACTACCGCTCTTCCGCAAGCTCTGGAGGCA 210  
QY 61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80

Db 211 ATGCGGCGCCAGAGATTCGTGCGCATGCTCTCGAGCAAGCAGGTGTGGCGAGCCACC 270  
QY 81 LeuArgThrGlnHisPheIleGlyLysThrArgTrpGluLysValSerGluAspGluVal 100  
Db 271 CTCGCGACGAGCACTTCATCGGCGGACCGGCTGGAGAGAGGTTGTCTCGAGAGAGTTC 330  
QY 101 IleGlyTrpHisGlnLeuArgValProHisGlnArgTyArgSerPheLeuMetLysGln 120  
Db 331 ATGCGGTACCAACGAGTGTGCGGCTCCGCAACAGAGTACAAAGACACCATGAGAGAG 390  
QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyArgLysValLeuAspGly 140  
Db 391 GTACACCATGAAAGGCGCACCGCCACTCGGCAAACTTCACTGTACAAAGAAATCGACGGC 450  
QY 141 ValTrpLysPheAlaGluLeuLysProAspIleArgTrpGluLysPheAspPheAspArg 160  
Db 451 GTCTGAGAGTTCGCCGCGCTCAAGCCGCAATTCGCGTGGGCGAGTTGACTTTGACAGG 510  
QY 161 IlePheGluAspGlyArgGluThrPhe 169  
Db 511 ATCTTGAGGACGAGCGGAGACCTTT 537

## RESULT 5

US-10-507-132-14  
; Sequence 14, Application US/10507132  
; Publication No. US2006022136A1  
; GENERAL INFORMATION:  
; APPLICANT: Koichiro KAKU et al.  
; TITLE OF INVENTION: GENE CODING FOR SCYTHALONE DEHYDRATASE EXHIBITTING RESISTANCE TO  
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT  
; FILE REFERENCE: 1254-0258PUS1  
; CURRENT APPLICATION NUMBER: US/10/507,132  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: JP 2002-66955  
; PRIOR FILING DATE: 2002-03-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 545  
; TYPE: DNA  
; ORGANISM: Pyricularia oryzae  
US-10-507-132-14

## Alignment Scores:

Pred. No.:	1,18e-176	Length:	545
Score:	169.00	Matches:	169
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	98.3%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x US-10-507-132-14 (1-545)

QY 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyArgLysLeuMet 20  
Db 38 ATGGGTTCCGAAAGTTCAAAGAGCGATGATTAACCTTCTCAGACTACGCGGCTCATG 97  
QY 21 ThrCysValTyArgLysPheValSerSerTyArgSerLysAspTrpAspArgLeuArgLys 40  
Db 98 ACTTGCTCTATAGTGGGAGACAGCTACGACTCCAGAGCTGGAGTAAAGCTCGCAAG 157  
QY 41 Val11leAlaProThrLeuArg11eAspTyArgSerPheLeuAspLysLeuTrpGluAla 60  
Db 158 GTGATTCGCGCTACTGCGCATTTGACTACCGCTCTTCCGCAAGCTCTGGAGGCA 217  
QY 61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80  
Db 218 ATGCGGCGCAGAGATTCGTGCGCATGCTCTGAGCAAGCAGGTGTGGGCGAGCCACC 277  
QY 81 LeuArgThrGlnHisPheIleGlyLysThrArgTrpGluLysValSerGluAspGluVal 100  
Db 278 CTCGCGACGAGCACTTCATCGGCGGACCGCTGGAGAGAGGTGTCTCGAGAGAGGTC 337

```
Oy 101 IleglytrrhiglnleuargValProhiglnargTyrlyAspThrThmetlysglu 120
Db 338 ATGGCTACACAGCTGCGCTCCGACCAAGATACAGACCAACCATGAAAGAG 397
Oy 121 ValThmetlysglyVhishAlahisSerAlaasleuHietrTyrlylyslleaapgly 140
Db 398 GTCAACATGAAAGGCGACGCCCATCGGCAACCTTCACTGATCAAGAAAGATCCAGCGC 457
Oy 141 ValTrrpyspheaAlglyleuLyProaspIleatgTrrpGlygluPheaspheaparg 160
Db 458 GCTCGAAGTTGCGCGCTCAAGCCCGACATCCGCTGGGCGAGTTGCACTTTGACAGG 517
Oy 161 IlephegluaspglyVargglunthrphe 169
Db 518 ATCTTTGAGACGACGAGGAGACCTTT 544

RESULT 6
US-10-507-132-18
; Sequence 18, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
US-10-507-132-18

Alignment Scores:
Pred. No.: 4 61e-128 Length: 729
Score: 125.00 Matches: 125
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 72.7% Indels: 0
Gaps: 0

US-10-507-132-4 (1-172) x US-10-507-132-18 (1-729)
Oy 48 IleaSPTrArgSerPheleuAspLyLeuTrrpGluAlaMetProAlaglunPheVal 67
Db 355 ATGACTACCGCTCTTCTCGACAAGCTCTGGAGGCAATGCCGCGAGGAGTTCTGC 414
Oy 68 GlymetValserSerlysglnValleuGlYAspProthrlleuargThrhniisphelle 87
Db 415 GGGATGCTCTCGAGCAAGAGGCTGGGGGACCCACCTCGCAGCGACGACCTTCATC 474
Oy 88 GlYglYThrArgTrrpGlygluYValserGluAspGluValIleglyTrrhiglnleuarg 107
Db 475 GGGGCGACGGCTCGGAGAGAGTCTCCGAGGACGAGTCTATCCGCTACCAACGCTCGC 534
Oy 108 ValProhiglnargTrrlyAspThrThmetlysgluValThrmetlysglyVhishAla 127
Db 535 GTCGCCGACAGAGTACAGACACCAACATGAAAGGATGACCATGAAAGGCGCCAGCC 594
Oy 128 HisSerAlaasleuHietrTrrlylyslleaapglyValTrrpyspheaAlaglYleu 147
Db 595 CACTCGCAAACTTCACTGATCAAGAAAGATGACGCGCTCGAAGTTGCGCGGCTTC 654
Oy 148 LyPProaspIleatgTrrpGlygluPheaspPheapargIlephegluaspglyVarglu 167
Db 655 AAGCCGCAKATCCGCTCGGCGAGTTGCACTTTGACAGATCTTTGAGAGCGGAGCGGAG 714
Oy 168 ThrPheglYAspLy 172
Db 718 ACCTTTGGCGACAAA 732
```

```
Db 715 ACCTTTGGCGACAAA 729

RESULT 7
US-10-507-132-17
; Sequence 17, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
US-10-507-132-17

Alignment Scores:
Pred. No.: 4 63e-128 Length: 732
Score: 125.00 Matches: 125
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 72.7% Indels: 0
Gaps: 0

US-10-507-132-4 (1-172) x US-10-507-132-17 (1-732)
Oy 48 IleaSPTrArgSerPheleuAspLyLeuTrrpGluAlaMetProAlaglunPheVal 67
Db 358 ATGACTACCGCTCTTCTCGACAAGCTCTGGAGGCAATGCCGCGAGGAGTTCTGC 417
Oy 68 GlymetValserSerlysglnValleuGlYAspProthrlleuargThrhniisphelle 87
Db 418 GGCATGCTCTCGAGCAAGAGTGTGGGCGACCCACCTCGCAGCGACGACCTTCATC 477
Oy 88 GlYglYThrArgTrrpGlygluYValserGluAspGluValIleglyTrrhiglnleuarg 107
Db 478 GGGGCGACGGCTCGGAGAGAGTCTCCGAGGACGAGTCTATCCGCTACCAACGCTCGC 537
Oy 108 ValProhiglnargTrrlyAspThrThmetlysgluValThrmetlysglyVhishAla 127
Db 538 GTCGCCGACAGAGTACAGACACCAACATGAAAGGATGACCATGAAAGGCGCCAGCC 597
Oy 128 HisSerAlaasleuHietrTrrlylyslleaapglyValTrrpyspheaAlaglYleu 147
Db 598 CACTCGCAAACTTCACTGATCAAGAAAGATGACGCGCTCGAAGTTGCGCGGCTTC 657
Oy 148 LyPProaspIleatgTrrpGlygluPheaspPheapargIlephegluaspglyVarglu 167
Db 658 AAGCCGCAKATCCGCTCGGCGAGTTGCACTTTGACAGATCTTTGAGAGCGGAGCGGAG 717
Oy 168 ThrPheglYAspLy 172
Db 718 ACCTTTGGCGACAAA 732

RESULT 8
US-10-507-132-1
; Sequence 1, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
```

;; PRIOR FILING DATE: 2002-03-12  
;; NUMBER OF SEQ ID NOS: 19  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 1  
;; LENGTH: 516  
;; TYPE: DNA  
;; ORGANISM: Pyricularia oryzae  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)..(516)  
US-10-507-132-1  
  
Alignment Scores:  
Pred. No.: 2,35e-97 Length: 516  
Score: 97.00 Matches: 97  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 56.4% Indels: 0  
DB: 6 Gaps: 0  
  
US-10-507-132-4 (1-172) x US-10-507-132-1 (1-516)  
  
QY 76 LeuGlyAspProThrIleuArgThrGlnHisPheIleGlyGlyThrArgTyrGlyVal 95  
DB 226 CTGGGGGACCCGACCTCCCGACGACGACCTTCATCGCGCGACGCGTGGAGAGGTG 285  
QY 96 SerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrGlyAsp 115  
DB 286 TCCGAGGACAGGTGTCATCGCTACCCACGACGCTGGCGCTCCCGACGAGAGTACAGGAC 345  
QY 116 ThrThrMetIleGlyValThrMetIleGlyHisAlaHisSerAlaSerLeuHisTyr 135  
DB 346 ACCACCATGAGAGGTGTCATGAGAGGCGCACGCCCACTCGGCAAACTTCACCTGGTAC 405  
QY 136 LysIleValLeuAspGlyValTyrPheAlaGlyLeuLysProAspIleArgTyrGlyGlu 155  
DB 406 AAGAAATTCACGCGCTGGAAGTTCGCGGCTCAAGCCGATATCCCGTGGGCGAG 465  
QY 156 PheAspPheAspArgIlePheGluAspGlyArgGluThrPheGlyAspLys 172  
DB 466 TTGCACTTTGACAGATCTTTGAGAGCGAGCGGAGACTTTGGCGACAAA 516  
  
RESULT 9  
US-11-266-748A-184560  
;; Sequence 184560, Application US/11266748A  
;; Publication No. US20060134663A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Harkin, Paul  
;; APPLICANT: Johnston, Patrick  
;; APPLICANT: Mulligan, Karl  
;; TITLE OF INVENTION: Transcriptome Microarray Technology and  
;; TITLE OF INVENTION: Methods of Using the Same  
;; FILE REFERENCE: 55815-0102 (319189)  
;; CURRENT APPLICATION NUMBER: US/11/266, 748A  
;; PRIOR FILING DATE: 2005-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105479.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105482.6  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105483.4  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105507.0  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105485.9  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105484.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: US 60/662,276  
;; PRIOR FILING DATE: 2005-03-14  
;; PRIOR APPLICATION NUMBER: US 60/700,293  
;; PRIOR FILING DATE: 2005-07-18  
;; NUMBER OF SEQ ID NOS: 483996  
;; SOFTWARE: Patentin version 3.3

;; SEQ ID NO 184560  
;; LENGTH: 497  
;; TYPE: DNA  
;; ORGANISM: Homo Sapiens  
US-11-266-748A-184560  
  
Alignment Scores:  
Pred. No.: 25.4 Length: 497  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-507-132-4 (1-172) x US-11-266-748A-184560 (1-497)  
  
QY 70 ValSerSerIleGlnValLeuGly 77  
DB 308 GTGAGCTCCCAACAACTTTAGGG 331  
  
RESULT 10  
US-11-266-748A-71004  
;; Sequence 71004, Application US/11266748A  
;; Publication No. US20060134663A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Harkin, Paul  
;; APPLICANT: Johnston, Patrick  
;; APPLICANT: Mulligan, Karl  
;; TITLE OF INVENTION: Transcriptome Microarray Technology and  
;; TITLE OF INVENTION: Methods of Using the Same  
;; FILE REFERENCE: 55815-0102 (319189)  
;; CURRENT APPLICATION NUMBER: US/11/266, 748A  
;; PRIOR FILING DATE: 2005-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105479.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105482.6  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105483.4  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105507.0  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105485.9  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: EP 04105484.2  
;; PRIOR FILING DATE: 2004-11-03  
;; PRIOR APPLICATION NUMBER: US 60/662,276  
;; PRIOR FILING DATE: 2005-03-14  
;; PRIOR APPLICATION NUMBER: US 60/700,293  
;; PRIOR FILING DATE: 2005-07-18  
;; NUMBER OF SEQ ID NOS: 483996  
;; SOFTWARE: Patentin version 3.3  
;; SEQ ID NO 71004  
;; LENGTH: 926  
;; TYPE: DNA  
;; ORGANISM: Homo Sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (144)..(446)  
;; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-71004  
  
Alignment Scores:  
Pred. No.: 45.4 Length: 926  
Score: 8.00 Matches: 8  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 4.7% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-507-132-4 (1-172) x US-11-266-748A-71004 (1-926)  
  
QY 70 ValSerSerIleGlnValLeuGly 77  
DB 308 GTGAGCTCCCAACAACTTTAGGG 331

DB 752 GTGAGCTCCAAACAGTTTAGGA 775

RESULT 11

US-11-266-748A-123815/C

Sequence 123815, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcription Microarray Technology and

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

PRIOR FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PatentIn version 3.3

SEQ ID NO 123815

LENGTH: 926

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (481)-(783)

OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-123815

Alignment Scores:

Pred. No.:	45.4	Length:	926
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	8	Gaps:	0

US-10-507-132-4 (1-172) x US-11-266-748A-123815 (1-926)

QY 70 ValSerSerLygInValleugly 77

DB 175 GTGAGCTCCAAACAGTTTAGGA 152

RESULT 12

US-11-218-305-4533/C

Sequence 4533, Application US/11218305

Publication No. US2006014195A1

GENERAL INFORMATION:

APPLICANT: MONSANTO TECHNOLOGY, LLC

APPLICANT: McIaird, Paul L.

APPLICANT: Tao, Nengsheng

APPLICANT: Wu, Kunsheng

TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping

FILE REFERENCE: 38-21 (53660)B

CURRENT APPLICATION NUMBER: US/11/218,305

PRIOR FILING DATE: 2005-09-01

PRIOR APPLICATION NUMBER: US 60/606,880

PRIOR FILING DATE: 2004-09-01

NUMBER OF SEQ ID NOS: 25043

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4533

LENGTH: 1586

TYPE: DNA

ORGANISM: Zea mays

US-11-218-305-4533

Alignment Scores:

Pred. No.:	75.1	Length:	1586
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	9	Gaps:	0

US-10-507-132-4 (1-172) x US-11-218-305-4533 (1-1586)

QY 69 MetValSerSerLygInValleu 76

DB 1217 ATGTGAGCTCCAAACAGTTTCTG 1194

RESULT 13

US-11-266-748A-32509

Sequence 32509, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcription Microarray Technology and

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

PRIOR FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PatentIn version 3.3

SEQ ID NO 32509

LENGTH: 3304

TYPE: DNA

ORGANISM: Homo Sapiens

US-11-266-748A-32509

Alignment Scores:

Pred. No.:	149	Length:	3304
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	8	Gaps:	0

US-10-507-132-4 (1-172) x US-11-266-748A-32509 (1-3304)

QY 70 ValSerSerLygInValleugly 77

DB 812 GTGAGCTCCAAACAGTTTAGGA 835



## RESULT 14

US-11-218-305-16760  
 ; Sequence 16760, Application US/11218305  
 ; Publication No. US20060141495A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MONSANTO TECHNOLOGY, LLC  
 ; APPLICANT: McIaird, Paul L.  
 ; APPLICANT: Tao, Nengbing  
 ; APPLICANT: Wu, Kunsheng  
 ; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
 ; FILE REFERENCE: 38-21 (53660)B  
 ; CURRENT APPLICATION NUMBER: US/11/218,305  
 ; CURRENT FILING DATE: 2005-09-01  
 ; PRIOR APPLICATION NUMBER: US 60/606,880  
 ; PRIOR FILING DATE: 2004-09-01  
 ; NUMBER OF SEQ ID NOS: 25043  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 16760  
 ; LENGTH: 4322  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 US-11-218-305-16760

## Alignment Scores:

Pred. No.:	192	Length:	4322
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	9	Gaps:	0

US-10-507-132-4 (1-172) x US-11-218-305-16760 (1-4322)

OY 94 LysValSerGluAspGluValIle 101

DB 70 AAGGTTCTCGAAGATGAAATCATT 93

## RESULT 15

US-10-507-132-8  
 ; Sequence 8, Application US/10507132  
 ; Publication No. US20060223136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koichiro KAKU et al.  
 ; TITLE OF INVENTION: GENE CODING FOR SCYTLONE DEHYDRATASE EXHIBITING RESISTANCE TO  
 ; FILE REFERENCE: 1254-0258PUS1  
 ; CURRENT APPLICATION NUMBER: US/10/507,132  
 ; CURRENT FILING DATE: 2004-09-10  
 ; PRIOR APPLICATION NUMBER: JP 2002-66955  
 ; PRIOR FILING DATE: 2002-03-12  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 8  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized primer  
 US-10-507-132-8

## Alignment Scores:

Pred. No.:	16.6	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x US-10-507-132-8 (1-21)

OY 1 MetGlySerGlnValGlnLys 7

|||||

DB 1 AAGGTTCCGAAGTTCAAAG 21

Search completed: December 4, 2006, 17:46:42  
 Job time: 173 secs

**This Page Blank (uspto)**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 4, 2006, 17:18:36 ; Search time 4365 Seconds  
(without alignments)  
3305.198 Million cell updates/sec

Title: US-10-507-132-4

Perfect score: 172

Sequence: 1 MGSQVQKSPDEITPFDYGLM.....MGEFDFDRIFFEDGRTFGDK 172

Scoring table:

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Xgapop 60.0 , Xgapext 60.0	
Ygapop 60.0 , Ygapext 60.0	
Fgapext 7.0	
Delop 60.0 , Delect 60.0	

Searched: 48236798 segs, 27959665780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96471816

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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-UNITS-bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs607  
-USER=US10507132 @CGN 1.1 6323 @runat\_04122006\_143511\_9655 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=60 -Fgapext=7  
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

EST.\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_est7:\*  
7: gb\_est8:\*  
8: gb\_est9:\*  
9: gb\_est10:\*  
10: gb\_est11:\*  
11: gb\_est12:\*  
12: gb\_est13:\*  
13: gb\_est14:\*  
14: gb\_est15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	619	3	BM863356 mgcm006x0
2	171	99.4	657	3	BM864194 mgcm008x0
3	168	97.7	664	3	BM863315 mgcm006x0
4	141	82.0	599	3	BM864156 mgcm008x0

5	132	76.7	510	3	BM863374	BM863374 mgcm006x0
6	132	76.7	530	3	BM863357	BM863357 mgcm006x0
7	132	76.7	643	3	BM864467	BM864467 mgcm010x0
8	129	75.0	571	3	BM863370	BM863370 mgcm007x0
9	125	72.7	486	3	BM863639	BM863639 mgcm007x0
10	115	66.9	473	3	BM864018	BM864018 mgcm008x0
11	106	61.6	600	3	BM864472	BM864472 mgcm010x0
12	104	60.5	504	3	BM863499	BM863499 mgcm006x0
13	102	59.3	366	3	BM864053	BM864053 mgcm008x0
14	101	58.7	649	3	BM863340	BM863340 mgcm006x0
15	96	55.8	398	3	BM861952	BM861952 mgcm001x0
16	96	55.8	781	3	BM864820	BM864820 mgcm007x0
17	91	52.9	593	3	BM863558	BM863558 mgcm006x0
18	91	52.9	602	3	BM861796	BM861796 mgcm001x0
19	85	49.4	515	3	BM863209	BM863209 mgcm005x0
20	85	49.4	523	3	BM863729	BM863729 mgcm011x0
21	74	43.0	541	4	CD034317	CD034317 mgcm015x0
22	74	43.0	570	4	CD034317	CD034317 mgcm015x0
23	71	41.3	441	3	BM871833	BM871833 mgcm015x0
24	55	32.0	486	4	CD035120	CD035120 mgcm018x0
25	55	32.0	489	3	BM863213	BM863213 mgcm005x0
26	55	32.0	491	4	CD035038	CD035038 mgcm018x0
27	35	20.3	430	4	CD028671	CD028671 mgcm007x0
28	17	9.9	377	5	CD276416	CD276416 T143B0271
29	17	9.9	429	5	CD274144	CD274144 T143B0403
30	17	9.9	499	5	CD273332	CD273332 T143B0196
31	17	9.9	507	5	CD275678	CD275678 T143B0071
32	17	9.9	530	5	CD275940	CD275940 T143B0156
33	17	9.9	552	5	CD275566	CD275566 T143B0121
34	17	9.9	588	5	CD275905	CD275905 T143B0122
35	14	8.1	573	3	BQ109916	BQ109916 V010E09
36	11	6.4	476	2	BG280255	BG280255 c2b06mp.r
37	9	5.2	363	3	BP100008	BP100008 BP100008
38	9	5.2	458	8	CO095673	CO095673 GR_Ea186
39	9	5.2	517	4	BY471348	BY471348 BY471348
40	9	5.2	571	13	C2697015	C2697015 OC_Ba001
41	9	5.2	634	10	DV027321	DV027321 ZM_Bf014
42	9	5.2	752	13	CZ781295	CZ781295 OC_Ba014
43	9	5.2	881	9	DN476575	DN476575 alt7207x0
44	8	4.7	181	3	BP686247	BP686247 BP686247
45	8	4.7	213	12	CG904247	CG904247 ZMMBB051

#### ALIGNMENTS

RESULT 1  
BM863356 619 bp mRNA linear EST 06-MAY-2003  
mgcm006x003.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
grisea cDNA clone mgcm006x03 5', mRNA sequence.  
BM863356  
BM863356.2 GI:30391591

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 619)  
Ebbolte,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe

grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19231038.

CONTACT: Ebbolte D.J.  
Department of Plant Pathology & Microbiology  
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Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483

EMAIL: d-ebbolte@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person.Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone

dehydratase >gi|1127197|pdb|1STD|. . . 367 e-101  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: 0 column: 03  
Seq primer: T3.

#### FEATURES

source

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Location/Qualifiers  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
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/clone\_id="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI, Site 2:  
XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
re-inoculated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to pnd files (0.05) and for vector segs."

#### ORIGIN

##### Alignment Scores:

Pred. No.: 1.08e-181  
Score: 172.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 100.0%  
DB: 3

Length: 619  
Matches: 172  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-507-132-4 (1-172) x BM863356 (1-619)

1 MetGlySerGlnValGlnYSerAspGluLeuThrPheSerAspTyrLeuGlyLeuMet 20  
53 ATGGGTTCCGAAAGATTGAAAGAGCATGAGATTAACCTTCCAGACTACCTGGGCTTCAG 112  
21 ThrCyValTyrGlnTyrPalaAspSerTyrAspSerLeuAspTyrPalaAspTyrGly 40  
113 ACTGGCTCTATAGAGGGGAGACAGCTACGATCCAGAGACGCGGATAGGCTGCCAAG 172  
41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspTyrLeuTyrGlnAla 60  
173 GTCATTGCCCTACTCTCGCGCATTTGACTACCGCTCTCTCGCAAGCTCTGGAGGCA 232  
61 MetProAlaGlnGluPheValGlyMetValSerSerLeuGlnValLeuGlyAspProThr 80  
233 ATGCCGCGCGAGAGATTGTCGGCATGCTTCAGAGAGAGGTGTGGCGGACCCACC 292  
81 LeuArgThrGlnIleAspHeileGlyGlyTyrArgTyrGlnValSerGluAspGluVal 100  
293 CTCGGACCGCAGACTTCATCCGCGGACCGCGTGGGAGAGAGTGTCCAGAGACGAGTTC 352  
101 IleGlyTyrHisGlnLeuArgValProHisGlnAlaTyrIleAspThrThrMetLeuGlu 120  
353 ATCGGCTACCAACAGCTGGCGCGTCCCGCACAGAGGTATCAAGAGACACCATGAGAGAG 412  
121 ValThrMetLeuGlyHisAlaHisSerAlaAsnLeuHisTyrTyrIleValIleAspGly 140  
413 GTCACCATGAAAGGCCACGCGCACTCGGCAAACTTCACGCTGACAGAGAGATCGACGC 472  
141 ValTyrLeuPheAlaGlyLeuLeuPheProAspIleArgTyrPalaGlnPheAspPala 160  
473 GTCGTGAAGATTCGCGGCTCAAGCCGACATCCGCTGGGCGCAGATTTCACCTTGACAG 532  
161 IlePheGluAspGlyArgGluThrPheGlyAspPala 172

Db 533 ATCTTGAGAGACGAGCGAGACTTTGGCGACAAA 568

RESULT 2  
BM864194 657 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm008xj12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm008xj12 5', mRNA sequence.  
ACCESSION BM864194  
VERSION BM864194.2 GI:30390885  
KEYWORDS EST  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
SORDARIOMYCETES; FUNGI; ASCOMYCOTA; PEZIZOMYCOTINA; SORDARIOMYCETES;  
Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.  
1 (bases 1 to 657)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhacterial,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea

REFERENCE  
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhacterial,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea

Unpublished (2002)

JOURNAL  
COMMENT On Mar 7, 2002 this sequence version replaced gi.19231876.  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact  
person; Beat nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 365 e-100

PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm008 row: J column: 12  
Seq primer: T3.

#### FEATURES

source

1. 657  
Location/Qualifiers  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
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/note="Vector: pBluescriptSK-; Site 1: EcoRI, Site 2:  
XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
re-inoculated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to pnd files (0.05) and for vector segs."

#### ORIGIN

##### Alignment Scores:

Pred. No.: 1.49e-180  
Score: 171.00  
Percent Similarity: 100.0%  
Best Local Similarity: 99.4%  
Query Match: 3  
DB: 3

Length: 657  
Matches: 171  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-507-132-4 (1-172) x BM864194 (1-657)

1 MetGlySerGlnValGlnYSerAspGluLeuThrPheSerAspTyrLeuGlyLeuMet 20

Db 91 ATGGGTTCCGAAGTTCAMAAAGCGATGAGATATACCTTCTCAGACTACCTGGGCTTCATG 150  
 Qy 21 ThCyValTYrGluTTPAlaAspSerTYrAspSerIysAspTPAspArgLeuArgLys 40  
 Db 151 ACTTGCGCTATGATGGGGACAGACTACGACTCCAGAGACGTGGATTAGCTGGCAAG 210  
 Qy 41 ValIleAlaProThrLeuArgIleAspTYrArgSerPheLeuAspLysLeuTPGluAla 60  
 Db 211 GTCAATTCGGCTACTCTGGCCATTCGATACCGCTCTTCTCCAGCAAGCTCTGGAGGCA 270  
 Qy 61 MetProAlaGluGluPheValGlyMetValSerSerIysGlnValLeuGlyAspProThr 80  
 Db 271 ATCCCGGCCAGAGAGTTCGTCCGCGATGCTCGAGCAAGAGAGGTGGCGGACCCCAACC 330  
 Qy 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTPGluLysValSerGluAspGluVal 100  
 Db 331 CTCGCGACGAGCACTTCATTCGGCGGACCGCGCTGGAGAGAGTTCGAGAGACGAGGTC 390  
 Qy 101 IleGlyTYrHisGlnLeuArgValProHisGlnArgTYrLysAspThrThrMetLysGlu 120  
 Db 391 ATCGGCTACACCAAGCTGGCGCGTCCGCGACAGAGGATCAAGAGCACCATGAAAGAG 450  
 Qy 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTPYrLysLysIleAspGly 140  
 Db 451 GTCAACCATGAGGGCCACGCCCACTTCGCAAACTTCATGATGATCAAGAAATCGACGGC 510  
 Qy 141 ValTPhyPheAlaGlyLeuLysProAspIleArgTPGluGluPheAspPheAspArg 160  
 Db 511 GTCTGAAAGTTCGCCGCTCCAGACCAGACATCCGCGGAGCGAGTTCGACTTGACAGG 570  
 Qy 161 IlePheGluAspGlyArgGluThrPheGlyAsp 171  
 Db 571 ATCTTTGAGAGCGAGCGAGAGACTTTGGCGAC 603  
 RESULT 3  
 BM863315 664 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm006x21f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm006x21 5', mRNA sequence.  
 ACCESSION BM863315.2 GI:30391622  
 VERSION EST.  
 KEYWORDS Magnaporthe grisea (anamorph: Pyricularia grisea)  
 SOURCE Magnaporthe grisea  
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
 1 (bases 1 to 664)  
 Bhatle,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhatle,R.K. and Dean,R.A.  
 Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 TITLE Unpublished (2002)  
 JOURNAL On Mar 7, 2002 this sequence version replaced gi:19230997.  
 COMMENT Contact: Ebdole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebdole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person; best hit (Apr 11, 22, 2003) sp|P56221|SCYD\_MAGR Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 364 e-100  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgcm006 row: B column: 21  
 Seq primer: T3.  
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 /strain="Guy11"

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 /sex="Mat1-2 hermaphrodite"  
 /cell\_type="mycelium"  
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 /note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
 XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 re inoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phred/rap version 991019 and trimmed  
 according to pnd files (0.05) and for vector seqs."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3,44e-177 Length: 664  
 Score: 168.00 Matches: 168  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 97.7% Indels: 0  
 DB: 3 Gaps: 0  
 US-10-507-132-4 (1-172) x BM863315 (1-664)  
 Qy 1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTYrLeuGlyLeuMet 20  
 Db 81 ATGGGTTCCGAAGTTCAMAAAGCGATGAGATATACCTTCTCAGACTACCTGGGCTTCATG 140  
 Qy 21 ThCyValTYrGluTTPAlaAspSerTYrAspSerIysAspTPAspArgLeuArgLys 40  
 Db 141 ACTTGCGCTATGATGGGGACAGACTACGACTCCAGAGACGTGGATTAGCTGGCAAG 200  
 Qy 41 ValIleAlaProThrLeuArgIleAspTYrArgSerPheLeuAspLysLeuTPGluAla 60  
 Db 201 GTCAATTCGGCTACTCTGGCCATTCGATACCGCTCTTCTCCAGCAAGCTCTGGAGGCA 260  
 Qy 61 MetProAlaGluGluPheValGlyMetValSerSerIysGlnValLeuGlyAspProThr 80  
 Db 261 ATCCCGGCCAGAGAGTTCGTCCGCGACAGAGGATCAAGAGCACCATGAAAGAG 320  
 Qy 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTPGluLysValSerGluAspGluVal 100  
 Db 321 CTCGCGACGAGCACTTCATTCGGCGGACCGCGCTGGAGAGAGTTCGAGAGACGAGTC 380  
 Qy 101 IleGlyTYrHisGlnLeuArgValProHisGlnArgTYrLysAspThrThrMetLysGlu 120  
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 Qy 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTPYrLysLysIleAspGly 140  
 Db 441 GTCACCATGAAAGGGCCAGCCCACTTCGCGCAAACTTCATGATGATCAAGAAATCGACGGC 500  
 Qy 141 ValTPhyPheAlaGlyLeuLysProAspIleArgTPGluGluPheAspPheAspArg 160  
 Db 501 GTCTGAAAGTTCGCCGCTCCAGACCAGATCCGCTGGGCGAGTTCGACTTGACAGG 560  
 Qy 161 IlePheGluAspGlyArgGluThr 168  
 Db 561 ATCTTTGAGAGCGAGCGAGAGACC 584  
 RESULT 4  
 BM864156 599 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgcm008x20f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
 DEFINITION grisea cDNA clone mgcm008x20 5', mRNA sequence.  
 ACCESSION BM864156  
 VERSION BM864156.2 GI:30390915  
 KEYWORDS EST.

SOURCE	Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM	Magnaporthe grisea (anamorph: Pyricularia grisea)
REFERENCE	Bakariyot, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 599)
AUTHORS	Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE	Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL	Unpublished (2002)
COMMENT	On Mar 7, 2002 this sequence version replaced gi:19231838. Contact: Ebbole DJ Department of Plant Pathology & Microbiology Texas A&M University Peterson Bldg, MS2132, College Station, TX 77843-2132, USA Tel: 979 845 4831 Fax: 979 845 6483 Email: d-ebbole@tamu.edu Chromatogram file of this sequence is available, see contact person:Best nr hit (April. 22, 2003) sp P56221 SCWD_MAGR Scytalone dehydrogenase >gi 1127197 pdb 1STD . . . 302 3e-87 PCR Primers FORWARD: T3 primer BACKWARD: T7 primer Plate: mgcm008 row: D column: 02 Seq primer: T3 Location/Qualifiers 1. .599

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/organism="Magnetaporthe grisea"
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/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_idb="Magnetaporthe grisea CM Uni-Zap XR Library"
/notes="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reincubated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the Bst sequence was trimmed
according to the alignment, otherwise sequence quality was
assessed using phredphrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."

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ORIGIN	
Alignment Scores:	
Pred. No.:	5.33e-147
Score:	141.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	82.0%
BB:	3
Length:	599
Matches:	141
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-507-132-4 (1-172) x BM864156 (1-599)

1 MetGlySerGlnValGlnIysSerAspGluLeuThrPheSerAspTyrLeuGlyLeuMet 20

Db 79 ATGGGTTCCGAGTCAAGAAGCATGAGATACCTTCTAGACTACCTGGGCTATG 138

21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40

Db 139 ACTTGGCTTATGAGTGGGAGACAGCTACAGACTCCAAGGACTGGGATAGCTGCCAAG 198

41 ValIleAlaProThrLeuArgIleaspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

Db 199 GTATTGGCCTACTCTGGCATTGACTACCGCTCCTTCTCGACAAGCTTGGAGGCA 258

61 MetProAlaGluGluPheValGlyMetValSerSerIysGlnValLeuGlyAspProThr 80

Protein	Accession	Position	Sequence	Position
Db	259	ATCCCGGCGGAGGAGTTGTCGTGGCAATGCTCTCGAGCAGCAGGAGTGTGGCGACCCACC	318	
Qy	81	LeuArgThrGlnHisPheIleGlyGlyThrArgTTrgLnLysValSerGluAaPgluVal	100	
Db	319	CTCCGACACGACATTCATCGGCGGACGCGCTGGGAGAAAGGTGTCCGAGACGAGATC	378	
Qy	101	IleGlyTrpHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu	120	
Db	379	ATGGGCTACACACGAGCGCGCTTCGCGACCAAGGTACAGGACACACATGAAAGAG	438	
Qy	121	ValThrMetLysGlyHisIleHisSerSerLysAsnLeuHisTrpTyrLysLysIleAspGly	140	
Db	439	GTCACCATGAAAGGCCACGCGCCACTCGGCAACCTTCACTGGTACAAAGAAATGACAGGC	498	
Qy	141	Val	141	
Db	499	GTT	501	

RESULT 5	BM863374	510 bp	mRNA	linear	EST 06-MAY-2003
LOCUS	BM863374				
DEFINITION	mgcm006xc10f.b Magnaporthe grisea CM Uni-Tag XR Library Magnaporthe				
ACCESSION	grisea cDNA clone mgcm006xc10 5', mRNA sequence.				
VERSION	BM863374				
KEYWORDS	BM863374.2 GI:30391576				
SOURCE	EST.				
ORGANISM	Magnaporthe grisea (anamorph: Pyricularia grisea)				
	Magnaporthe grisea				

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 510)  
Ebbels, D. J., Yuan, J., Thomas, T. L., Bobrowicz, P., Lu, G., Bhatnagar, K., and Dean, R. A.  
Expressed sequence tags from the rice blast fungus, *Magnaporthe grisea*.  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19331056.

Contact: Ebbbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person:best nr hit (April, 22, 2003) EP|P66221|SCYD\_MAGGR Scytalone  
dehydroatase >g11127197|pdb|1STO|. . . 276 1e-73

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FEATURES
source
  PCR Primers
  FORWARD: T3 primer
  BACKWARD: T7 primer
  Plate: mgcm006 row: C column: 10
  Seq primer: T3.
  Location/Qualifiers
    1..510

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/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xCl0"
/sex="mat-2 hermaphrodite"
/cell_type="mycelium"
/clone_id="Magnaporthe grisea CM Uni-Zap XR library"
/notes="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the BSI sequence was trimmed according to the alignment. Otherwise sequence quality was

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assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

## ALIGNMENT SCORES:

Pred. No.:	5,586-137	Length:	510
Score:	132.00	Matches:	132
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	76.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x BM863374 (1-510)

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QY 1 MetGlySerGlnValGlnYssSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
DB 83 ATGGGTTCCGAAAGTTCAAAAGACGAGTGAATTAACCTTCCAGACTACCTGGGCTTCATG 142
QY 21 ThrCyValTyrGlnTyrAlaAspSerTyrAspSerTyrAspTyrAlaGly 40
DB 143 ACTTGCGTCTATGAGTGGGAGACAGCTACGACTCCAGAGACTGGGATAGGCTGCCAAG 202
QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTyrGluAla 60
DB 203 GTCATTGGCCCTACTCTGGCGCATTTGACTACCGCTCTCTCCGACAGGCTCTGGAGGCA 262
QY 61 MetProAlaGlnGluPheValGlyMetValSerSerTyrGlnValLeuGlyAspProThr 80
DB 263 ATGCCCGCCGAGAGTTCGTCGGCATGCTTCAGAGAGAGGTGTCGGCGACCCACC 322
QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTyrGlnValSerGluAspGluVal 100
DB 323 CTCGCGACCGAGACTTCACTCCGCGGACCGCGCTGGGAGAGAGGTGTCGAGAGCAGAGTC 382
QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrIleAspThrThrMetLysGlu 120
DB 383 ATCGGCTACCAACAGCGCGCTCCGCGACAGAGGATCAAGAGACCAATGAAGAG 442
QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
DB 443 GTCACCATGAAGGCGCACGCTCACTCGGCMAACCTT 478
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RESULT 6 BM863357 530 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm006x005f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm006x005 5', mRNA sequence.  
ACCESSION BM863357 GI:19231039  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Magnaporthe grisea (anamorph: Pyricularia grisea)

REFERENCE  
AUTHORS Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 510)

TITLE  
JOURNAL  
COMMENT Ebbole, J., Yuan, J., Thomas, T. L., Bobrowicz, P., Lu, G.,  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person's e-mail (April, 22, 2003) ap|p56221|SCYD\_MAGR\_Scytalone  
dehydratase >gi|11271937|pdb|1stm|. . . 276 1e-73  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer

Plate: mgcm006 row: 0 column: 05  
Seq primer: T3.  
Location/Qualifiers  
1.530  
Source

/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm006x005"  
/sex="Mati-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_1b="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI, Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
re-inoculated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

## ALIGNMENT SCORES:

Pred. No.:	5,756-137	Length:	530
Score:	132.00	Matches:	132
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	76.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x BM863357 (1-530)

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QY 1 MetGlySerGlnValGlnYssSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
DB 83 ATGGGTTCCGAAAGTTCAAAAGACGAGTGAATTAACCTTCCAGACTACCTGGGCTTCATG 142
QY 21 ThrCyValTyrGlnTyrAlaAspSerTyrAspSerTyrAspTyrAlaGly 40
DB 143 ACTTGCGTCTATGAGTGGGAGACAGCTACGACTCCAGAGAGAGGTGTCGAGAGCAGAGTC 202
QY 41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTyrGluAla 60
DB 203 GTCATTGGCCCTACTCTGGCGCATTTGACTACCGCTCTCTCCGACAGGCTCTGGAGGCA 262
QY 61 MetProAlaGlnGluPheValGlyMetValSerSerTyrGlnValLeuGlyAspProThr 80
DB 263 ATGCCCGCCGAGAGTTCGTCGGCATGCTTCAGAGAGAGGTGTCGGCGACCCACC 322
QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTyrGlnValSerGluAspGluVal 100
DB 323 CTCGCGACCGAGACTTCACTCCGCGGACCGCGCTGGGAGAGAGGTGTCGAGAGCAGAGTC 382
QY 101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrIleAspThrThrMetLysGlu 120
DB 383 ATCGGCTACCAACAGCGCGCTCCGCGACAGAGGATCAAGAGACCAATGAAGAG 442
QY 121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
DB 443 GTCACCATGAAGGCGCACGCTCACTCGGCMAACCTT 478
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RESULT 7 BM864467 643 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm010xh12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm010xh12 5', mRNA sequence.  
ACCESSION BM864467  
VERSION  
KEYWORDS  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
1 (bases 1 to 643)  
AUTHORS Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatterai, K. and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:1923149.  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person: Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 320 8e-87  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm010 row: H column: 12  
Seq primer: T3.  
Location/Qualifiers  
1..643  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm010xH12"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-, Site\_1: EcoRI; Site\_2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phred/rap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

FEATURES  
source  
Alignment Scores:  
Pred. No.: 6,71e-137 Length: 643  
Score: 132.00 Matches: 132  
Percent Similarity: 100.0% Conservatative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 76.7% Indels: 0  
Gaps: 0  
DB: 3  
US-10-507-132-4 (1-172) x BM64467 (1-643)

ORIGIN  
1 MetGlySerGlnValGlnLysSerAspGluLeuThrPheSerAspTyrLeuGlyLeuMet 20  
145 ATGGGTTGCCCAAGTTCAAAAGAGCGATGAGATTAACCTTCACAGACTACCTGGGCGCCATG 204  
21 ThrGValTyrGlnTyrAlaAspSerTyrAspSerLysValThrAspArgLeuArgLys 40  
205 ACTTGCGCTTATGAGTGGGACACACTTCGACTCCAAAGAGCTGGGATGGGCTGCAAAAG 264  
41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTyrGlnAla 60  
265 GTCATTGGCGCTACTCTGGCGATTGACTACCGCTCTTCTCTGACCAAGCTCTGGAGGGA 324  
61 MetProAlaGluGlnPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80  
|||||

DB 325 ATGCCGCGCAGAGATTCTGCGCATGTCTCGAGCAAGCAGGTCTGGGCGACCCACC 384  
QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTyrGlnLysValSerGluAspGluVal 100  
DB 385 CTCGGACGACGACACTTATATCGCGGACGCGCTCGGAGAAAGTGTCTCGAAGACAGAGTC 444  
QY 101 TleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120  
DB 445 ATCGGCTACCAACAGCTCGCGTCCCGACAGAGGTCAAGACACACCATGAAAGAG 504  
QY 121 ValThrMetLysGlyHisAlaHisSerLysAsnLeu 132  
DB 505 GTCACCATGAAGGCGCAGCCCATCTGGCAACCTT 540

RESULT 8  
BM63710  
LOCUS  
DEFINITION BM63710 571 bp mRNA linear EST 06-MAY-2003  
mgcm007xH24f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
grisea cDNA clone mgcm007xH24 5', mRNA sequence.  
ACCESSION BM63710  
VERSION BM63710.2 GI:30391295  
KEYWORDS  
SOURCE  
ORGANISM  
Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
1 (bases 1 to 571)  
AUTHORS Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatterai, K. and Dean, R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19231392.  
COMMENT Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person: Best nr hit (April. 22, 2003) sp|P56221|SCYD\_MAGGR Scytalone  
dehydratase >gi|1127197|pdb|1STD|. . . 336 1e-91  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm007 row: E column: 24  
Seq primer: T3.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm007xH24"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-, Site\_1: EcoRI; Site\_2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods.  
Where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phred/rap version 991019 and trimmed  
according to phd files (0.05) and for vector segs."

FEATURES  
source  
Alignment Scores:  
ORIGIN  
1 MetProAlaGluGlnPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80  
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Pred. No.: 1.39e-133 Length: 571  
Score: 129.00 Matches: 129  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 75.0% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x BM863710 (1-571)

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QY 1 MetG|SeG|InVal|InLyS|SerA|P|G|U|L|E|Th|P|He|S|e|A|P|T|Y|L|e|U|Met 20
DB 92 ATGGGTTCCGAAGTTCAAAAGACGATGAGATTAACCTTCTCAACATCACTGGGCTTCAG 151
QY 21 ThrC|Val|T|G|U|T|P|A|A|S|e|S|e|T|Y|A|S|e|S|e|T|P|A|S|P|H|e|U|A|T|G|L|S 40
DB 152 ACTTGCGTCTATGAGTGGGCAACACCTACGACTCCAAAGCATGGGATGAGCTGCCAAG 211
QY 41 Val|Le|A|P|ro|Th|r|Leu|A|rg|I|e|A|P|T|Y|A|S|e|S|e|P|H|e|U|A|S|P|L|e|U|T|P|G|U|A| 60
DB 212 GTCATTGGCCCTACTCTGGCGCATTTGACTACCGCTCCTTCTCGACAAGCTCTGGAGGCA 271
QY 61 MetP|ro|A|G|U|G|U|P|H|e|A|G|I|Y|Met|V|A|S|e|S|e|T|Y|G|I|N|Val|Leu|G|I|A|S|P|ro|Th|r 80
DB 272 ATGCCGCGCGAGAGTTCTGCGCATGCTCTGAGCAAGAGGTGCTGGCGCACTCCACCC 331
QY 81 LeuA|T|G|T|G|I|N|H|I|S|P|H|e|I|e|G|I|Y|T|H|A|T|G|T|P|G|U|L|Y|S|e|G|I|A|S|P|G|U|A| 100
DB 332 CTCGGACCGACACTTCACTCGCGGCGACCGCTGGAGAGAGGTGCTCCAGACGAGGTC 391
QY 101 I|L|e|G|I|Y|T|H|I|S|G|I|N|Leu|A|rg|V|A|P|ro|H|I|S|G|I|N|A|T|Y|L|Y|S|A|P|H|e|T|H|Met|Y|S|G|I|N 120
DB 392 ATCGGCTACCAACAGCTGGCGCTCCGCGACAGAGGTAACAGGACCAACATGAGAGAG 451
QY 121 Val|Th|r|Met|Y|S|G|I|N|H|I|S|S|e| 129
DB 452 GTCACCATGAAGGCGCACGCCACTCG 478
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RESULT 9  
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LOCUS mgcm007xg13.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm007xg13 5', mRNA sequence.  
ACCESSION BM863639  
VERSION BM863639.2 GI:30391353  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
1 (bases 1 to 486)  
Bhobole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhaterai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea

TITLE Unpublished (2002)  
JOURNAL On Mar 7, 2002 this sequence version replaced gi:19231321.  
COMMENT Contact: Bhobole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-bhobole@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person:Best hit (Apr11. 22, 2003) sp|F56221|SCYD\_MAGGR\_Scytalone  
denudataae>gi|1127197|pdb|1stnd|. . . 293 5e-79  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm007 row: G column: 13  
Seq primer: T3.

FEATURES  
source 1. .486  
Location/Qualifiers

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/organism="Magnaporthe grisea"  
/mol_type="mRNA"  
/strain="Guy11"  
/db_xref="taxon:148305"  
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/sex="Mat1-2 hermaphrodite"  
/cell_type="mycelium"  
/clone_1ib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI, Site 2:  
XhoI; unidirectional cloning. EcoRI site has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days  
at room temperature, 150 rpm, harvested, blended,  
reincubated into complete medium 24 h, room temperature,  
150 rpm. Sequences were processed by one of two methods,  
where a full-length alignment to the M. grisea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredphrap version 991019 and trimmed  
according to phd files (0.05) and for vector seqs."
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#### ORIGIN

Alignment Scores:  
Pred. No.: 3.68e-129 Length: 486  
Score: 125.00 Matches: 125  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 72.7% Indels: 0  
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x BM863639 (1-486)

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QY 1 MetG|Y|S|e|G|I|N|V|A|L|I|N|Y|S|e|S|e|A|P|G|U|L|E|Th|P|H|e|S|e|A|P|T|Y|L|e|U|Met 20
DB 55 ATGGGTTCCGAAGTTCAAAAGACGATGAGATTAACCTTCTCAACATCACTGGGCTTCAG 114
QY 21 ThrC|Val|T|G|U|T|P|A|A|S|e|S|e|T|Y|A|S|e|S|e|T|P|A|S|P|H|e|U|A|T|G|L|S 40
DB 115 ACTTGCGTCTATGAGTGGGCAACACCTACGACTCCAAAGCATGGGATGAGCTGCCAAG 174
QY 41 Val|Le|A|P|ro|Th|r|Leu|A|rg|I|e|A|P|T|Y|A|S|e|S|e|P|H|e|U|A|S|P|L|e|U|T|P|G|U|A| 60
DB 175 GTCATTGGCCCTACTCTGGCGCATTTGACTACCGCTCCTTCTCGACAAGCTCTGGAGGCA 234
QY 61 MetP|ro|A|G|U|G|U|P|H|e|A|G|I|Y|Met|V|A|S|e|S|e|T|Y|G|I|N|Val|Leu|G|I|A|S|P|ro|Th|r 80
DB 235 ATGCCGCGCGAGAGTTCTGCGCATGCTCTGAGCAAGAGGTGCTGGCGCACTCCACCC 294
QY 81 LeuA|T|G|T|G|I|N|H|I|S|P|H|e|I|e|G|I|Y|T|H|A|T|G|T|P|G|U|L|Y|S|e|G|I|A|S|P|G|U|A| 100
DB 295 CTCGGACCGACACTTCACTCGCGGCGACCGCTGGAGAGAGGTGCTCCAGACGAGGTC 354
QY 101 I|L|e|G|I|Y|T|H|I|S|G|I|N|Leu|A|rg|V|A|P|ro|H|I|S|G|I|N|A|T|Y|L|Y|S|A|P|H|e|T|H|Met|Y|S|G|I|N 120
DB 355 ATCGGCTACCAACAGCTGGCGCTCCGCGACAGAGGTAACAGGACCAACATGAGAGAG 414
QY 121 Val|Th|r|Met|Y|S|G|I|N|H|I|S|S|e| 125
DB 415 GTCACCATGAAGGCG 429
```

RESULT 10  
BM864018 473 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm008xg12.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea cDNA clone mgcm008xg12 5', mRNA sequence.  
ACCESSION BM864018  
VERSION BM864018.2 GI:30391030  
KEYWORDS EST.  
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
ORGANISM Magnaporthe grisea  
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.  
1 (bases 1 to 473)

**AUTHORS** Ebbbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Shatterai,K. and Dean,R.A.  
**TITLE** Expressed sequence tags from the rice blast fungus, *Magnaporthe grisea*.  
**JOURNAL** unpublished (2002)  
**COMMENT** On Mar 7, 2002 this sequence version replaced gi:1921700.

FEATURES	Location/Qualifiers
source	1. .473

**ORIGIN**

### Alignment Scores:

Pred. No.:	5.65e-118	Length:	473
Score:	115.00	Matches:	115
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	66.9%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) X BM864018 (1-473)

Qy	1	MeG1SerGlnValGlnYssSerApjUuIetRhpSerAspYrLeuGlyLeuMet	20
Db	69	ATGGGTTCCGACGATCCAAAAGACGATGAGTACCTTCTCGACTACCTCGGGCCATG	128
Qy	21	ThhCysValYrcUuTrpUlaaSpSerYrAaSpSerYsAaPTTrpAspArUleuArGlys	40
Db	129	ACTGCGCTCATATAGAGGGCGACACACTCGACTCCAGACATCGGAGATAGGCTCGAAG	188
Qy	41	ValIlealabProThrLeuArGllleaPryrArGserPheLeuAspYlsLeuTrpGluAla	60
Db	189	GTCATTCGCGCTACTCTCGCCATGTACTACCCCTCTCTCGAACAACCTCGGAGGCA	248
Qy	61	MeCProAlaGluGluPheValGlyMetValSerSerYsGlnValIleuGlyAaSPProThr	80
Db	249	ATGCGCGCCAGAGATTCGTCGSCCAAGCTCTCGAAGAACAGAGTCTCGGCGAACCACC	308
Qy	81	LeuArGThrGlnHisPheIleGlyValYThrArGTrpGluYsValSerGluAspGluVal	100

D<sub>b</sub> 309 CTCGCCAGCAGCATTTATCGGCGGCGACGGCGCTGGGAGAAAGTGTCCGAGACGAGGTC 368

Q<sub>Y</sub> 101 ILeGLYrHieGlnleuAryfaProHieGlnAryTyrlysaap 115

D<sub>b</sub> 369 ATGGTTACACACAGCTGGCGCTCCCGACCAAGGTGCAAGAGC 413

RESULT 11	BM864472	LOCUS	DEFINITION
	BM864472	600 bp	mRNA
	mgcm010xj04f.b	Magnaporthe grisea	CM Uni-Zap XR Library
	grisea cDNA clone mgcm010xj04 5'		mRNA sequence.

**AUTHORS** Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Battarrai,K. and Dean,R.A.  
**TITLE** Expressed sequence tags from the rice blast fungus, *Magnaporthe grisea*  
**JOURNAL** unpublished (2002)  
**COMMENT** On Mar 7, 2002 this sequence version replaced gi:19222154.

FEATURES	Location/Qualifiers
source	1. .600

**ORIGIN**

Alignment Scores:

Pred. No.:	8,12e-108	Length:	600
Score:	106.00	Matches:	106
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	61.6%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) X BM864472 (1-600)

QY 1 MetGlySerGlnValGlnIlySerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20  
DB 145 ATGGGTTCCGCAAGTTCAAAAGACGATGAGATTAACCTTTCAGACTACCTGGGCTTCATG 204  
QY 21 ThrCysValTyrGlnUtrpAlaAspSerTyrAspSerIlyAspTTPaSpArlgLeuArlglys 40  
DB 205 ACTTGCGTCTATAGTGGGAGACAGCTACGACTCCAAAGACGGAATAGGCTGCAGAAAG 264  
QY 41 ValIleAlaProThrLeuArlgIleAspTyrArlgSerPheLeuAspIlyLeuTTPgIuaIa 60  
DB 265 GTCATTGGCGCTCTCTGGCATTGACTACCGCTCTCTTCTTCCAGACAGCTCTGGAGGCA 324  
QY 61 MetProAlaGlnIlyAspValGlyMetValSerSerIlyGlnValIleuGlyAspProThr 80  
DB 325 ATGCCGCGCAGAGAGTTCCGTGGCAGTGTCTCCAGACAGAGAGTGTGCTGGCGACCCCAACC 384  
QY 81 LeuArlgThrGlnHisPheIleGlyGlyThrArlgTTPgIulysValSerGluAspGluVal 100  
DB 385 CTCGCGACCGACACTTCATCGCGGACCGCTGGAGAGAGTGTCCGAGAGAGAGTTC 444  
QY 101 IleGlyTyrHisGlnLeu 106  
DB 445 ATCGGCTACCAACGACTG 462

RESULT 12 504 bp mRNA linear EST 06-MAY-2003  
BM63499 mgcm006xm18f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
LOCUS grisea CDNA clone mgcm006xm19 5', mRNA sequence.  
DEFINITION BM63499  
ACCESSION BM63499.2 GI:30391475  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

EST.  
Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 504)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.

Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
On Mar 7, 2002 this sequence version replaced gi:19231181.  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, WS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact  
person.Best nr hit (April. 22, 2003) sp|56221|SCYP\_MAGGR Scyralone  
dehydratase >gi|1127197|pdb|1STD|. . . 260 7e-69  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgcm006 row: L column: 19  
Seq primer: T3

Location/Qualifiers  
1. 504

FEATURES  
source  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm006xm19"  
/sex="Mali-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:
1,22e-105	504
Score:	104.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	60.5%
DB:	3
Gaps:	0

US-10-507-132-4 (1-172) x BM63499 (1-504)

QY 1 MetGlySerGlnValGlnIlySerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20  
DB 86 ATGGGTTCCGCAAGTTCAAAAGACGATGAGATTAACCTTTCAGACTACCTGGGCTTCATG 145  
QY 21 ThrCysValTyrGlnUtrpAlaAspSerTyrAspSerIlyAspTTPaSpArlgLeuArlglys 40  
DB 146 ACTTGCGTCTATAGTGGGAGACAGCTACGACTCCAAAGACGGAATAGGCTGCAGAAAG 205  
QY 41 ValIleAlaProThrLeuArlgIleAspTyrArlgSerPheLeuAspIlyLeuTTPgIuaIa 60  
DB 206 GTCATTGGCGCTCTCTGGCATTGACTACCGCTCTCTTCTTCCAGACAGCTCTGGAGGCA 265  
QY 61 MetProAlaGlnIlyAspValGlyMetValSerSerIlyGlnValIleuGlyAspProThr 80  
DB 266 ATGCCGCGCAGAGAGTTCCGTGGCAGTGTCTCCAGACAGAGTGTGCTGGCGACCCCAACC 325  
QY 81 LeuArlgThrGlnHisPheIleGlyGlyThrArlgTTPgIulysValSerGluAspGluVal 100  
DB 326 CTCGCGACCGACACTTCATCGCGGACCGCTGGAGAGAGTGTCCGAGAGAGAGTTC 385  
QY 101 IleGlyTyrHis 104  
DB 386 ATCGGCTACCAAC 397

## RESULT 13

BM64053 366 bp mRNA linear EST 06-MAY-2003  
LOCUS mgcm008xm18f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe  
DEFINITION grisea CDNA clone mgcm008xm18 5', mRNA sequence.  
ACCESSION BM64053  
VERSION BM64053.1 GI:19231735  
KEYWORDS  
SOURCE  
ORGANISM

EST.  
Magnaporthe grisea (anamorph: Pyricularia grisea)  
Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.  
1 (bases 1 to 366)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.

Expressed sequence tags from the rice blast fungus, Magnaporthe  
grisea  
Unpublished (2002)  
Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, WS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact  
person.Best nr hit (April. 22, 2003) pdb|4STD|A Chain A, High  
Resolution Structures Of Scyralone Deny. . . 223 6e-58  
PCR Primers

## JOURNAL

COMMENT  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgcm008xm18"  
/sex="Mali-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea CM Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:  
XhoI; Unidirectional cloning. EcoRI side has T3 primer and  
predominantly 5' reads. T7 primer on XhoI side of insert.  
Strain inoculated into complete medium grown for two days

```

FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm008 row: M column: 18
Seq primer: T3.

```

**ORIGIN**

according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector segs."

Alignment Scores:	
Pred. No.:	1,65e-103
Score:	102.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	59.3%
DB:	3
	Gaps: 0
	Matches: 366
	Length: 102
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

US-10-507-132-4 (1-172) X BM864053 (1-366)

Oy	71	IGSERLTVSGIIVallengIYAspProthLeuArgThGHIshellegIyLTtr	90
Db	3	TCGACCAAGCAGGTGTGGGGCCACCACCCCTTCGACCGCAGCATTTCACTGGCGGCACG	62
Oy	91	ArgTgPIuLyVasIserGIuAspGIuValIIegIYThISGLeuArgValProHis	110
Db	63	CGCTGGAGAAAGGTGTCCGAGGACGAGGTCACTCGGTACACACGCTGGCGGTCCGCAC	122
Oy	111	GIuArgIYLyIAspThThrMetLySGIuValIThMeLyegIyHisIaHisSeraIa	130
Db	123	CAGAGGTACAAAGACACCCACCATGAAAGAGGTCAACATGAAGGCCAACCCGCACTGGCA	182
Oy	131	AsnLeuHISITPIYLyIyLySIIeAspGIyValITrPlyPheAlaGlyLeuLySProAsp	150
Db	183	AACCTTCACTGTGTACAAAGATTCGACGGCGTCTGAAATTCCCGCGCTCAAGCCCGAC	242
Oy	151	IIeaRTPGIIyGIuPheAspPheAspArgIIePheGIuAspGIyArgGIuThrPheGIy	170
Db	243	ATCCGCTGGGGGAGGTTCGACTTTGACAGAGTCTTTGAAGGACGAGCGGAGACTTTGGC	302
Oy	171	AspLyS	172
Db	303	GACCAA	308

RESULT	14
BM863340	
LOCUS	649 bp mRNA linear EST 06-MAY-2003
DEFINITION	mgmcm006xk09.f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
ACCESSION	grisea cDNA clone mgmcm006xk09 5', mRNA sequence.
VERSION	BM863340
KEYWORDS	BM863340.2 GI:30391603
SOURCE	EST.
ORGANISM	Magnaporthe grisea (anamorph: Pyricularia grisea)
	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
	Eurhizaria; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

## REFERENCE AUTHORS

## FEATURES

**Source**

FORWARD: T3 primer  
 BACKWARD: T7 primer  
 plate: mgcm006 row: K column: 09  
 Seq primer: T3.

## ORIGIN

### Alignment Scores:

Pred. No.:	3.42e-102	Length:	649
Score:	101.00	Matches:	101
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	58.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) X BM863340 (1-649)

QY	32	Set1yaaSPTraspAphrguemaArgyVal11lea1aPProThrLeuAqG11leaSPYArg	51
Db	177	TCCAGAGACTGGGATATAGCTGCGAAAGGACATGGCGCTACTCTGCGCATTTGACTACCC	236
QY	52	SetPheLeuAspIysLeuTrpGluu1aMetPro1aGluGluuPheValG1yMetValSer	71
Db	237	TCTTCTCTGACACAGCTCTGAGGAGCATGGCGGCGAGAGATTGTCGTGGGATGCTTCG	266
QY	72	Set1yag1Val1eug1IyAspProThrLeuArgThrglnH1sPhe11leg1yG1yThnArg	91
Db	297	AGCAGAGAGGTGCTGGGACACCCACCTCCGCAAGCAGCACTTCATCTGGGGGACCGC	356
QY	92	TrpGluu1yValSerGluuAspGluVal11leg1yTh1sGln1euaArgValProH1sGln	111
Db	357	TGGAGAAAGGTGTCACAGGACAGAGGTCATCGGCTACCAACAGCTGCGGTCTCCGACACAG	416

QY 112 ArgTYLYEAAPThrThreLYSGluValThreLYSGlyHisAlaHisSerAlaAsn 131  
 DB 417 AGTACAGACACCAACCATGAAGAGTCACATCAAGGCGCACCCCACTCGGAAC 476  
 QY 132 Leu 132  
 DB 477 CTT 479  
 RESULT 15  
 BM861952  
 LOCUS 398 bp mRNA linear EST 06-MAY-2003  
 DEFINITION mgcm001XL17.f.b Magnaporthe grisea CM Uni-Zap XR library Magnaporthe  
 grisea cDNA clone mgcm001XL17 5', mRNA sequence.  
 ACCESSION BM861952  
 VERSION BM861952.2 GI:30392735  
 KEYWORDS EST.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
 1 (bases 1 to 398)  
 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
 Bhacterai,K. and Dean,R.A.  
 Expressed sequence tags from the rice blast fungus, Magnaporthe  
 grisea  
 Unpublished (2002)  
 On Mar 7, 2002 this sequence version replaced gi:19229634.  
 JOURNAL Contact: Ebbole DJ  
 COMMENT Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
 Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu  
 Chromatogram file of this sequence is available, see contact  
 person:best nr hit (Apr11. 22, 2003) sp|P56221|SCYD\_MAGR\_Scytalone  
 dehydratase >gi|1127197|pdb|1STD|. . . 209 7e-54  
 PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Place: mgcm001 row: L column: 17  
 Seq primer: T3.  
 FEATURES  
 source Location/Qualifiers  
 1..398  
 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgcm001XL17"  
 /sex="Mati-2 hermaphrodite"  
 /cell\_type="mycelium"  
 /clone\_lib="Magnaporthe grisea CM Uni-Zap XR library"  
 /note="Vector: pBluescriptSK-; Site\_1: EcoRI; Site\_2:  
 XhoI; Unidirectional cloning. EcoRI site has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Strain inoculated into complete medium grown for two days  
 at room temperature, 150 rpm, harvested, blended,  
 reinoculated into complete medium 24 h, room temperature,  
 150 rpm. Sequences were processed by one of two methods.  
 Where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredphrap version 991019 and trimmed  
 according to phd files (0.05) and for vector segs."

## ORIGIN

## Alignment Scores:

Pred. No.: 9,17e-97 Length: 398  
 Score: 96.00 Matches: 96  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 55.8% Indels: 0  
 DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x BM861952 (1-398)  
 QY 1 MetGlySerGlnValGlnLYSSerAspGluIleThrPheSerAspTyrIleuGlyLeuMet 20  
 DB 88 ATGGGTTCCAGAGTTCAAAGAGCGATGAGTAACCTTCTCGACACTCGGCGCTCATG 147  
 QY 21 ThrCyValTyrGluTrpAlaAspSerTyrAspSerTyrAspTrpAspArgLeuArgLys 40  
 DB 148 ACTTGCGTCTATGAGTGGGCAACAGCTACGACTCCAAAGACTGGATAGCTGCGAAAG 207  
 QY 41 ValIleAlaProThrIleuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60  
 DB 208 GTCAATTGCGCTACTCTGCGCAATTGACTACCGCTCTCTCGACAAAGCTTGGGAGGCA 267  
 QY 61 MetProAlaGluGluPheValGlnMetValSerSerTyrGlnValLeuGlyAspProThr 80  
 DB 268 ATGCCGCGCAGAGAGTTCGTGCGAGTGTCTGAGCAGACAGTGTCTGGCGACCCGACC 327  
 QY 81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSer 96  
 DB 328 CTTGCGACGACAGACTTCATCGCGGACGCGCTGGGAGAGGTGTCC 375

Search completed: December 4, 2006, 18:35:44  
 Job time : 4369 secs

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